

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:43:32 ; Search time 74.6015 seconds  
(without alignments)  
627.306 Million cell updates/sec

Title: US-10-660-357A-1

Perfect score: 649

Sequence: 1 QVQLQSGFGLVKPSTLSL.....WLLPDAFDIWGQGTWVTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	649	100.0	121	7 ADC99772	Adc99772 Anti-huma
2	649	100.0	121	7 ADC99788	Adc99788 Anti-huma
3	649	100.0	121	7 ADD05376	Add05376 Anti-MUC1
4	649	100.0	121	7 ADD05392	Add05392 Anti-MUC1
5	649	100.0	121	7 ADF09814	Adf09814 Human ant
6	649	100.0	121	7 ADF09830	Adf09830 Human ant
7	643	99.1	121	7 ADF09780	Adf09780 Anti-huma
8	643	99.1	121	7 ADD05384	Add05384 Anti-MUC1
9	643	99.1	121	7 ADF09822	Adf09822 Human ant
10	597	92.0	121	7 ADC99808	Adc99808 Anti-huma
11	597	92.0	121	7 ADD05412	Add05412 Anti-MUC1
12	597	92.0	121	7 ADF09850	Adf09850 Human ant
13	565.5	87.1	243	8 ADO58076	Ado58076 S9 cell d
14	547	84.3	121	5 ABG92884	Abg92884 Human imm
15	545.5	84.1	121	5 ABB07171	Abb07171 ebvHlgM M
16	545.5	84.1	121	8 ADI26658	Adi26658 Human ant
17	545.5	84.1	122	7 ADP03887	Adp03887 Murine-ex
18	545.5	84.1	122	7 ADP03884	Adp03884 Murine-ex
19	544.5	83.9	122	7 ADP03885	Adp03885 Murine-ex
20	544.5	83.9	122	7 ADP03889	Adp03889 Murine-ex
21	540	83.2	119	2 AA27554	Aaw27554 Human Ab
22	540	83.2	119	6 ABJ18676	Abj18676 Human ant
23	540	83.1	118	8 ADP22272	Adp22272 Human ant
24	540	83.1	123	6 ADA9258	Ada9258 Human ant
25	83.0	83.0	122	7 ADP03931	Adp03931 Murine-ex

ALIGNMENTS

RESULT 1

ADC99772

ID ADC99772 standard; protein; 121 AA.

XX AC ADC99772;

XX DT 01-JAN-2004 (first entry)

XX DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 1.

XX KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;

KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;

KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;

KW lung cancer; human.

XX OS Homo sapiens.

XX PN WO2003057838-A2.

XX PD 17-JUL-2003.

XX PF 26-DEC-2002; 2002WO-US041581.

XX PR 28-DEC-2001; 2001US-0346299P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudae J;

XX DR WPI; 2003-587113/55.

XX N-PSDB; ADC99774.

XX PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease

PT or condition associated with expression of MUC18 in a patient, e.g.

PT tumors, cancers, and other malignancies.

XX Claim 1; SEQ ID NO 1; 78pp; English.

XX CC The invention relates to a novel isolated monoclonal antibody comprising

CC a heavy or light chain amino acid or a heavy or light chain variable

CC domain where the antibody binds to MUC18. The monoclonal antibody of the

CC invention demonstrates cytostatic activity and may be useful for treating

CC a disease or condition associated with the expression of MUC18 on the

CC cell surface such as tumours, specifically melanoma, oesophageal,

CC pancreatic or colorectal tumours, carcinomas, particularly cervical

CC carcinomas and cervical intraepithelial neoplasia and cancers including

CC colorectal, breast or lung cancer, as well as other malignancies. The

CC current sequence is that of the anti-human MUC18 monoclonal antibody

CC

CC heavy chain protein of the invention.

XX Sequence 121 AA;

Query Match 100.0%; Score 649; DB 7; Length 121;

Best Local Similarity 100.0%; Pred. No. 6.4e-46;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIROPKGLGWIGYIYYTTSN 60

Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIROPKGLGWIGYIYYTTSN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120

Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120

QY 121 S 121

Db 121 S 121

RESULT 2

ADC99788

ID ADC99788 standard; protein; 121 AA.

XX

AC ADC99788;

XX

DT 01-JAN-2004 (first entry)

XX

DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 17.

XX

KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;

KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;

KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;

KW lung cancer; human.

XX

OS Homo sapiens.

XX

XX WO2003057838-A2.

PN

XX 17-JUL-2003.

XX

PF 26-DEC-2002; 2002WO-US041581.

XX

PR 28-DEC-2001; 2001US-0346299P.

XX

XX (ABGE-) ABGENIX INC.

PA

XX Gudas J;

XX

PI

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XX WPI; 2003-587113/55.

XX

DR N-PSDB; ADC99790.

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CC heavy chain protein of the invention.

XX Sequence 121 AA;

Query Match 100.0%; Score 649; DB 7; Length 121;

Best Local Similarity 100.0%; Pred. No. 6.4e-46;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIROPKGLGWIGYIYYTTSN 60

Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIROPKGLGWIGYIYYTTSN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120

Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120

QY 121 S 121

Db 121 S 121

RESULT 3

ADD05376

ID ADD05376 standard; protein; 121 AA.

XX

AC ADD05376;

XX

DT 01-JAN-2004 (first entry)

XX

DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 1.

XX

KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;

KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.

XX

OS Homo sapiens.

XX

XX WO2003057006-A2.

PN

XX 17-JUL-2003.

XX

PF 26-DEC-2002; 2002WO-US041582.

XX

PR 28-DEC-2001; 2001US-0346460P.

XX

XX (ABGE-) ABGENIX INC.

PA

XX Gudas J, Bar-Eli M;

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PI

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XX WPI; 2003-577496/54.

XX

DR N-PSDB; ADD05378.

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Query Match

Best Local Similarity 100.0%; Score 649; DB 7; Length 121;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIROPKGLGWIGYIYYTTSN 60

Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIROPKGLGWIGYIYYTTSN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120

Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120

QY 121 S 121

Db 121 S 121

RESULT 3

ADD05376

ID ADD05376 standard; protein; 121 AA.

XX

AC ADD05376;

XX

DT 01-JAN-2004 (first entry)

XX

DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 1.

XX

KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;

KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.

XX

OS Homo sapiens.

XX

XX WO2003057006-A2.

PN

XX 17-JUL-2003.

XX

PF 26-DEC-2002; 2002WO-US041582.

XX

PR 28-DEC-2001; 2001US-0346460P.

XX

XX (ABGE-) ABGENIX INC.

PA

XX Gudas J, Bar-Eli M;

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PI

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XX WPI; 2003-577496/54.

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DR N-PSDB; ADD05378.

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Query Match

Best Local Similarity 100.0%; Score 649; DB 7; Length 121;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIROPKGLGWIGYIYYTTSN 60

Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIROPKGLGWIGYIYYTTSN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120

Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120

QY 121 S 121

Db 121 S 121

RESULT 3

ADD05376

ID ADD05376 standard; protein; 121 AA.

XX

AC ADD05376;

XX

DT 01-JAN-2004 (first entry)

XX

DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 1.

XX

KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;

KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.

XX

OS Homo sapiens.

XX

XX WO2003057006-A2.

PN

XX 17-JUL-2003.

XX

PF 26-DEC-2002; 2002WO-US041582.

XX

PR 28-DEC-2001; 2001US-0346460P.

XX

XX (ABGE-) ABGENIX INC.

PA

XX Gudas J, Bar-Eli M;

XX

PI

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XX WPI; 2003-577496/54.

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DR N-PSDB; ADD05378.

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Query Match

Best Local Similarity 100.0%; Score 649; DB 7; Length 121;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIROPKGLGWIGYIYYTTSN 60

Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIROPKGLGWIGYIYYTTSN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120

Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120

QY 121 S 121

Db 121 S 121

RESULT 3

ADD05376

ID ADD05376 standard; protein; 121 AA.

XX

AC ADD05376;

XX

DT 01-JAN-2004 (first entry)

XX

DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 1.

XX

KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;

KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.

XX

OS Homo sapiens.

XX

XX WO2003057006-A2.

PN

XX 17-JUL-2003.

XX

PF 26-DEC-2002; 2002WO-US041582.

XX

PR 28-DEC-2001; 2001US-0346460P.

XX

XX (ABGE-) ABGENIX INC.

PA

XX Gudas J, Bar-Eli M;

XX

PI

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XX WPI; 2003-577496/54.

XX

DR N-PSDB; ADD05378.

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XX OS Homo sapiens.
XX PN WO2003057837-A2.
XX PD 17-JUL-2003.
XX PF 26-DEC-2002; 2002WO-US041580.
XX PR 28-DEC-2001; 2001US-0346414P.
XX PA (ABGE-) ABGENIX INC.
XX PI Gudas J;
XX WPI; 2003-598367/56.
XX DR N-PSDB; ADF09852.
XX PT Inhibiting cell proliferation associated with expression of MUC18 tumor
XX PT MUC18 monoclonal antibody.
XX PS Claim 1; SEQ ID NO 37; 83pp; English.
XX CC The invention comprises a method for inhibiting cell proliferation
XX CC associated with expression of MUC18 tumour antigen. The method involves
XX CC administering anti-MUC18 monoclonal antibody. The method of the invention
XX CC is useful for inhibiting cell (e.g. melanoma or tumour cell)
XX CC proliferation associated with the expression of MUC18 tumour antigen, the
XX CC method is preferably useful for inhibiting tumour metastasis. The method
XX CC is useful for inhibiting cell proliferation in patients with tumours,
XX CC carcinomas, cancer and other malignancies. The present amino acid
XX CC sequence represents a heavy chain from an MUC18 tumour antigen-specific
XX CC monoclonal antibody.
XX SQ Sequence 121 AA;
Query Match 92.0%; Score 597; DB 7; Length 121;
Best Local Similarity 90.9%; Pred. No. 1.2e-41;
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKLEWIGYIYTTSTNNYN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKLEWIGYIYTTSTNNYN 60
QY 61 PSLKSRVTISVDTSKNQFSLRSLSSVTAADTAVYYCARDQGWLLPDAFDIWGGQTMVTS 120
Db 61 PSLKSRVTISVDTSKNQFSLKLSNSVTAADTAVYYCARDQGWLLPDAFDIWGGQTMVTS 120
QY 121 S 121
Db 121 S 121
QY S9 cell derived human scFvL-VH protein.
XX B cell; surface immunoglobulin; Ig; binding site; antigen; human CD28;
XX closed system; detection laser-beam; catcher tube;
XX electrochemical device; fluorescence activated cell sorter; FACS;
XX antibody variable region; human.
XX Homo sapiens.
XX WO200404584-A1.
XX
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PD 27-MAY-2004.
XX 12-NOV-2003; 2003WO-EP012664.
XX PR 13-NOV-2002; 2002EP-00025335.
XX PA (MICR-) MICROMET AG.
XX PI Baeuerle P, Hoffmann P, Weinberger S, Kischel R;
XX WPI; 2004-449579/42.
XX DR N-PSDB; ADO58077.
XX PT Identifying a B cell carrying a surface immunoglobulin molecule having a
XX PT binding site for an antigen of interest, useful for constructing
XX PT therapeutic antibodies, comprises contacting a sample with the antigen
XX PT and a receptor.
XX Claim 22; SEQ ID NO 76; 156pp; English.
XX CC The invention relates to a novel method for identifying a B cell carrying
XX CC a surface immunoglobulin (Ig) molecule having a binding site for an
XX CC antigen of interest. The method comprises contacting a sample putatively
XX CC containing the B cell with the antigen of interest and with a receptor
XX CC specifically binding to the Ig molecule, and assessing the presence of
XX CC the detectable signal. The invention further comprises: an antibody
XX CC generated by the method above which is specific for human CD28 or
XX CC comprising an amino acid(s) sequence(s) given in the specification,
XX CC and/or are encoded by a nucleic acid sequence(s) also given in the
XX CC specification; and a device for assessing the presence of a detectable
XX CC signal defined above, where the device comprises a closed system for the
XX CC detection laser-beam and a catcher tube, and where the B cell of interest
XX CC can be collected as a single cell by means of an electrochemical device,
XX CC which is triggered by an electric signal generated by the fluorescence
XX CC activated cell sorter (FACS) device, where the electrochemical device
XX CC moves the nozzle of the steady catcher tube liquid stream for a
XX CC programmed time over a collecting tube, microtiter plate or other
XX CC container after a B cell is sorted. The method is useful for identifying
XX CC a B cell carrying a surface Ig molecule having a binding site for an
XX CC antigen of interest. The method is also useful for cloning of antibody
XX CC variable regions from the identified B cells, which may subsequently be
XX CC employed in the construction of proteins such as antibodies or its
XX CC fragments or derivatives useful in therapeutic approaches. The method is
XX CC useful as an alternative to phage display for the gain of antibodies or
XX CC its fragments. This sequence represents an S2 cell derived human
XX CC polypeptide of the invention.
XX SQ Sequence 243 AA;
Query Match 87.1%; Score 565.5; DB 8; Length 243;
Best Local Similarity 90.1%; Pred. No. 9.5e-39;
Matches 109; Conservative 6; Mismatches 5; Indels 1; Gaps 1;
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKLEWIGYIYTTSTNNYN 60
Db 124 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKLEWIGYIYSGSTNNYN 183
QY 61 PSLKSRVTISVDTSKNQFSLRSLSSVTAADTAVYYCARDQGWLLPDAFDIWGGQTMVTS 120
Db 184 PSLKSRVTISVDTSKNQFSLKLSNSVTAADTAVYYCARDQGWLLPDAFDIWGGQTMVTS 242
QY 121 S 121
Db 243 S 243
RESULT 14
ID ABG92884
XX ABG92884 standard; protein; 121 AA.
XX AC ABG92884;
XX DT 19-NOV-2002 (first entry)
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XX DE Human immunoglobulin variable light domain #1.
XX DE
XX KW Immunoglobulin; variable heavy chain; variable light chain; human;
KW G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;
KW immunologic deficiency syndrome; blood protein disorder; nephritis;
KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;
KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;
KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;
KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;
KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;
KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;
XX LYmphocytopenia.
XX OS Homo sapiens.
XX XX
XX PN WO200264612-A2.
XX XX
XX PD 22-AUG-2002.
XX XX
XX PF 08-FEB-2002; 2002WO-US003634.
XX XX
XX PR 09-FEB-2001; 2001US-00779880.
XX PR 09-FEB-2001; 2001WO-US004153.
XX PR 12-JUN-2001; 2001US-0297257P.
XX PR 08-AUG-2001; 2001US-0310458P.
XX PR 12-OCT-2001; 2001US-032847P.
XX PR 21-DEC-2001; 2001US-0341725P.
XX XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX XX
XX PI Roschke V, Rosen CA, Ruben SM;
XX XX
XX DR WPI; 2002-643455/69.
XX DR N-PSDB; ABS68607.
XX XX
XX PT New human G-protein Chemokine Receptor gene (HDGNR10) useful for
XX PT treating, preventing, ameliorating or monitoring diseases or disorders
XX PT associated with aberrant expression of HDGNR10 e.g. cancer.
XX XX
XX PS Example 55; Fig 4; 562pp; English.
XX XX
XX CC The invention describes an isolated polynucleotide encoding a first
XX CC antibody at least 95-100% identical to a second antibody consisting of an
XX CC amino acid sequence comprising at least one, two or three CDR regions of
XX CC a variable heavy (VH) or variable light (VL) domain of the antibody
XX CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1P8,
XX CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9B6, XF27/28.7D5, XF27/28.18B5,
XX CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody
XX CC is useful treating, preventing, ameliorating, prognosing or monitoring
XX CC cancers or other diseases or disorders e.g. immunologic deficiency
XX CC syndromes such as blood protein disorders and ataxia telangiectasia,
XX CC inflammation associated disorders such as endotoxin lethality, nephritis
XX CC and inflammatory bowel disease, conditions associated with an increase in
XX CC certain haematopoietic cells such as histiocytosis, defective or aberrant
XX CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,
XX CC an infectious disease, an autoimmune disease such as Addison's disease,
XX CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative
XX CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or
XX CC poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma,
XX CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a
XX CC disease or disorder associated with aberrant expression of novel human G-
XX CC protein chemokine receptor (CCR5) HDGNR10. This is the amino acid
XX CC sequence of human immunoglobulin sequence associated with the antibodies
XX CC against HDGNR10
XX XX
XX SQ Sequence 121 AA:
XX
XX Query Match 84.3%; Score 547; DB 5; Length 121;
XX Best Local Similarity 86.0%; Pred. No. 1.6e-37;
XX Matches 104; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
XX
XX QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYFWSWIRQPGKGLDWIGRIYTSNNTYN 60

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CC damaged as by trauma. The present sequence represents the ebvHigM  
CC MS119D10 heavy chain variable region amino acid sequence  
XX  
SQ Sequence 121 AA;

Query Match 84.1%; Score 545.5; DB 5; Length 121;  
Best Local Similarity 87.6%; Pred. No. 2.1e-37;  
Matches 106; Conservative 6; Mismatches 8; Indels 1; Gaps 1;  
Qy 1 QVQLQESGPGLVKRPSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGYIYYTWTSTNYN 60  
Db 1 QVQLQESGPGLVKRPSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGYIYYTWTSTNYN 60  
Qy 61 PSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARDQGWLLIPDAFDIWGQGTMTVTS 120  
Db 61 PSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARDQGWLLIPDAFDIWGQGTMTVTS 120  
Qy 121 S 121  
Db 120 S 120

Search completed: November 9, 2005, 12:55:23  
Job time : 76.6015 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:29:55 ; Search time 18.802 Seconds  
(without alignments)  
480.403 Million cell updates/sec

Title: US-10-660-357A-1

Perfect score: 649

Sequence: 1 QVQLQSSGCLVKPSETLSL.....WLLPDAFDIWGQGTMTVTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pcp.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pcp.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pcp.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pcp.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCITUS COMB.pcp.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfilees1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	540	83.2	119	3	US-09-025-769B-39
2	540	83.2	119	3	US-09-025-769B-65
3	540	83.2	119	4	US-09-490-070A-39
4	540	83.2	119	4	US-09-490-070A-65
5	540	83.2	119	4	US-09-490-153-39
6	540	83.2	119	4	US-09-490-153-65
7	540	83.2	119	4	US-09-490-324-39
8	540	83.2	119	4	US-09-490-324-65
9	531.5	81.9	118	3	US-09-025-769B-25
10	531.5	81.9	118	4	US-09-490-070A-25
11	531.5	81.9	118	4	US-09-490-153-25
12	531.5	81.9	120	4	US-09-490-324-25
13	531.5	81.9	120	4	US-09-424-840B-20
14	529.5	81.6	244	3	US-08-918-148-79
15	529.5	81.6	244	4	US-09-138-091A-77
16	515.5	79.4	473	3	US-09-049-672A-4
17	502	77.3	142	2	US-08-480-774B-2
18	500	77.0	117	4	US-09-720-493-2
19	499.5	77.0	139	4	US-09-471-276-837
20	498.5	76.8	122	1	US-08-360-125-11
21	498.5	76.8	122	2	US-08-450-578-11
22	498.5	76.8	122	2	US-09-017-628-11
23	498.5	76.8	122	2	US-09-014-880-11
24	498.5	76.8	122	4	US-08-450-363-11
25	498.5	76.8	122	4	US-09-467-903-11
26	494.5	76.2	487	4	US-09-800-729-145
27	488	75.2	116	3	US-08-545-809A-140

28	485	74.7	119	1	US-08-360-125-5	Sequence 5, Appli
29	485	74.7	119	2	US-08-450-578-5	Sequence 5, Appli
30	485	74.7	119	2	US-09-017-628-5	Sequence 5, Appli
31	485	74.7	119	2	US-09-014-880-5	Sequence 5, Appli
32	485	74.7	119	4	US-08-450-363-5	Sequence 5, Appli
33	485	74.7	119	4	US-09-467-903-5	Sequence 10, Appli
34	484	74.6	119	2	US-08-652-816A-10	Sequence 7, Appli
35	479.5	73.9	172	4	US-09-472-087-7	Sequence 10, Appli
36	479.5	73.9	172	4	US-09-472-087-86	Sequence 86, Appli
37	479	73.8	123	3	US-08-793-450-4	Sequence 4, Appli
38	477	73.5	118	3	US-08-545-809A-142	Sequence 142, App
39	476	73.3	472	3	US-08-793-450-8	Sequence 2, Appli
40	472.5	72.8	139	4	US-09-203-768A-2	Sequence 888, App
41	471	72.6	155	4	US-09-471-276-888	Sequence 6, Appli
42	470.5	72.5	118	4	US-09-343-698-6	Sequence 6, Appli
43	470.5	72.5	118	4	US-08-325-955-6	Sequence 7, Appli
44	469.5	72.3	832	3	US-08-630-820-7	Sequence 7, Appli
45	469.5	72.3	832	4	US-09-273-453-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1  
US-09-025-769B-39  
; Sequence 39, Application US/09025769B  
; Patent No. 630064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge. Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-39

Query Match 83.2%; Score 540; DB 3; Length 119;  
Best Local Similarity 86.8%; Pred. No. 7.3e-45;  
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRPPGKGLEWIGYIYVYTWTSNYN 60  
|  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRPPGKGLEWIGYIYVYSGSTNYN 60  
|  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGQTMVTYS 120  
|  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGQTMVTYS 118  
|  
QY 121 S 121  
|  
Db 119 S 119

## RESULT 2

US-09-025-769B-65  
; Sequence 65, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-65

Query Match 83.2%; Score 540; DB 3; Length 119;  
Best Local Similarity 86.8%; Pred. No. 7.3e-45;  
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRPPGKGLEWIGYIYVYTWTSNYN 60  
|  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRPPGKGLEWIGYIYVYSGSTNYN 60  
|  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGQTMVTYS 120  
|  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGQTMVTYS 118  
|  
QY 121 S 121  
|

Db 119 S 119  
|  
RESULT 3  
US-09-490-070A-39  
; Sequence 39, Application US/09490070A  
; Patent No. 6696248  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
; STREET: 1666 K Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,070A  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Colin G. Sandercock, Esq.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37629-0005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 912-2000  
TELEFAX: (202) 912-2020  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-490-070A-39

Query Match 83.2%; Score 540; DB 4; Length 119;  
Best Local Similarity 86.8%; Pred. No. 7.3e-45;  
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRPPGKGLEWIGYIYVYTWTSNYN 60  
|  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRPPGKGLEWIGYIYVYSGSTNYN 60  
|  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGQTMVTYS 120  
|  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGQTMVTYS 118  
|  
QY 121 S 121  
|  
Db 119 S 119

## RESULT 4

US-09-490-070A-65  
; Sequence 65, Application US/09490070A



Patent No. 6696248  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
White & McAuliffe  
STREET: 1666 K Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,070A  
FILING DATE: 24-Jan-2000  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Colin G. Sandercock, Esq.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37629-0005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 912-2000  
TELEFAX: (202) 912-2020  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 65:  
US-09-490-070A-65  
Query Match 83.2%; Score 540; DB 4; Length 119;  
Best Local Similarity 86.8%; Pred. No. 7.3e-45;  
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRPPGKLEWIGYIYVTSNYN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRPPGKLEWIGYIYVTSNYN 60  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDGQWLLPDAFDIWGGTMTVTS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDGQWLLPDAFDIWGGTMTVTS 120  
QY 121 S 121  
Db 119 S 119  
RESULT 5  
US-09-490-153-39  
Sequence 39, Application US/09490153  
Patent No. 6706484  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,153  
FILING DATE: 24-Jan-2000  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-490-153-39  
Query Match 83.2%; Score 540; DB 4; Length 119;  
Best Local Similarity 86.8%; Pred. No. 7.3e-45;  
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRPPGKLEWIGYIYVTSNYN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRPPGKLEWIGYIYVTSNYN 60  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDGQWLLPDAFDIWGGTMTVTS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDGQWLLPDAFDIWGGTMTVTS 120  
QY 121 S 121  
Db 119 S 119  
RESULT 6  
US-09-490-153-65  
Sequence 65, Application US/09490153  
Patent No. 6706484  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York

```
;
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
;
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-153-65

Query Match 83.2%; Score 540; DB 4; Length 119;
Best Local Similarity 86.8%; Pred. No. 7.3e-45;
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLWIGIYYTTSNN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLWIGIYYSGSTNN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFIMQGGMVTVS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFIMQGGMVTVS 120

QY 121 S 121
Db 119 S 119

RESULT 7
US-09-490-324-39
; Sequence 39, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
;
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
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;
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
;
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-324-39

Query Match 83.2%; Score 540; DB 4; Length 119;
Best Local Similarity 86.8%; Pred. No. 7.3e-45;
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLWIGIYYTTSNN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLWIGIYYSGSTNN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFIMQGGMVTVS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFIMQGGMVTVS 120

QY 121 S 121
Db 119 S 119

RESULT 8
US-09-490-324-65
; Sequence 65, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
;
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
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/
/ FILING DATE: 18-FEB-1998
/ APPLICATION NUMBER: EP 95 11 3021.0
/ FILING DATE: 18-AUG-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: James F. Haley, Jr., Esq.
/ REGISTRATION NUMBER: 27,794
/ REFERENCE/DOCKET NUMBER: MORPHO/5
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)596-9000
/ TELEFAX: (212)596-9090
/ INFORMATION FOR SEQ ID NO: 65:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 119 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-324-65

Query Match      83.2%; Score 540; DB 4; Length 119;
Best Local Similarity 86.8%; Pred. No. 7.3e-45;
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIRQPPGKGLWIGIYYTWTSTN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIRQPPGKGLWIGIYYTWTSTN 60
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 118
QY 121 S 121
Db 119 S 119

RESULT 9
US-09-025-769B-25
/ Sequence 25, Application US/09025769B
/ Patent No. 630064
/ GENERAL INFORMATION:
/ APPLICANT: Knappik, Achim
/ APPLICANT: Pack, Peter
/ APPLICANT: Ilag, Vic
/ APPLICANT: Ge, Liming
/ APPLICANT: Moroney, Simon
/ APPLICANT: Plueckthun, Andreas
/ TITLE OF INVENTION: Protein/(Poly)peptide libraries
/ NUMBER OF SEQUENCES: 373
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
/ STREET: 1251 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10021
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/025,769B
/ FILING DATE: 18-FEB-1998
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 95 11 3021.0
/ FILING DATE: 18-AUG-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: James F. Haley, Jr., Esq.
/ REGISTRATION NUMBER: 27,794
/ REFERENCE/DOCKET NUMBER: MORPHO/5
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)596-9000

/
/ FILING DATE: (212)596-9090
/ INFORMATION FOR SEQ ID NO: 25:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 118 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-025-769B-25

Query Match      81.9%; Score 531.5; DB 3; Length 118;
Best Local Similarity 85.1%; Pred. No. 4.8e-44;
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Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIRQPPGKGLWIGIYYTWTSTN 60
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 117
QY 121 S 121
Db 118 S 118

RESULT 10
US-09-490-070A-25
/ Sequence 25, Application US/09490070A
/ Patent No. 6696248
/ GENERAL INFORMATION:
/ APPLICANT: Knappik, Achim
/ APPLICANT: Pack, Peter
/ APPLICANT: Ilag, Vic
/ APPLICANT: Ge, Liming
/ APPLICANT: Moroney, Simon
/ APPLICANT: Plueckthun, Andreas
/ TITLE OF INVENTION: Protein/(Poly)peptide libraries
/ NUMBER OF SEQUENCES: 373
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
/ STREET: 1666 K Street, N.W., Suite 300
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20006
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/490,070A
/ FILING DATE: 24-Jan-2000
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 95 11 3021.0
/ FILING DATE: 18-AUG-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Colin G. Sandercock, Esq.
/ REGISTRATION NUMBER: 31,298
/ REFERENCE/DOCKET NUMBER: 37629-0005
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 912-2000
/ TELEFAX: (202) 912-2020
/ INFORMATION FOR SEQ ID NO: 25:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 118 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
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SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-070A-25
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Best Local Similarity 85.1%; Pred. No. 4.8e-44;
Matches 103; Conservative 7; Mismatches 8; Indels 3; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWISWIRPPGKGLEWIGYIYTTWTSN 60
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QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARGGG---GGVFDYWGQGLTVTVS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARGGG---GGVFDYWGQGLTVTVS 120
QY 121 S 121
Db 118 S 118

RESULT 12
US-09-490-324-25
; Sequence 25, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-324-25
Query Match      81.9%; Score 531.5; DB 4; Length 118;
Best Local Similarity 85.1%; Pred. No. 4.8e-44;
Matches 103; Conservative 7; Mismatches 8; Indels 3; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWISWIRPPGKGLEWIGYIYTTWTSN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWISWIRPPGKGLEWIGYIYTTWTSN 60
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARGGG---GGVFDYWGQGLTVTVS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARGGG---GGVFDYWGQGLTVTVS 120
QY 121 S 121
Db 118 S 118

RESULT 11
US-09-490-153-25
; Sequence 25, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-153-25
Query Match      81.9%; Score 531.5; DB 4; Length 118;
Best Local Similarity 85.1%; Pred. No. 4.8e-44;
Matches 103; Conservative 7; Mismatches 8; Indels 3; Gaps 1;
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121 S 121  
118 S 118

RESULT 13  
US-09-424-840B-20  
; Sequence 20, Application US/09424840B  
; Patent No. 6790938  
; GENERAL INFORMATION:  
; APPLICANT: Berchtold, Peter  
; APPLICANT: Escher, Robert F. A.  
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES  
; FILE REFERENCE: 100564-09049  
; CURRENT APPLICATION NUMBER: US/09/424,840B  
; PRIOR FILING DATE: 1999-12-03  
; PRIOR APPLICATION NUMBER: DE 19820663.1  
; PRIOR FILING DATE: 1998-05-08  
; PRIOR APPLICATION NUMBER: DE 19755227.7  
; PRIOR FILING DATE: 1997-12-12  
; PRIOR APPLICATION NUMBER: DE 19723904.8  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 120  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-424-840B-20

Query Match 81.9%; Score 531.5; DB 4; Length 120;  
Best Local Similarity 84.4%; Pred. No. 4.9e-44;  
Matches 103; Conservative 6; Mismatches 10; Indels 3; Gaps 2;  
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Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGIYYTWTN 60  
Qy 61 PSLKSRVTISVDTSKNQFSLKLSVTAADTAVVYCARDOQO-WLLPDAFDIWGQGTMTV 119  
Db 61 PSLKSRATISVDTSKNQFSLKLSVTAADTAVVYCARLNDGW--NDGFDIWGQGTMTV 118  
Qy 120 SS 121  
Db 119 SS 120

RESULT 14  
US-08-918-148-79  
; Sequence 79, Application US/08918148A  
; Patent No. 6342220  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Camellia  
; APPLICANT: W.  
; APPLICANT: Carter, Paul J.  
; APPLICANT: Fendly, Brian M.  
; APPLICANT: Gurney, Austin L.  
; TITLE OF INVENTION: Agonist Antibodies  
; FILE REFERENCE: P0979  
; CURRENT APPLICATION NUMBER: US/08/918,148A  
; CURRENT FILING DATE: 1997-08-25  
; NUMBER OF SEQ ID NOS: 79  
; SEQ ID NO 79  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: artificial  
US-08-918-148-79

Query Match 81.6%; Score 529.5; DB 3; Length 244;  
Best Local Similarity 84.3%; Pred. No. 1.7e-43;

Matches 102; Conservative 10; Mismatches 2; Indels 7; Gaps 2;  
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Db 3 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGIYYTWTN 62  
Qy 61 PSLKSRVTISVDTSKNQFSLKLSVTAADTAVVYCARDOQO-WLLPDAFDIWGQGTMTV 120  
Db 63 PSLKSRVTISVDTSKNQFSLKLSVTAADTAVVYCAR--GRY-----FDVWGRGTMTV 115  
Qy 121 S 121  
Db 116 S 116

RESULT 15  
US-09-138-091A-77  
; Sequence 77, Application US/09138091A  
; Patent No. 6737249  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Camellia W.  
; APPLICANT: Carter, Paul J.  
; APPLICANT: Fendly, Brian M.  
; APPLICANT: Gurney, Austin L.  
; TITLE OF INVENTION: Agonist Antibodies  
; FILE REFERENCE: 9491-013-27  
; CURRENT APPLICATION NUMBER: US/09/138,091A  
; CURRENT FILING DATE: 1998-08-21  
; PRIOR APPLICATION NUMBER: US 60/056,736  
; PRIOR FILING DATE: 1997-08-22  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 77  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: single chain antibody (scFv) fragments  
US-09-138-091A-77

Query Match 81.6%; Score 529.5; DB 4; Length 244;  
Best Local Similarity 84.3%; Pred. No. 1.7e-43;  
Matches 102; Conservative 10; Mismatches 2; Indels 7; Gaps 2;  
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Db 3 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGIYYTWTN 62  
Qy 61 PSLKSRVTISVDTSKNQFSLKLSVTAADTAVVYCARDOQO-WLLPDAFDIWGQGTMTV 120  
Db 63 PSLKSRVTISVDTSKNQFSLKLSVTAADTAVVYCAR--GRY-----FDVWGRGTMTV 115  
Qy 121 S 121  
Db 116 S 116

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

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Title: US-10-660-357A-1

Perfect score: 649

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Searched: 1867879 segs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	649	100.0	121	14	US-10-330-613-17
3	649	100.0	121	14	US-10-330-530-1
4	649	100.0	121	14	US-10-330-530-17
5	649	100.0	121	16	US-10-660-357-1
6	649	100.0	121	16	US-10-660-357-17
7	643	99.1	121	14	US-10-330-613-9
8	643	99.1	121	14	US-10-330-530-9
9	643	99.1	121	16	US-10-660-357-9
10	597	92.0	121	14	US-10-330-613-37
11	597	92.0	121	14	US-10-330-530-37

12	597	92.0	121	16	US-10-660-357-37	Sequence 37, Appl
13	553.5	85.3	118	15	US-10-292-088-142	Sequence 142, App
14	549.5	84.7	118	15	US-10-292-088-109	Sequence 109, App
15	547	84.3	121	14	US-10-067-800-60	Sequence 60, Appl
16	547	84.3	121	18	US-10-994-679-60	Sequence 60, Appl
17	545.5	84.1	121	14	US-10-010-729-11	Sequence 11, Appl
18	545.5	84.1	122	15	US-10-309-762-24	Sequence 24, Appl
19	545.5	84.1	122	15	US-10-309-762-27	Sequence 27, Appl
20	545	84.0	119	17	US-10-937-596-23	Sequence 23, Appl
21	544.5	83.9	122	15	US-10-309-762-25	Sequence 25, Appl
22	544.5	83.9	122	15	US-10-309-762-29	Sequence 29, Appl
23	540	83.2	119	14	US-10-125-687-5	Sequence 5, Appli
24	540	83.2	119	18	US-10-996-191-5	Sequence 5, Appli
25	539.5	83.1	118	17	US-10-727-155-178	Sequence 178, App
26	539	83.1	123	15	US-10-371-942-102	Sequence 102, App
27	538.5	83.0	122	15	US-10-309-762-71	Sequence 71, Appl
28	538.5	83.0	141	15	US-10-309-762-90	Sequence 90, Appl
29	536.5	82.7	120	15	US-10-309-762-4	Sequence 4, Appli
30	536.5	82.7	120	15	US-10-309-762-102	Sequence 102, App
31	536.5	82.7	121	15	US-10-309-762-154	Sequence 154, App
32	536	82.6	119	15	US-10-309-762-143	Sequence 143, App
33	536	82.6	125	15	US-10-309-762-11	Sequence 11, Appl
34	536	82.6	142	17	US-10-893-576-37	Sequence 37, Appl
35	534.5	82.4	122	15	US-10-309-762-73	Sequence 73, Appl
36	534.5	82.4	141	15	US-10-309-762-94	Sequence 94, Appl
37	533.5	82.2	116	18	US-10-822-306A-5	Sequence 5, Appli
38	533.5	82.2	124	15	US-10-309-762-26	Sequence 26, Appl
39	533.5	82.2	193	15	US-10-264-049-4331	Sequence 4331, Ap
40	532.5	82.0	118	17	US-10-706-689-10	Sequence 10, Appl
41	532.5	82.0	118	18	US-10-988-360-10	Sequence 10, Appl
42	532.5	82.0	128	15	US-10-173-551-24	Sequence 24, Appl
43	531.5	81.9	120	16	US-10-844-424-20	Sequence 20, Appl
44	531.5	81.9	121	17	US-10-805-177-56	Sequence 56, Appl
45	531.5	81.9	126	14	US-10-067-800-68	Sequence 68, Appl

ALIGNMENTS

RESULT 1  
US-10-330-613-1  
; Sequence 1, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; US-10-330-613-1

Query Match 100.0%; Score 649; DB 14; Length 121;  
Best Local Similarity 100.0%; Pred. No. 1.8e-50;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 QVQLQESGPGLVKPSSTLSLCTVSGGSISSYWSWIROPKGLWIGYIYTTWSNYN 60  
QY 61 PSLKSRVTISVDTSKNQRSLRSSVTAADTAVYVCARDQGWLLPDAFDIWGGTMTVTVS 120  
Db 61 PSLKSRVTISVDTSKNQRSLRSSVTAADTAVYVCARDQGWLLPDAFDIWGGTMTVTVS 120  
QY 121 S 121

Db 121 S 121

## RESULT 2

US-10-330-613-17  
; Sequence 17, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-17

Query Match 100.0%; Score 649; DB 14; Length 121;  
Best Local Similarity 100.0%; Pred. No. 1.8e-50;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGYIYYTTSN 60  
  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDINGQGTMTV 120  
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QY 121 S 121  
Db 121 S 121

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US-10-330-530-1  
; Sequence 1, Application US/10330530  
; Publication No. US20030152514A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES  
; FILE REFERENCE: ABGENIX.031A  
; CURRENT APPLICATION NUMBER: US/10/330,530  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: US 60/346414  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-530-1

Query Match 100.0%; Score 649; DB 14; Length 121;  
Best Local Similarity 100.0%; Pred. No. 1.8e-50;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDINGQGTMTV 120  
  
QY 121 S 121

Db 121 S 121

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US-10-330-530-17  
; Sequence 17, Application US/10330530  
; Publication No. US20030152514A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES  
; FILE REFERENCE: ABGENIX.031A  
; CURRENT APPLICATION NUMBER: US/10/330,530  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: US 60/346414  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-530-17

Query Match 100.0%; Score 649; DB 14; Length 121;  
Best Local Similarity 100.0%; Pred. No. 1.8e-50;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGYIYYTTSN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGYIYYTTSN 60  
  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDINGQGTMTV 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDINGQGTMTV 120  
  
QY 121 S 121  
Db 121 S 121

## RESULT 5

US-10-660-357-1  
; Sequence 1, Application US/10660357  
; Publication No. US20040115205A1  
; GENERAL INFORMATION:  
; APPLICANT: Bar-Eli, Menashe  
; APPLICANT: Green, Larry L.  
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18  
; FILE REFERENCE: ABGENIX.030C1  
; CURRENT APPLICATION NUMBER: US/10/660,357  
; CURRENT FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 10/330,580  
; PRIOR FILING DATE: 2002-12-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-660-357-1

Query Match 100.0%; Score 649; DB 16; Length 121;  
Best Local Similarity 100.0%; Pred. No. 1.8e-50;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGYIYYTTSN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGYIYYTTSN 60  
  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDINGQGTMTV 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDINGQGTMTV 120  
  
QY 121 S 121



Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVVYCARDQGWLLPDAFDIWGGTMTVTS 120  
 QY 121 S 121  
 Db 121 S 121

RESULT 6  
 US-10-660-357-17  
 ; Sequence 17, Application US/10660357  
 ; Publication No. US20040115205A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bar-Eli, Menashe  
 ; APPLICANT: Green, Larry L.  
 ; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18  
 ; FILE REFERENCE: ABGENIX 030C1  
 ; CURRENT APPLICATION NUMBER: US/10/660,357  
 ; CURRENT FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 10/330,580  
 ; PRIOR FILING DATE: 2002-12-26  
 ; NUMBER OF SEQ ID NOS: 40  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 17  
 ; LENGTH: 121  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 US-10-660-357-17

Query Match 100.0%; Score 649; DB 16; Length 121;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-50;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIROPKGLWIGYIYYTTSNYN 60  
 Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIROPKGLWIGYIYYTTSNYN 60  
 QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVVYCARDQGWLLPDAFDIWGGTMTVTS 120  
 Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVVYCARDQGWLLPDAFDIWGGTMTVTS 120  
 QY 121 S 121  
 Db 121 S 121

RESULT 7  
 US-10-330-613-9  
 ; Sequence 9, Application US/10330613  
 ; Publication No. US20030147809A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gudas, Jean  
 ; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
 ; FILE REFERENCE: ABGENIX.022A  
 ; CURRENT APPLICATION NUMBER: US/10/330,613  
 ; CURRENT FILING DATE: 2002-12-26  
 ; PRIOR APPLICATION NUMBER: 60/346299  
 ; PRIOR FILING DATE: 2001-12-18  
 ; NUMBER OF SEQ ID NOS: 40  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 9  
 ; LENGTH: 121  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 US-10-330-613-9

Query Match 99.1%; Score 643; DB 14; Length 121;  
 Best Local Similarity 98.3%; Pred. No. 6.1e-50;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIROPKGLWIGYIYYTTSNYN 60  
 Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIROPKGLWIGYIYYTTSNYN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVVYCARDQGWLLPDAFDIWGGTMTVTS 120  
 Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVVYCARDQGWLLPDAFDIWGGTMTVTS 120  
 QY 121 S 121  
 Db 121 S 121

RESULT 8  
 US-10-330-530-9  
 ; Sequence 9, Application US/10330530  
 ; Publication No. US20030152514A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gudas, Jean  
 ; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES  
 ; FILE REFERENCE: ABGENIX.031A  
 ; CURRENT APPLICATION NUMBER: US/10/330,530  
 ; CURRENT FILING DATE: 2002-12-26  
 ; PRIOR APPLICATION NUMBER: US 60/346414  
 ; PRIOR FILING DATE: 2001-12-18  
 ; NUMBER OF SEQ ID NOS: 40  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 9  
 ; LENGTH: 121  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 US-10-330-530-9

Query Match 99.1%; Score 643; DB 14; Length 121;  
 Best Local Similarity 98.3%; Pred. No. 6.1e-50;  
 Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIROPKGLWIGYIYYTTSNYN 60  
 Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIROPKGLWIGYIYYTTSNYN 60  
 QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVVYCARDQGWLLPDAFDIWGGTMTVTS 120  
 Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVVYCARDQGWLLPDAFDIWGGTMTVTS 120  
 QY 121 S 121  
 Db 121 S 121

RESULT 9  
 US-10-660-357-9  
 ; Sequence 9, Application US/10660357  
 ; Publication No. US20040115205A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bar-Eli, Menashe  
 ; APPLICANT: Green, Larry L.  
 ; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18  
 ; FILE REFERENCE: ABGENIX 030C1  
 ; CURRENT APPLICATION NUMBER: US/10/660,357  
 ; CURRENT FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 10/330,580  
 ; PRIOR FILING DATE: 2002-12-26  
 ; NUMBER OF SEQ ID NOS: 40  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 9  
 ; LENGTH: 121  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 US-10-660-357-9

Query Match 99.1%; Score 643; DB 16; Length 121;  
 Best Local Similarity 98.3%; Pred. No. 6.1e-50;  
 Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy	1	QVQLQESGGPGLVKPSETLSLTCTVSSGSGISYYNSWIRQPPEGKLEWIGIYIYTWSNYN	60
Dd	1	QVQLQESGGPGLVKPSETLSLTCTVSSGSGISYYNSWIRQPPEGKLEWIGIYIYTWTINYN	60
Qy	61	PSLKSRTVISDVTSTKNQFSLRLSSVTAADTAVYYCARDQGQWLPLPAFDINGOGTWMTVS	120
Dd	61	PSLKSRTVISDVTSTKNQFSLRLSSVTAADTALYYCARDQGQWLLPDAFDINGOGTWMTVS	120
Qy	121	S 121	
Dd	121	S 121	

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RESULT 10
US-10-330-613-37
; Sequence 37, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCES: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2003-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-37

```

```

Query Match      92.0%; Score 597; DB 14; Length 121;
Best Local Similarity 90.9%; Pred. No. Be-46;
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

1 QVQLSESGPLVKPSETLSLCTVSGGSISSYYKSWIRPPKGLIEWIGIYYTWTN 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 QVQLSESGPLVKPSETLSLCTVSGGSISSYYKSWIRPPKGLIEWIGIYYTGN 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARDQGGWLLPDAFDIW 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 PSLKSRVTISVDTSKNQFSLKLSNVTAADTAVYVCARDPGQWLVPDAFDIW 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

121 S 121
|
121 S 121

```

```

RESULT 11
US-10-330-530-37
; Sequence 37, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-37

```

Query Match 92.0%; Score 597; DB 14; Length 121;  
Best Local Similarity 90.9%; Pred. No. 8e-46;  
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy	1	QVQLQESGPGLVKPSETLSLTCTVSGGSI	SYYSW	IRQPPCKGLEWIGYIYYTWT	SNYN	60
Db	1	QVQLQESGPGLVKPSETLSLTCTVSGGSI	STYYN	SWIRQPPCKGLEWIGYIYYTGT	NTYN	60
Qy	61	PSLKSRTVITSDVTSKNQPSFLSL	SVTAADTAVYVCARDQGQGW	LLPD	FDI	120
Db	61	PSLKSRTVITSDVTSKNQPSFLK	NSVTAADTAVYVCARDPGQ	GWLPD	FDI	120
Qy	121	S	121			
Db	121	S	121			

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RESULT 12
US-10-660-357-37
; Sequence 37, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660.357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-37

```

Query Match	92.0%;	Score 597;	DB 16;	Length 121;
Best Local Similarity	90.9%;	Pred. No. 8e-46;		
Matches 110;	Conservative 7;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	1	QVQLQESGPGGLVLRPSETLSLTCTVSGGSISSYYWWSWIRQPPGKLEWIGYIYYTWTN	60	
Db	1	QVQLQESGPGGLVLRPSETLSLTCTVSGGSISSYYWWSWIRQPPGKLEWIGYIYYTNTYYN	60	
Qy	61	PSLKSRTVISVDTSKNOFSLRLSSVTAAADTAVYYCARDQDQGWLLLPDAFDIWGQGTMTVTS	120	
Db	61	PSLKSRTVTSVDTSKNOFSLKLSVTAADTAVYYCARDPGQWLVPDAFDIWGQGTMTSVS	120	
Qy	121	S 121		
Db	121	S 121		

RESULT 13  
 US-10-292-088-142  
 ; Sequence 142, Application US/10292088  
 ; Publication No. US20030211100A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BEDIAN, VAHE  
 ; APPLICANT: GLADUE, RONALD P.  
 ; APPLICANT: CORVALAN, JOSE  
 ; APPLICANT: JIA, XIAO-CHI  
 ; APPLICANT: FENG, XIAO  
 ; TITLE OF INVENTION: ANTIBODIES TO CD40  
 ; FILE REFERENCE: ABX-PP/3 US  
 ; CURRENT APPLICATION NUMBER: US/10/292,088  
 ; CURRENT FILING DATE: 2003-03-14  
 ; PRIOR APPLICATION NUMBER: 60/348,980  
 ; PRIOR FILING DATE: 2001-11-09  
 ; NUMBER OF SEQ ID NOS: 147  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 142  
 ; LENGTH: 118

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; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/341,725
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-067-800-60

Query Match      84.3%; Score 547; DB 14; Length 121;
Best Local Similarity 86.0%; Pred. No. 2.4e-41;
Matches 104; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy      1 QVQLQESGPGLVKPSETLSLTCTCTVSGGSISSYYMSWIRPPGKGLEWIGYIYYTWTSNYN 60
Db      1 QVQLQESGPGLVKPSETLSLTCTCTVSGGSISSFYMSWIRQPGAGLWDWIGRIYTSGNNTYN 60

Qy      61 PSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGGTMTVTS 120
Db      61 PSLKSRVTMSVDTSKKNRFSKLSSVTAADTAVYYCARDGSSWYPDAFDIWGGGTMTVTS 120

Qy      121 $ 121
Db      121 $ 121

Search completed: November 9, 2005, 12:42:57
Job time : 68.2222 secs

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-142

Query Match      85.3%; Score 553.5; DB 15; Length 118;
Best Local Similarity 87.6%; Pred. No. 6.2e-42;
Matches 106; Conservative 7; Mismatches 5; Indels 3; Gaps 1;

Qy 1 QVQLQESGPGLVKPESETLSLTCTVSGGSISSYYMSWIRQPPGKGLEWIGIYYTWTSNYN 60
Db 1 QVQLQESGPGLVKPESETLSLTCTVSGGSISSYYMSWIRQPPGKGLEWIGIYYSGTNYN 60

Qy 61 PSLKSRVTISVDTSKNQFSLSLSSVTAADTAVYYCARDQGWLLPDADFINGQGTMVTVS 120
Db 61 PSLKSRVTISVDTSKNQFSLSLSSVTAADTAVYYCARDYGDY---NWFDPWGQGLTIVTS 117

Qy 121 S 121
Db 118 S 118

RESULT 14
US-10-292-088-109
; Sequence 109, Application US/10292088
; Publication No. US2003021100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 109
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-109

Query Match      84.7%; Score 549.5; DB 15; Length 118;
Best Local Similarity 87.6%; Pred. No. 1.4e-41;
Matches 106; Conservative 5; Mismatches 7; Indels 3; Gaps 1;

Qy 1 QVQLQESGPGLVKPESETLSLTCTVSGGSISSYYMSWIRQPPGKGLEWIGIYYTWTSNYN 60
Db 1 QVQLQESGPGLVKPESETLSLTCTVSGGSISSYYMSWIRQPPGKGLEWIGIYYSGTNYN 60

Qy 61 PSLKSRVTISVDTSKNQFSLSLSSVTAADTAVYYCARDQGWLLPDADFINGQGTMVTVS 120
Db 61 PSLKSRVTISVDTSKNQFSLSLSSVTAADTAVYYCARDYGG---NSYFDYWGQGLTIVTS 117

Qy 121 S 121
Db 118 S 118

RESULT 15
US-10-067-800-60
; Sequence 60, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.1150001
; CURRENT APPLICATION NUMBER: US/10/067,800

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 12:25:58 ; Search time 13.0401 seconds  
(without alignments)  
892.802 Million cell updates/sec

Title: US-10-660-357A-1  
Perfect score: 649  
Sequence: 1 QVQLQESGPGLVKPSSETLSL.....WLLPDAFDIWGQGTWTVSS 121

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	543	83.7	140	2 I37782	Ig variable region
2	536	82.6	155	2 S31512	Ig heavy chain - h
3	533	82.1	130	2 S31690	Ig heavy chain v r
4	533	82.1	155	2 S31511	Ig heavy chain - h
5	526.5	81.1	139	2 S31586	Ig heavy chain v r
6	518.5	79.9	130	2 S30534	Ig heavy chain v r
7	512.5	79.0	137	2 S31676	Ig heavy chain v r
8	509.5	78.5	118	2 S20780	Ig heavy chain v r
9	505	77.8	147	2 S13519	Ig heavy chain v r
10	498.5	76.8	140	2 S78052	Ig heavy chain pre
11	495	76.3	135	2 S78051	Ig heavy chain pre
12	490	75.5	105	2 S44125	Ig lambda chain v
13	489	75.3	97	2 S26906	Ig heavy chain v r
14	489	75.3	146	2 S09711	Ig heavy chain v r
15	488	75.2	116	2 B26340	Ig heavy chain pre
16	486	74.9	97	2 S12416	Ig heavy chain v r
17	486	74.9	121	2 S44113	Ig heavy chain v r
18	485	74.7	140	2 A49045	Ig heavy chain v r
19	481	74.1	123	2 S30530	Ig heavy chain v r
20	481	74.1	139	2 S31696	Ig heavy chain v r
21	477	73.5	118	2 A26340	Ig heavy chain pre
22	474.5	73.1	129	2 S44114	Ig heavy chain v r
23	473.5	73.0	126	2 S47010	Ig heavy chain v r
24	473.5	73.0	145	2 S78055	Ig heavy chain pre
25	468.5	72.2	118	2 S24443	Ig heavy chain v r
26	467	72.0	99	2 S26802	Ig heavy chain v r
27	467	72.0	99	2 S26803	Ig heavy chain v r
28	467	72.0	220	2 A49444	Ig gamma-1 heavy c
29	466	71.8	97	2 PH0876	Ig heavy chain v r

30	465	71.6	99	2 S12412	Ig heavy chain v r
31	462	71.2	143	2 B49028	Ig heavy chain v-i
32	460	70.9	97	2 S26804	Ig heavy chain v r
33	460	70.9	116	2 S18557	Ig heavy chain v r
34	459.5	70.8	122	2 D41287	Ig heavy chain v-i
35	458	70.6	99	2 S26801	Ig heavy chain v r
36	458	70.6	134	2 S54906	Ig heavy chain v r
37	458	70.6	146	2 S09710	Ig heavy chain v r
38	455.5	70.2	110	2 S44110	Ig heavy chain v-D
39	454.5	70.0	146	1 G1H02	Ig heavy chain pre
40	454	70.0	99	2 S12418	Ig heavy chain v r
41	453.5	69.9	122	2 S69912	Ig v-D-J region (N
42	452	69.6	140	2 A24770	hypothetical hybri
43	451	69.5	109	2 PH1673	Ig heavy chain v r
44	451	69.5	135	2 S31604	Ig heavy chain v r
45	449	69.2	115	2 S57464	Ig heavy chain v-J

ALIGNMENTS

RESULT 1  
I37782  
Ig variable region (VDJ) (clone T23-9) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999  
C:Accession: I37782; S25476  
R:Demaison, C.; Chastagner, P.; There, J.; Zouali, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994  
A>Title: Somatic diversification in the heavy chain variable region genes expressed by F;46-128/Domain: immunoglobulin homology <IMM>  
A:Accession: I37782  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140 <RES>  
A:Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F;46-128/Domain: immunoglobulin homology <IMM>

Query Match 83.7%; Score 543; DB 2; Length 140;  
Best Local Similarity 86.0%; Pred. No. 3.5e-41;  
Matches 104; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLCTVSGGSISSYVWSWIRPPGKGLWIGYIVYTWTSNYN 60  
Db 20 QVQLQESGPGLVKPSSETLSLCTVSGGSISSYVWSWIRPPGKGLWIGYIVYSGSTNYN 79  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAIVYCARDQGGQWLLPDAFDIWGQGTWTVVS 120  
Db 80 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAIVYCARDHNSSSWYGRYFDYWGQGTWTVVS 139  
QY 121 S 121  
Db 140 S 140

RESULT 2  
S31512  
Ig heavy chain - human  
C:Species: Homo sapiens (man)  
C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S31512  
R:Chastagner, P.; Demaison, C.; There, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA aut  
A:Reference number: S31509  
A:Accession: S31512  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-155 <CHA>  
A:Cross-references: EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PID:g33083  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

F;47-129/Domain: immunoglobulin homology <IMM>

Query Match	82.6%;	Score 536;	DB 2;	Length 155;
Best Local Similarity	82.9%;	Pred. No. 1.6e-40;		
Matches 102;	Conservative 7;	Mismatches 12;	Indels 2;	Gaps 1;
Qy	1	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYMSWIRQPPGKGLEWIGYIYYTWTSNYN	60	
Db	33	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYMSWIRQPPGKGLEWIGYIYYTGSATYN	92	
Qy	61	PPLKSRVTIISVDTSKQNPFLSLRSLVSTAADTAIVYICARDQG--QWLLPDAFDIWGGTWMVT	118	
Db	93	PPLKSRVTIISVDTSKQNPFLSKVSSSTAADTAIVYICARGGISSWVYVYGMVDWVGQGITVT	152	
Qy	119	VSS	121	
Db	153	VSS	155	

```

RESULT 3
S31690
Ig heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31690
R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31595
A/Accession: S31690
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-130 <CDI>
A/Cross-references: EMBL:Z14199; NID:G30984; PIDN:CAA78568.1; PID:G30985
C/Superfamily: immunoglobulin v region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/20-102/Domain: immunoglobulin homology <IMW>

```

Query Match	82.1%;	Score 533;	DB 2;	Length 130;
Best Local Similarity	84.0%;	Pred. No. 2.5e-40;		
Matches 105;	Conservative 5;	Mismatches 11;	Indels 4;	Gaps 1;
Qy	1	QVQLQESGPGLVKPSETLSLTCTVSGSISYYKSWIRQPPGKGLEWIGYIYYTWSNYN	60	
Db	6	QVQLQESGPGLVKPSETLSLTCTVSGSISYYKSWIRQPPGKGLEWIGYIYYSGSYN	65	
Qy	61	PSLKSRYTISVDTSKNQFSLKLSVTTAADTAVYYCARDQGWL----	LPDAFDIWGGQTM	116
Db	66	PSLKSRYTISVDTSKNQFSLKLSVTTAADTAVYYCARGSSVLLWFGELLYYFDIWGGQTL	125	
Qy	117	VTWSS	121	
Db	126	VTWSS	130	

RESULT 4

S31511

IG heavy chain - human

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999

C:Accession: S31511

R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.

A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto

A:Reference number: S31509

A:Accession: S31511

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-155 <CHA>

A:Cross-references: EMBL:X69866; NID:G33094; PID:CAA49500.1; PID:G33095

C:Superfamily: immunoglobulin v region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:47-129/Domain: immunoglobulin homology <IMM>

Query Match	82.1%;	Score 533;	DB 2;	Length 155;
Best Local Similarity	83.7%;	Pred. No. 3e-40;		
Matches 103;	Conservative 5;	Mismatches 13;	Indels 2;	Gaps 1
Qy	1	QVQLQESGPGLVKPSETLSLTCTVSGGISISSYVYWSWIRPPGKGLEWIGYLYYTWTSNN	60	
Db	33	QVQLQESGPGLVKPSETLSLTCTVSGGISISSYVYWSWIRPPGKGLEWIGYLYYTGSA	92	
Qy	61	PSLKSRTVISVDTSKNOFSLRLSVTTAADTAVVYCARDQG--QWLLPDAFDIWGGTWM	118	
Db	93	PPLKSRTVISVDTSKNOFSLKVSSTTAADTAVVYCARGGGISSWDYDGMDVWVG	152	
Qy	119	VSS 121		
Db	153	VSS 155		

```

RESULT 5
S31586
Ig heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31586
R/Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31586
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-139 <CUI>
A/Cross-references: EMBL:Z14196; NID:G30978; PIDN:CAA78565.1; PID:G30979
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:34-116/Domain: immunoglobulin homology <IMW>

```

	Query Match	81.1%	Score 526.5	DB 2	Length 139
	Best Local Similarity	86.0%	Pred. No. 1e-39		
	Matches 104	Conservative	6	Mismatches 10	Indels 1
					Gaps 1
Qy	1	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYMSWIRPPGKGLEWIGVYVYTWTSNN	60		
Db	20	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYMSWIRPPGKGLEWIGVYVYTWTSNN	79		
Qy	61	PSLKSRTVTSVDTSKNQPSLRLSSVTAAATVAVYCARDQGWLLPDAFDIWGGTWTVTS	120		
Db	80	PSLKSRTVMSVDTSKNQPSLRLSSVTAAATVAVYCAEG-GLGIRGAFDIWGGTWTVTS	138		
Qy	121	S 121			
Db	139	S 139			

```

RESULT 6
S30534
IG heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1995
C:Accession: S30534
R:Marlette, X.
submitted to the EMBL Data Library, October 1992
A:Reference number: S30520
A:Accession: S30534
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-130 <MAR>
A:Cross-references: EMBL:Z18320
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 79.9% Score 518.5 DB 2: Length 130:

```

```
Best Local Similarity 81.5%; Pred. No. 4.8e-39;
Matches 106; Conservative 6; Mismatches 9; Indels 9; Gaps 3;

QY 1 QVQLQESGPGLVKPSETLSLTCTVSGGIS--SYNWSWIROPKGLGWIGYIYTWTSN 58
Db 1 QVQLQESGPGLVKPSETLSLTCTVSGGIS--SYNWSWIROPKGLGWIGYIYTWTSN 60
QY 59 YNPSLSRVITISVDTSKNQFSLRLSSVTAADTAVYYCARDQGO-WL-----LPDAFDIW 111
Db 61 YNPSLSRVITISVDTSKNQFSLRLSSVTAADTAVYYCARDKGGFWSGYITNSRAAFDIW 120
QY 112 QGTMVTVSS 121
Db 121 QGTMVTVSS 130

RESULT 7
S31676
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31676
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31676
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-137 <CUI>
A:Cross-references: EMBL:Z14182; NID:G31031; PIDN:CAA78551.1; PID:G31032
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 512.5; DB 2; Length 137;
Best Local Similarity 83.5%; Pred. No. 1.7e-38;
Matches 101; Conservative 6; Mismatches 11; Indels 3; Gaps 1;

QY 1 QVQLQESGPGLVKPSETLSLTCTVSGGIS--SYNWSWIROPKGLGWIGYIYTWTSN 60
Db 20 QVQLQESGPGLVKPSETLSLTCTVSGGIS--SYNWSWIROPKGLGWIGYIYTWTSN 79
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGO-WLLPDAFDIWGGTMTVTS 120
Db 80 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDAP---LMYGMVWGQGTMTVTS 136
QY 121 S 121
Db 137 S 137

RESULT 8
S20780
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S20780
R:Mortari, F.; Wang, J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A:Description: Analysis of human cord blood Ig heavy chain IgA and IgG repertoire.
A:Reference number: S20764
A:Accession: S20780
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-118 <MOR>
A:Cross-references: EMBL:Z11958; NID:G33893; PIDN:CAA78015.1; PID:G33894
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 78.5%; Score 509.5; DB 2; Length 118;
Best Local Similarity 81.0%; Pred. No. 2.7e-38;
```

```
Matches 98; Conservative 11; Mismatches 9; Indels 3; Gaps 1;

QY 1 QVQLQESGPGLVKPSETLSLTCTVSGGIS--SYNWSWIROPKGLGWIGYIYTWTSN 60
Db 1 QVQLQESGPGLVKPSETLSLTCTVSGGIS--SYNWSWIROPKGLGWIGYIYTWTSN 60
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGO-WLLPDAFDIWGGTMTVTS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDGR---DGGFDIWGGTMTVTS 117
QY 121 S 121
Db 118 S 118

RESULT 9
S13519
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S13519
R:Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.
Nucleic Acids Res. 19, 673, 1991
A:Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked
A:Reference number: S13519; MUID:91187691; PMID:2011536
A:Accession: S13519
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-147 <MOR>
A:Cross-references: EMBL:X56158; NID:G37724; PIDN:CAA39626.1; PID:G37725
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:41-125/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 505; DB 2; Length 147;
Best Local Similarity 82.1%; Pred. No. 8.6e-38;
Matches 101; Conservative 7; Mismatches 11; Indels 4; Gaps 3;

QY 1 QVQLQESGPGLVKPSETLSLTCTVSGGI--SSYYWSWIROPKGLGWIGYIYTWTSN 58
Db 27 QVQLQESGPGLVKPSETLSLTCTVSGGIS--SSYYWSWIROPKGLGWIGYIYSGTY 86
QY 59 YNPSLSRVITISVDTSKNQFSLRLSSVTAADTAVYYCARDQGO-WLLPDAFDIWGGTMTV 118
Db 87 YNPSLSRVITISVDTSKNQFSLRLSSVTAADTAVYYCARPL-LW-FGELFDIWGGTMTV 144
QY 119 VSS 121
Db 145 VSS 147

RESULT 10
S78052
Ig heavy chain precursor V-D-J region (clone mAB 63VH) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78052; S3717
R:Harindranath, N.
submitted to the EMBL Data Library, August 1990
A:Reference number: S78051
A:Accession: S78052
A:Molecule type: mRNA
A:Residues: 1-140 <HAR>
A:Cross-references: EMBL:X54441; NID:G37815; PIDN:CAA38308.1; PID:G930118
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin
Int. Immunol. 3, 865-875, 1991
A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and
patient.
A:Reference number: S23716; MUID:92031262; PMID:1718404
A:Accession: S23717
A:Molecule type: mRNA
A:Residues: 15-111 <HAW>
A:Cross-references: EMBL:X54441
```





## RESULT 14

Query Match 75.3%; Score 489; DB 2; Length 146;  
Best Local Similarity 74.0%; Pred. No. 2.2e-36;  
Matches 97; Conservative 11; Mismatches 9; Indels 14; Gaps 3;

[illegible]

## RESULT 15

```
Query Match      75.2%; Score 488; DB 2; Length 116;
Best Local Similarity 93.8%; Pred. No. 2.1e-36;
Matches 91; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

QY 61 PSLKSRVTISVDTSKNFSIRLSSVTAADTAVYYCAR 97  
|||:|||||

Db 80 PSLKSRVTISVDTSKNFSIKLSSVTAADTAVYYCAR 116

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:46:52 ; Search time 62.4712 Seconds  
(without alignments)  
991.843 Million cell updates/sec

Title: US-10-660-357A-1

Perfect score: 649

Sequence: 1 QVQLQESGPGLVKPSSETLSL.....WLLPDAFDIWGQGTMTVTSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	516	79.5	476	2	Q6GMX1 homo sapien
2	515	79.4	119	2	Q9UL73 homo sapien
3	508.5	78.4	465	2	Q6GMX6 homo sapien
4	501.5	77.3	620	2	Q96EV0
5	498.5	76.8	477	2	Q6GMX7 homo sapien
6	495	76.3	139	2	Q86SX2
7	493.5	76.0	478	2	Q7Z379
8	482.5	74.3	150	2	Q95973
9	472.5	72.8	576	2	Q6P418
10	472	72.7	492	2	Q7Z374
11	460.5	71.0	496	2	Q96KX8
12	454.5	70.0	146	1	HV21 HUMAN
13	451	69.5	595	2	Q8WUX4
14	451	69.5	597	2	Q6GMX5
15	451	69.5	597	2	Q9BU10
16	451	69.5	625	2	Q96AA6
17	450	69.3	478	2	Q6NTH3
18	449	69.2	597	2	Q9BQB8
19	445	68.6	117	1	HV2G HUMAN
20	444	68.4	129	1	HV2F HUMAN
21	435.5	67.1	130	2	Q81ZD7
22	416.5	64.2	116	2	Q7Z3Y6
23	411.5	63.4	122	2	Q9UL75
24	407	62.7	479	2	Q99M22
25	398	61.3	476	2	Q6MZK7
26	394.5	60.8	136	2	Q6LBQ5
27	394	60.7	137	1	HV46 MOUSE
28	390.5	60.2	473	2	Q8TC63
29	375	57.8	113	1	HV47 MOUSE
30	372	57.3	262	2	Q65Z11
31	369.5	56.9	482	2	Q91X92

32	366.5	56.5	116	1	HV60 MOUSE
33	355	54.7	117	1	HV62 MOUSE
34	354.5	54.6	116	1	HV61 MOUSE
35	348	53.6	118	2	Q9UL74
36	348	53.6	144	1	HV43 MOUSE
37	347.5	53.5	118	2	Q811U5
38	345.5	53.2	121	2	Q99NG4
39	343.5	52.9	135	1	HV02 XENLA
40	333	51.3	121	2	Q9UL96
41	332	51.2	470	2	Q6PJA4
42	330.5	50.9	613	2	Q8WUK1
43	328.5	50.6	118	2	Q9UL91
44	324.5	50.0	606	2	Q6GMV2
45	320	49.3	240	2	Q65ZC9

P18531	mus musculus
P18533	mus musculus
P18532	mus musculus
Q9UL74	homo sapien
P01819	mus musculus
Q811U5	mus musculus
Q99NG4	mus musculus
P20957	xenopus lae
Q9UL96	homo sapien
Q6PJA4	homo sapien
Q8WUK1	homo sapien
Q9UL91	homo sapien
Q6GMV2	homo sapien
Q65ZC9	homo sapien

#### ALIGNMENTS

RESULT 1  
Q6GMX1 PRELIMINARY; PRT; 476 AA.  
ID Q6GMX1  
AC Q6GMX1;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Bouffard G.G.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BC073773; AAH73773.1; -.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF07654; C1-set; 3.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 3.  
DR SMART; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.

```
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DD59D CRC64;

Query Match 79.5%; Score 516; DB 2; Length 476;
Best Local Similarity 79.7%; Pred. No. 3.6e-43;
Matches 102; Conservative 10; Mismatches 8; Indels 8; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISS--YYHWSWIROPKGLWIGIYYTWTN 58
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: ||
20 QVQLQESGPGLVKPSOTLSLTCTVSGGSISSGDIYWSWIROPKGLWIGIYYSGSTY 79
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: ||

QY 59 YNPSLKSRVTISVDTSKNQFSLRSSVTAADTAIVYCARDQGW----LLDPADFIWG 113
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: ||
80 YNPSLKSRVTISLDTSKNQFSLKNSVTAADTAIVYFCAR-AGVWGSRFSAIDGFNIWG 138
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: ||

QY 114 GTWMTVSS 121
Db |||||
139 GTWMTVSS 146

RESULT 2
ID Q9UL73 PRELIMINARY; PRT; 119 AA.
AC Q9UL73;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DS (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]

SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RC MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RX Wu X., Liu B., Van der Marwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetuses.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035041; AAD56277.1; -.
DR PIR; PH0876; PH0876.
DR PIR; S12416; S12416.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;

Query Match 79.4%; Score 515; DB 2; Length 119;
Best Local Similarity 82.6%; Pred. No. 1e-43;
Matches 100; Conservative 8; Mismatches 11; Indels 2; Gaps 2;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYWSWIROPKGLWIGIYYTWTN 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: ||
1 QVQLQESGPGLVKPSSETLSLTCTVSGGSICSYWSWIROPKGLWIGIYYSGSTNYT 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: ||

QY 61 PSLKSRVTISVDTSKNQFSLRSSVTAADTAIVYCARDQGWLLPDAFIWGCGTMTVS 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: ||
61 PSLKSRVTISVDRSKNQFSLKLTSLTAADTAIVYFCAR-LSNW-GPYFYDWGQGLTIVTS 118
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: ||

QY 121 $ 121
Db 119 $ 119

RESULT 3
ID Q6GMX6 PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]

SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RC MEDLINE=22388357; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]

SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RC Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 78.4%; Score 508.5; DB 2; Length 465;
Best Local Similarity 81.8%; Pred. No. 2e-42;
Matches 99; Conservative 8; Mismatches 9; Indels 5; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYWSWIROPKGLWIGIYYTWTN 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: ||
20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISGYWSWIROPKGLWIGIRITSGSTNN 79
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: ||

QY 61 PSLKSRVTISVDTSKNQFSLRSSVTAADTAIVYCARDQGWLLPDAFIWGCGTMTVS 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: ||
80 PSLKSRVTISVDTSKNQFSLKLTSLTAADTAIVYCARDQGWLLPDAFIWGCGTMTVS 134
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: ||

QY 121 $ 121
Db 135 $ 135

RESULT 4
ID Q96EYO
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ID Q96EY0 PRELIMINARY; PRT; 620 AA.
AC Q96EY0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011857; AAH11857.2; -.
DR PIR; S15590; S15590.
DR HSP; P01820; IG7J.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 620 AA; 68125 MW; 990A1A4A6E8FF27B CRC64;

Query Match 77.3%; Score 501.5; DB 2; Length 620;
Best Local Similarity 82.0%; Pred. No. 1.4e-41;
Matches 100; Conservative 6; Mismatches 13; Indels 3; Gaps 2;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGYIYTWTSNYN 60
DB 27 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGYIYTWTSNYN 86
QY 61 PSLSKRVITISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPD-AFDIWGGTMTV 119
DB 87 PSLSKRVITMSVDTSKNQFSLRLSSVTAADTAVYYCASQ--PWELPTVGLFPYGGGLTV 144
QY 120 SS 121
DB 145 SS 146
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RESULT 5

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Q6GMX7 PRELIMINARY; PRT; 477 AA.
ID Q6GMX7;
AC Q6GMX7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073765; AAH73765.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein.
SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CFF85 CRC64;

Query Match 76.8%; Score 498.5; DB 2; Length 477;
Best Local Similarity 81.0%; Pred. No. 2e-41;
Matches 98; Conservative 8; Mismatches 12; Indels 3; Gaps 2;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGYIYTWTSNYN 60
DB 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGYIYTWTSNYN 79
QY 61 PSLSKRVITISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPD-AFDIWGGTMTV 120
DB 80 PSLSKRVITSLDTSKNQFSLRLSSVTAADTAVYYCAHG--SSW--DFAFDWGGTTLTV 136
QY 121 S 121
DB 137 S 137
```

RESULT 6	
Q86SX2	Q86SX2 PRELIMINARY; PRT; 139 AA.
ID	Q86SX2
AC	Q86SX2; AC
DT	01-JUN-2003 (TrEMBLrel. 24, Created)
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Full-length cDNA clone CSDDL0047M19 of B cells (Ramos cell line) of
DE	Homo sapiens (human) (Fragment).
OS	Homo sapiens (human)
OS	Eukaryota; Metazoa
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=B cells;
RA	Li W.B., Gruber C., Jessee J., Polayes D.;
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=B cells;
RA	Genoscope;
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BX248300; CAD62627.1; -
DR	HSSP; P01820; IG7J
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003596; Ig_v.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS50835; IG_LIKE; 1.
FT	NON_TER 1
QY	SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;
Query Match 76.3%; Score 495; DB 2; Length 139;	
Best Local Similarity 94.9%; Pred. No. 1.2e-41;	
Matches 93; Conservative 4; Mismatches 1; Indels 0; Gaps 0;	
QY	1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKLEWIGYIYYTWTSN 60
Db	33 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKLEWIGYIYYSGSTNYN 92
QY	61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARD 98
Db	93 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARD 130
RESULT 7	
Q72379	Q72379 PRELIMINARY; PRT; 478 AA.
ID	Q72379
AC	Q72379; AC
DT	01-OCT-2003 (TrEMBLrel. 25, Created)
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Hypothetical protein DKFZp686K04218 (Fragment).
GN	Name=DKFZp686K04218;
OS	Homo sapiens (human)
OC	Eukaryota; Metazoa
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Human rectum tumor;
RA	Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA	Fobo G., Han M., Wiemann S.;
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BX538066; CAD97996.1; -
DR	HSSP; P01820; IG7J
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003597; Ig-cl.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF07654; C1-set; 2.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS50835; IG_LIKE; 4.
Query Match 74.3%; Score 482.5; DB 2; Length 150;	
Best Local Similarity 79.7%; Pred. No. 2.3e-40;	
Matches 98; Conservative 6; Mismatches 12; Indels 7; Gaps 2;	
QY	1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISS--YYWMIROPPGKLEWIGYIYYTWTSN 58
Db	20 QLQLQESGPGLVKPSSETLSLTCTVSGGSISSNNYYWMIROPPGKLEWIGSLHNSGSDY 79
QY	59 YNPISLKSRTVISVDTSKNQFSLRLSSVTAADTAVYYCARDQDQWLLPDAFDIWGQGTWYT 118
Db	80 YNPISLKSRTVISVDTSKNQFSLRLSSVTAADTAVYYCAR-----LGMGAFDFWGHGTWYT 134
QY	119 VSS 121
Db	135 VSS 137
RESULT 9	
Q6P4I8	Q6P4I8 PRELIMINARY; PRT; 576 AA.
ID	Q6P4I8

AC Q6P4I8;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE IGH domain protein.  
 GN Name=IGHD;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywicki M.I., Skalska U., Smutuz J., Schnerch D.E., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC063384; AB463384.1; -;  
 DR HSSP; P01820; 1A7N.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF07654; C1-set; 2.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00407; IGC1; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
 SQ SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;  
 Query Match 72.8%; Score 472.5; DB 2; Length 576;  
 Best Local Similarity 76.2%; Pred. No. 1e-38;  
 Matches 96; Conservative 9; Mismatches 10; Indels 11; Gaps 3;  
 QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSIS--SSYWSWIRQPPGKLEWIGYIYVWTSNY 59  
 DB 27 QVQLQESGPGLVKPSGTLSTCAVSGSISSSNWSVRQPPGKLEWIGIYVHSGSTNY 86  
 QY 60 NPSLKSRTVISVDTSKNQFSLRLSSVTAADTAIVYCARDGQWLLPDAF-----DIWGQGT 115  
 DB 87 NPSLKSRTVISVDTSKNQFSLRLSSVTAADTAIVYCARDGQWLLPDAF-----DIWGQGT 140  
 QY 116 MVTVSS 121  
 DB 141 TVTVSS 146  
 RESULT 10

Q7Z374  
 ID Q7Z374 PRELIMINARY; PRT; 492 AA.  
 AC Q7Z374;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein DKFZp686C02218 (Fragment).  
 GN Name=DKFZp686C02218;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Human rectum tumor;  
 RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Fobo G., Han M., Wiemann S.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX538077; CAD98001.1; -;  
 DR HSSP; P01820; 1G7J.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig v.  
 DR Pfam; PF07654; C1-set; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR SMART; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
 KW Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;  
 Query Match 72.7%; Score 472; DB 2; Length 492;  
 Best Local Similarity 75.4%; Pred. No. 9.5e-39;  
 Matches 95; Conservative 9; Mismatches 12; Indels 10; Gaps 4;  
 QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSIS--SYWSWIRQPPGKLEWIGYIYVWTSN 58  
 DB 32 QVQLQESGPGLVKPSSETLSLTCTVSGSVSNRYNGWIRQPPGKLEWIGSIYNYNTY 91  
 QY 59 YNPGLKSRVTISVDTSKNQFSLRLSSVTAADTAIVYCARD-QGQ--WLPDAFDIWGQGT 115  
 DB 92 YSPSLKSLRTIFVDTSKNHFSLRLSVTAADTAIVYCVRHVEGPGYGM-----FDPWQGT 146  
 QY 116 MVTVSS 121  
 DB 147 LVTVSS 152  
 RESULT 11  
 Q96KX8  
 ID Q96KX8 PRELIMINARY; PRT; 496 AA.  
 AC Q96KX8;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE MGC27165 protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,





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DR Pfam; PF07654; Cl-set; 4.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGc1; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
DR KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65304 MW; 2A1E75F6AED85230 CRC64;

Query Match 69.5%; Score 451; DB 2; Length 597;
Best Local Similarity 69.8%; Pred.No.1.5e-36;
Matches 90; Conservative 10; Mismatches 17; Indels 12; Gaps 2

Qy 1 QVQLQESGGPGLVKPSETLSLTCTVSGGISISSYKWSWIRQPPGKGLEWIGYIYVTTSNYN 60
Db 20 QVQLQESGGPGLVKPSETLSLTCTVSGGSFGSYGWSWIRQPPGKGLEWIGTINHSGSTNYN 79
Qy 61 PSLKSRVTISVDTSKNQFSLRSLSSVTAADTAVYYCAR-----DQGWLLPDAFDIWG 112
Db 80 PSLKSRVTISVDTSKKQLSLKLSVNAADTAVYYCARVITRASPTGDRY----GMDVWG 135
Qy 113 QGTVMTVSS 121
Db 136 QGTVMTVSS 144

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RESULT 15	
Q9BU10	PRELIMINARY; PRT; 597 AA.
ID	Q9BU10
AC	Q9BU10; 2001 (TrEMBLrel. 17, Created)
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT	01-JAN-2004 (TrEMBLrel. 26, Last annotation update)
DE	IGHM protein.
OS	Homo sapiens (Human)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Lymph;
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.C., Touchman J.W., Green E.D., Dickens M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skalka U., Smillus D.E., Schnerch A., Schein J.E.,
RA	Jones S.J., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences."
RP	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Lymph;
RC	TISSUE=Lymph;
RA	Strausberg R.;
RL	Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BC002963; AA02963.1; -
DR	HSSP; P01861; IADQ.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003597; Ig cl.
DR	InterPro; IPR003006; Ig MHC.



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:43:32 ; Search time 72.1353 Seconds  
(without alignments)  
627.306 Million cell updates/sec

Title: US-10-660-357A-5  
Perfect score: 625  
Sequence: 1 QVQLQSGPGLVKPSQTL...ARGGDGKYWGQTLVTSS 117

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_16Dec04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	625	100.0	117	7	ADC99776	Adc99776 Anti-huma
2	625	100.0	117	7	ADD05380	Adf05380 Anti-MUC1
3	625	100.0	117	7	ADF09818	Adf09818 Human ant
4	604	96.6	117	7	ADC99804	Adc99804 Anti-huma
5	604	96.6	117	7	ADD05408	Adf05408 Anti-MUC1
6	604	96.6	117	7	ADF09846	Adf09846 Human ant
7	587	93.9	117	7	ADC99784	Adc99784 Anti-huma
8	587	93.9	117	7	ADD05388	Adf05388 Anti-MUC1
9	587	93.9	117	7	ADF09826	Adf09826 Human ant
10	571.5	91.4	118	7	ADC93968	Adp03968 Murine-ex
11	571	91.4	123	7	ADP03870	Adp03870 Murine-ex
12	567.5	90.8	120	7	ADP03974	Adp03974 Murine-ex
13	567.5	90.8	120	7	ADP03873	Adp03873 Murine-ex
14	561	89.8	120	4	AAB62775	Aab62775 Human HIV
15	559.5	89.5	121	7	ADJ80377	Adj80377 Antibody
16	559	89.4	119	7	ADP03970	Adp03970 Murine-ex
17	557	89.1	122	4	AAB62765	Aab62765 Human HIV
18	556.5	89.0	123	4	AAB62745	Aab62745 Human HIV
19	556.5	89.0	124	7	ADP03935	Adp03935 Murine-ex
20	555.5	88.9	110	7	ADP03934	Adp03934 Murine-ex
21	555.5	88.9	122	7	ADP03977	Adp03977 Murine-ex
22	555	88.8	121	7	ADP03981	Adp03981 Murine-ex
23	555	88.8	123	2	AAW78433	Aaw78433 Antibody
24	555	88.8	123	5	ABB97976	Abb97976 Heavy cha
25	555	88.8	123	7	ADG88414	Adg88414 anti-Ob-R

ALIGNMENTS

RESULT 1

ADC99776

ID ADC99776 standard; protein; 117 AA.

XX AC

XX ADC99776;

DT 01-JAN-2004 (first entry)

DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 5.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
KW lung cancer; human.

XX Homo sapiens.

XX WO2003057838-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

XX Gudas J;

XX WPI; 2003-587113/55.

XX N-PSDB; ADC99778.

XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
or condition associated with expression of MUC18 in a patient, e.g.  
tumors, cancers, and other malignancies.

XX Claim 1; SEQ ID NO 5; 78pp; English.

XX The invention relates to a novel isolated monoclonal antibody comprising  
a heavy or light chain amino acid or a heavy or light chain variable  
domain where the antibody binds to MUC18. The monoclonal antibody of the  
invention demonstrates cytostatic activity and may be useful for treating  
a disease or condition associated with the expression of MUC18 on the  
cell surface such as tumours, specifically melanoma, oesophageal,  
pancreatic or colorectal tumours, carcinomas, particularly cervical  
carcinomas and cervical intraepithelial neoplasia and cancers including  
colorectal, breast or lung cancer, as well as other malignancies. The  
current sequence is that of the anti-human MUC18 monoclonal antibody

CC heavy chain protein of the invention.

XX Sequence 117 AA;

Query Match 100.0%; Score 625; DB 7; Length 117;

Best Local Similarity 100.0%; Pred. No. 1.7e-45; Mismatches 0; Indels 0; Gaps 0;

Matches 117; Conservative 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGKLEWIGYIYSGSTY 60

DB 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGKLEWIGYIYSGSTY 60

QY 61 YNPPLSKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYKYWGQGLTVTVSS 117

DB 61 YNPPLSKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYKYWGQGLTVTVSS 117

RESULT 2

ADD05380

ID ADD05380 standard; protein; 117 AA.

XX AC

XX ADD05380;

DT 01-JAN-2004 (first entry)

XX DE

XX Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 5.

XX monoclinal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;

XX antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.

XX OS

XX Homo sapiens.

XX WO2003057006-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041582.

XX 28-DEC-2001; 2001US-0346460P.

XX (ABGE-) ABGENIX INC.

XX Gudas J, Bar-Eli M;

XX WPI; 2003-577496/54.

XX N-PSDB; ADD05382.

XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and

XX treating tumors, inhibiting tumor growth, inhibiting cell invasion

XX associated with melanoma, or increasing survival of an animal having a

XX metastatic tumor.

XX Claim 1; SEQ ID NO 5; 87pp; English.

XX The invention relates to a novel monoclonal antibody used for inhibiting

XX tumour growth in an animal. The tumour inhibition process comprises

XX selecting an animal in need of treatment for a tumour, providing a

XX monoclonal antibody comprising a heavy chain amino acid, where the

XX antibody consists of any one of 10 fully defined sequences of 117-123

XX amino acids given in the specification, and where the monoclonal antibody

XX binds MUC18, and contacting the tumour with the antibody resulting in

XX inhibited proliferation of the cells. The monoclonal antibody has

XX cytostatic and can be used in the production of a vaccine. The monoclonal

XX antibodies against the MUC18 antigen are useful for diagnosing and

XX treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or

XX tumour metastasis), inhibiting cell invasion associated with melanoma, or

XX increasing survival of an animal having a metastatic tumour. This

XX sequence represents an anti-MUC18 antibody heavy chain, variable region,

XX protein of the invention.

XX Sequence 117 AA;

Query Match 100.0%; Score 625; DB 7; Length 117;

Best Local Similarity 100.0%; Pred. No. 1.7e-45;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGKLEWIGYIYSGSTY 60

DB 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGKLEWIGYIYSGSTY 60

QY 61 YNPPLSKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYKYWGQGLTVTVSS 117

DB 61 YNPPLSKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYKYWGQGLTVTVSS 117

RESULT 3

ADF09818

ID ADF09818 standard; protein; 117 AA.

XX AC

XX ADF09818;

DT 12-FEB-2004 (first entry)

XX DE

XX Human anti-MUC18 monoclonal antibody heavy chain #2.

XX cell proliferation inhibition; MUC18 tumour antigen;

XX anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;

XX carcinoma; cancer; malignancy; heavy chain; human.

XX OS

XX Homo sapiens.

XX WO2003057837-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041580.

XX 28-DEC-2001; 2001US-0346414P.

XX (ABGE-) ABGENIX INC.

XX Gudas J;

XX WPI; 2003-598367/56.

XX N-PSDB; ADF09820.

XX Inhibiting cell proliferation associated with expression of MUC18 tumour

XX antigen, involves incubating and inhibiting cell by administering anti-

XX MUC18 monoclonal antibody.

XX Claim 1; SEQ ID NO 5; 83pp; English.

XX The invention comprises a method for inhibiting cell proliferation

XX associated with expression of MUC18 tumour antigen. The method involves

XX administering anti-MUC18 monoclonal antibody. The method of the invention

XX is useful for inhibiting cell (e.g. melanoma or tumour cell)

XX proliferation associated with the expression of MUC18 tumour antigen, the

XX method is preferably useful for inhibiting tumour metastasis. The method

XX is useful for inhibiting cell proliferation in patients with tumours,

XX carcinomas, cancer and other malignancies. The present amino acid

XX sequence represents a heavy chain from an MUC18 tumour antigen-specific

XX monoclonal antibody.

XX Sequence 117 AA;

Query Match 100.0%; Score 625; DB 7; Length 117;

Best Local Similarity 100.0%; Pred. No. 1.7e-45;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGKLEWIGYIYSGSTY 60

DB 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGKLEWIGYIYSGSTY 60

QY 61 YNPPLSKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYKYWGQGLTVTVSS 117

DB 61 YNPPLSKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYKYWGQGLTVTVSS 117



KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
 KW carcinoma; cancer; malignancy; heavy chain; human.  
 OS Homo sapiens.  
 XX WO2003057837-A2.  
 PN 17-JUL-2003.  
 PD  
 XX 26-DEC-2002; 2002WO-US041580.  
 PF  
 XX 28-DEC-2001; 2001US-0346414P.  
 PR  
 XX (ABGE-) ABGENIX INC.  
 PA  
 XX Gudas J;  
 PI  
 XX WPI; 2003-598367/56.  
 DR N-PSDB; ADF09848.  
 DR  
 XX Inhibiting cell proliferation associated with expression of MUC18 tumor  
 PT antigen, involves incubating and inhibiting cell by administering anti-  
 PT MUC18 monoclonal antibody.  
 PT  
 XX  
 XX Claim 1; SEQ ID NO 33; 83pp; English.  
 PS  
 XX The invention comprises a method for inhibiting cell proliferation  
 CC associated with expression of MUC18 tumour antigen. The method involves  
 CC administering anti-MUC18 monoclonal antibody. The method of the invention  
 CC is useful for inhibiting cell (e.g. melanoma or tumour cell)  
 CC proliferation associated with the expression of MUC18 tumour antigen, the  
 CC method is preferably useful for inhibiting tumour metastasis. The method  
 CC is useful for inhibiting cell proliferation in patients with tumours,  
 CC carcinomas, cancer and other malignancies. The present amino acid  
 CC sequence represents a heavy chain from an MUC18 tumour antigen-specific  
 CC monoclonal antibody.  
 XX  
 SQ Sequence 117 AA;  
 Query Match 96.6%; Score 604; DB 7; Length 117;  
 Best Local Similarity 94.0%; Pred. No. 1.1e-43;  
 Matches 110; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSY 60  
 Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSY 60  
 QY 61 YNPFLSKSRVTISVDTSKNQFSLKSSVTAADTAVYVCARGDGYKYWGQGLTVTVSS 117  
 Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 61 HNPFLSKSRVTISVDTSKNQFSLKSSVTAADTAVYVCARGDGYKYWGQGLTVTVSS 117  
 RESULT 7  
 ADC99784  
 ID ADC99784 standard; protein; 117 AA.  
 AC  
 XX ADC99784;  
 XX  
 DT 01-JAN-2004 (first entry)  
 DE  
 XX Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 13.  
 XX  
 KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
 KW cytotatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
 KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
 KW lung cancer; human.  
 XX  
 OS Homo sapiens.  
 XX WO2003057838-A2.  
 PN 17-JUL-2003.  
 PD  
 XX

PF 26-DEC-2002; 2002WO-US041581.  
 XX  
 PR 28-DEC-2001; 2001US-0346299P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Gudas J;  
 XX  
 DR WPI; 2003-587113/55.  
 DR N-PSDB; ADC99786.  
 DR  
 XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
 PT or condition associated with expression of MUC18 in a patient, e.g.  
 PT tumors, cancers, and other malignancies.  
 PT  
 XX  
 XX Claim 1; SEQ ID NO 13; 78pp; English.  
 PS  
 XX The invention relates to a novel isolated monoclonal antibody comprising  
 CC a heavy or light chain amino acid or a heavy or light chain variable  
 CC domain where the antibody binds to MUC18. The monoclonal antibody of the  
 CC invention demonstrates cytostatic activity and may be useful for treating  
 CC a disease or condition associated with the expression of MUC18 on the  
 CC cell surface such as tumours, specifically melanoma, oesophageal,  
 CC pancreatic or colorectal tumours, carcinomas, particularly cervical  
 CC carcinomas and cervical intraepithelial neoplasia and cancers including  
 CC colorectal, breast or lung cancer, as well as other malignancies. The  
 CC current sequence is that of the anti-human MUC18 monoclonal antibody  
 CC heavy chain protein of the invention.  
 XX  
 SQ Sequence 117 AA;  
 Query Match 93.9%; Score 587; DB 7; Length 117;  
 Best Local Similarity 94.0%; Pred. No. 2.9e-42;  
 Matches 110; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSY 60  
 Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSY 60  
 QY 61 YNPFLSKSRVTISVDTSKNQFSLKSSVTAADTAVYVCARGDGYKYWGQGLTVTVSS 117  
 Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 61 YNPFLSKSRVTISVDTSKNQFSLKSSVTAADTAVYVCARGDGYKYWGQGLTVTVSS 117  
 RESULT 8  
 ADD05388  
 ID ADD05388 standard; protein; 117 AA.  
 XX  
 AC ADD05388;  
 XX  
 DT 01-JAN-2004 (first entry)  
 DE  
 XX Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 13.  
 XX  
 KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
 KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.  
 XX  
 OS Homo sapiens.  
 XX WO2003057006-A2.  
 PN 17-JUL-2003.  
 PD  
 XX 26-DEC-2002; 2002WO-US041582.  
 PF  
 XX 28-DEC-2001; 2001US-0346460P.  
 PR  
 XX (ABGE-) ABGENIX INC.  
 PA  
 XX Gudas J, Bar-Eli M;  
 XX WPI; 2003-577496/54.  
 DR N-PSDB; ADD05390.  
 DR

XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
 PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
 PT associated with melanoma, or increasing survival of an animal having a  
 PT metastatic tumor.

XX Claim 1; SEQ ID NO 13; 87pp; English.

XX The invention relates to a novel monoclonal antibody used for inhibiting  
 CC tumour growth in an animal. The tumour inhibition process comprises  
 CC selecting an animal in need of treatment for a tumour, providing a  
 CC monoclonal antibody comprising a heavy chain amino acid, where the  
 CC antibody consists of any one of 10 fully defined sequences of 117-123  
 CC amino acids given in the specification, and where the monoclonal antibody  
 CC binds MUC18, and contacting the tumour with the antibody resulting in  
 CC inhibited proliferation of the cells. The monoclonal antibody has  
 CC cytostatic and can be used in the production of a vaccine. The monoclonal  
 CC antibodies against the MUC18 antigen are useful for diagnosing and  
 CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or  
 CC tumour metastasis), inhibiting cell invasion associated with melanoma, or  
 CC increasing survival of an animal having a metastatic tumour. This  
 CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
 CC protein of the invention.

XX Sequence 117 AA;

Query Match 93.9%; Score 587; DB 7; Length 117;  
 Best Local Similarity 94.0%; Pred. No. 2.9e-42;  
 Matches 110; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60

Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60

Qy 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYICARGDGYKYWGQGLTVTVSS 117

Db 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYICAREGDGDFYWGQGLTVTVSS 117

RESULT 9

ID ADF09826

XX ADF09826 standard; protein; 117 AA.

XX ADF09826;

XX 12-FEB-2004 (first entry)

XX Human anti-MUC18 monoclonal antibody heavy chain #4.

XX cell proliferation inhibition; MUC18 tumour antigen;  
 KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
 KW carcinoma; cancer; malignancy; heavy chain; human.

XX Homo sapiens.

XX WO2003057837-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041580.

XX 28-DEC-2001; 2001US-0346414P.

XX (ABGE-) ABGENIX INC.

XX Gudas J;

XX WPI; 2003-598367/56.

XX N-PSDB; ADF09828.

XX Inhibiting cell proliferation associated with expression of MUC18 tumor  
 PT antigen, involves incubating and inhibiting cell by administering anti-  
 PT MUC18 monoclonal antibody.

XX

PS Claim 1; SEQ ID NO 13; 83pp; English.

XX The invention comprises a method for inhibiting cell proliferation  
 CC associated with expression of MUC18 tumour antigen. The method involves  
 CC administering anti-MUC18 monoclonal antibody. The method of the invention  
 CC is useful for inhibiting cell (e.g. melanoma or tumour cell)  
 CC proliferation associated with the expression of MUC18 tumour antigen. The method  
 CC is preferably useful for inhibiting tumour metastasis. The method  
 CC is useful for inhibiting cell proliferation in patients with tumours,  
 CC carcinomas, cancer and other malignancies. The present amino acid  
 CC sequence represents a heavy chain from an MUC18 tumour antigen-specific  
 CC monoclonal antibody.

XX Sequence 117 AA;

Query Match 93.9%; Score 587; DB 7; Length 117;  
 Best Local Similarity 94.0%; Pred. No. 2.9e-42;  
 Matches 110; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60

Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60

Qy 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYICARGDGYKYWGQGLTVTVSS 117

Db 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYICAREGDGDFYWGQGLTVTVSS 117

RESULT 10

ID ADF03968

XX ADF03968 standard; protein; 118 AA.

XX ADF03968;

XX 29-JUL-2004 (first entry)

XX Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 138.

XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KW cytostatic; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;  
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; heavy chain variable domain.

XX Unidentified.

XX WO2003048328-A2.

XX 12-JUN-2003.

XX 02-DEC-2002; 2002WO-US038550.

XX 03-DEC-2001; 2001US-0337275P.

XX (ABGE-) ABGENIX INC.

XX Gudas J, Foltz I, Handa M, Gallo M;

XX WPI; 2003-523295/49.

XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX Example 2; SEQ ID NO 138; 89pp; English.

XX The invention relates to a novel isolated monoclonal antibody (mab)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
 CC demonstrates cytostatic activity and may be useful for treating a tumour,

CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.

XX SQ Sequence 118 AA;  
Query Match 91.4%; Score 571.5; DB 7; Length 118;  
Best Local Similarity 94.1%; Pred. No. 6.1e-41;  
Matches 111; Conservative 1; Mismatches 5; Indels 1; Gaps 1;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYTHMSWIRQHPGKGLEWIGYIYSGSTY 60  
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYTHMSWIRQHPGKGLEWIGYIYSGSTY 60  
QY 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYICAR-GGDGYKYGQGTILVTYSS 117  
DB 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYICARYYGGSDYWGQGTILVTYSS 118

RESULT 11  
ADP03870  
ID ADP03870 standard; protein; 123 AA.  
XX AC ADP03870;  
XX DT 29-JUL-2004 (first entry)  
XX DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 10.  
XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
XX KW cytosstatic; colorectal neoplasm; renal cell carcinoma;  
XX KW cervical intraepithelial squamous neoplasia;  
XX KW cervical intraepithelial glandular neoplasia;  
XX KW gene therapy; murine; mouse; human; heavy chain variable domain.  
XX OS Unidentified.  
XX PN WO2003048328-A2.  
XX PD 12-JUN-2003.  
XX PF 02-DEC-2002; 2002WO-US038550.  
XX PR 03-DEC-2001; 2001US-0337275P.  
XX PA (ABGE-) ABGENIX INC.  
XX PI Gudas J, Foltz I, Handa M, Gallo M;  
XX DR WPI; 2003-523295/49.  
XX PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
XX PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
XX PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
XX PS Claim 1; SEQ ID NO 10; 89pp; English.

XX The invention relates to a novel isolated monoclonal antibody (mAb)  
XX comprising a heavy chain polypeptide and light chain polypeptide having a  
XX sequence chosen from one of 53 fully defined amino acid sequences given  
XX in the specification, where the antibody specifically binds carbonic  
XX anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
XX demonstrates cytostatic activity and may be useful for treating a tumour,  
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
XX cervical intraepithelial squamous and glandular neoplasia, oesophageal  
XX tumour or breast cancer, possibly via gene therapy. The current sequence  
XX is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
XX (heavy chain variable domain) protein of the invention. The protein was  
XX generated via the introduction of the human CA IX protein into a

CC transgenic mouse strain.  
XX SQ Sequence 123 AA;  
Query Match 91.4%; Score 571; DB 7; Length 123;  
Best Local Similarity 90.2%; Pred. No. 7e-41;  
Matches 111; Conservative 1; Mismatches 5; Indels 6; Gaps 1;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYTHMSWIRQHPGKGLEWIGYIYSGSTY 60  
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYTHMSWIRQHPGKGLEWIGYIYSGSTY 60  
QY 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYICARGGDGY-----KYWGQGTILVT 114  
DB 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYICARGGDGY-----KYWGQGTILVT 120  
QY 115 VSS 117  
DB 121 VSS 123  
RESULT 12  
ADP03974  
ID ADP03974 standard; protein; 120 AA.  
XX AC ADP03974;  
XX DT 29-JUL-2004 (first entry)  
XX DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 144.  
XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
XX KW cytosstatic; colorectal neoplasm; renal cell carcinoma;  
XX KW cervical intraepithelial squamous neoplasia;  
XX KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
XX KW gene therapy; murine; mouse; human; heavy chain variable domain.  
XX OS Unidentified.  
XX PN WO2003048328-A2.  
XX PD 12-JUN-2003.  
XX PF 02-DEC-2002; 2002WO-US038550.  
XX PR 03-DEC-2001; 2001US-0337275P.  
XX PA (ABGE-) ABGENIX INC.  
XX PI Gudas J, Foltz I, Handa M, Gallo M;  
XX DR WPI; 2003-523295/49.  
XX PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
XX PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
XX PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
XX PS Example 2; SEQ ID NO 144; 89pp; English.  
XX The invention relates to a novel isolated monoclonal antibody (mAb)  
XX comprising a heavy chain polypeptide and light chain polypeptide having a  
XX sequence chosen from one of 53 fully defined amino acid sequences given  
XX in the specification, where the antibody specifically binds carbonic  
XX anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
XX demonstrates cytostatic activity and may be useful for treating a tumour,  
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
XX cervical intraepithelial squamous and glandular neoplasia, oesophageal  
XX tumour or breast cancer, possibly via gene therapy. The current sequence  
XX is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
XX (heavy chain variable domain) protein of the invention. The protein was  
XX generated via the introduction of the human CA IX protein into a  
XX transgenic mouse strain.



SQ Sequence 120 AA;  
 Query Match 90.8%; Score 567.5; DB 7; Length 120;  
 Best Local Similarity 91.0%; Pred. No. 1.4e-40;  
 Matches 111; Conservative 2; Mismatches 2; Indels 7; Gaps 2;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKGLEWIGYIYSGSTY 60  
 Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKGLEWIGYIYSGSTY 60  
 Qy 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYKY-----WGQGLTVTV 115  
 Db 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCAR--DGYNWYFDFLWGRGLTVTV 118  
 Qy 116 SS 117  
 ||  
 Db 119 SS 120  
 ||

RESULT 13  
 ADP03873  
 ID ADP03873 standard; protein; 120 AA.  
 XX  
 AC ADP03873;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 13.  
 XX  
 KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KW cytosolic; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;  
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; heavy chain variable domain.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2003048328-A2.  
 XX  
 PD 12-JUN-2003.  
 XX  
 PF 02-DEC-2002; 2002WO-US038550.  
 XX  
 PR 03-DEC-2001; 2001US-0337275P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Gudas J, Foltz I, Handa M, Gallo M;  
 XX  
 DR WPI; 2003-523295/49.  
 XX  
 PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
 XX  
 PS Claim 1; SEQ ID NO 13; 89pp; English.  
 XX  
 CC The invention relates to a novel isolated monoclonal antibody (mAb)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
 CC demonstrates cytostatic activity and may be useful for treating a tumour,  
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumour or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
 CC (heavy chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.  
 XX  
 SQ Sequence 120 AA;

Query Match 90.8%; Score 567.5; DB 7; Length 120;  
 Best Local Similarity 91.0%; Pred. No. 1.4e-40;  
 Matches 111; Conservative 2; Mismatches 2; Indels 7; Gaps 2;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKGLEWIGYIYSGSTY 60  
 Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKGLEWIGYIYSGSTY 60  
 Qy 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYKY-----WGQGLTVTV 115  
 Db 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCAR--DGYNWYFDFLWGRGLTVTV 118  
 Qy 116 SS 117  
 ||  
 Db 119 SS 120  
 ||

RESULT 14  
 AAB62775  
 ID AAB62775 standard; protein; 120 AA.  
 XX  
 AC AAB62775;  
 XX  
 DT 03-APR-2001 (first entry)  
 XX  
 DE Human HIV-1 monoclonal antibody SEQ ID NO: 74.  
 XX  
 KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;  
 KW envelope glycoprotein; gp120; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200100678-A1.  
 XX  
 PD 04-JAN-2001.  
 XX  
 PF 23-JUN-2000; 2000WO-US017327.  
 XX  
 PR 30-JUN-1999; 99US-0141701P.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Watkins BA, Reitz MS;  
 XX  
 DR WPI; 2001-112438/12.  
 DR N-PSDB; AAF29076.  
 XX  
 PT Novel human monoclonal antibody immunoreactive with human  
 PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1  
 PT in biological sample and providing passive immunotherapy to HIV-1  
 PT infected mammal.  
 XX  
 PS Claim 1; Page 69; 81pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences for the  
 CC variable regions of human monoclonal antibodies which are immunoreactive  
 CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.  
 CC These can be used in diagnosis and therapy of HIV-1 infection  
 XX  
 SQ Sequence 120 AA;

Query Match 89.8%; Score 561; DB 4; Length 120;  
 Best Local Similarity 91.8%; Pred. No. 4.8e-40;  
 Matches 109; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKGLEWIGYIYSGSTY 60  
 Db 2 EVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKGLEWIGYIYSGSTY 61  
 Qy 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARG--GDGKYWGQGLTVTVSS 117  
 Db 62 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGVVVDWDFPWQGLTVTVSS 120

RESULT 15  
ADJ80377 standard; protein; 121 AA.  
XX AC ADJ80377;  
XX DT 06-MAY-2004 (first entry)  
XX DE Antibody variable heavy chain with homology to mouse anti-human antibody.  
XX KW hybrid antibody; antibody; framework region; homology; immunogenicity.  
XX OS Unidentified.  
XX PN WO2003048321-A2.  
XX PD 12-JUN-2003.  
XX PF 03-DEC-2002; 2002WO-US038450.  
XX PR 03-DEC-2001; 2001US-0336591P.  
XX PA (ALEX-) ALEXION PHARM INC.  
XX PI Rother R, Wu D;  
XX DR WPI; 2003-513753/48.  
XX PT Producing a hybrid antibody or hybrid antibody fragment by operatively  
PT linking the selected framework sequences to one or more complementarity  
PT determining regions of the initial antibody.  
XX  
XX Example 1; SEQ ID NO 137; 77pp; English.  
XX  
XX The invention relates to a method of producing a hybrid antibody or  
CC hybrid antibody fragment by: (i) providing an initial antibody having  
CC specificity for a target; (ii) determining the sequence of a variable  
CC region of the initial antibody; (iii) selecting a first component of the  
CC variable region consisting of FR1, FR2, FR3 and FR4; (iv) comparing the  
CC sequence of the first component to sequences contained in a reference  
CC database of antibody sequences or antibody fragment sequences from a  
CC target species; (v) selecting a sequence from an antibody in the database  
CC which demonstrates a high degree of homology to the first component; (vi)  
CC selecting a second component of the variable region which is different  
CC than the first component, the second component selected from the group  
CC consisting of FR1, FR2, FR3 and FR4; (vii) comparing the sequence of the  
CC second component to sequences contained in a reference database of  
CC antibody sequences or antibody fragment sequences from the target species  
CC; (viii) selecting a sequence from the database which demonstrates a high  
CC degree of homology to the second component and which is from a different  
CC antibody than the selected antibody; and (ix) operatively linking the  
CC selected framework sequences to one or more complementarity determining  
CC regions (CDRs) of the initial antibody to produce a hybrid antibody or  
CC hybrid antibody fragment. The method is useful for producing a hybrid  
CC antibody or hybrid antibody fragment (claimed). The antibody and  
CC fragments are useful for therapeutic and diagnostic purposes. The method  
CC uses entire framework regions from a single antibody variable heavy or  
CC variable light chain to receive the CDRs. This produces antibodies that  
CC are highly homologous and exhibit reduced immunogenicity while  
CC maintaining an optimum binding profile. This sequence represents an  
CC antibody variable heavy chain which has good homology to an initial  
CC murine anti-human mannose binding lectin antibody (ADJ80371). The  
CC sequence was used to generate a hybrid antibody of the invention.  
XX  
XX Sequence 121 AA;

Query Match 89.5%; Score 559.5; DB 7; Length 121;  
Best Local Similarity 89.3%; Pred. No. 6.5e-40;  
Matches 108; Conservative 3; Mismatches 5; Indels 5; Gaps 1;  
QY 2 VQLQESGPGLVKPSQTLSTCTVSGSISGSGYWNWIRQHPGKGLWIGIYVSGSTYY 61  
||||| :|||||

Db 1 VQLQESGPGLVKPSQTLSTCTVSGSISGSGYWNWIRQHPGKGLWIGIYVSGSTYY 60  
QY 62 NPSLKSRTIISVDTSKNQPSLKLSSVTAADTAVVYCARG-----GDGYKYWGQGLTAVTS 116  
Db 61 NPSLKSRTIISVDTSKNQPSLKLSSVTAADTAVVYCARGLKWGNHNFYDYWGQGLTAVTS 120  
QY 117 S 117  
Db 121 S 121

Search completed: November 9, 2005, 12:55:24  
Job time : 73.1353 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:29:55 ; Search time 18.1805 Seconds  
(without alignments)  
480.403 Million cell updates/sec

Title: US-10-660-357A-5

Perfect score: 625

Sequence: 1 QVQLQSGPGLVKPSQTL...ARGGDKYKMGQTLVTSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	543	86.9	119	3	US-09-025-769B-39
2	543	86.9	119	3	US-09-025-769B-65
3	543	86.9	119	4	US-09-490-070A-39
4	543	86.9	119	4	US-09-490-070A-65
5	543	86.9	119	4	US-09-490-153-39
6	543	86.9	119	4	US-09-490-153-65
7	543	86.9	119	4	US-09-490-324-39
8	543	86.9	119	4	US-09-490-324-65
9	535	85.6	119	1	US-08-360-125-5
10	535	85.6	119	2	US-08-450-578-5
11	535	85.6	119	2	US-09-017-628-5
12	535	85.6	119	2	US-09-014-880-5
13	535	85.6	119	4	US-08-450-363-5
14	535	85.6	119	4	US-09-467-903-5
15	532.5	85.2	122	1	US-08-360-125-11
16	532.5	85.2	122	2	US-08-450-578-11
17	532.5	85.2	122	2	US-09-017-628-11
18	532.5	85.2	122	2	US-09-014-880-11
19	532.5	85.2	122	4	US-08-450-363-11
20	532.5	85.2	122	4	US-09-467-903-11
21	532.5	85.2	473	3	US-09-049-672A-4
22	525.5	84.1	487	4	US-09-800-729-145
23	524.5	83.9	118	3	US-09-025-769B-145
24	524.5	83.9	118	4	US-09-490-070A-25
25	524.5	83.9	118	4	US-09-490-153-25
26	524.5	83.9	118	4	US-09-490-324-25
27	516	82.6	117	4	US-09-720-493-2

28	511	81.8	118	3	US-08-545-809A-116	Sequence 116, Appl
29	509.5	81.5	172	4	US-09-472-087-7	Sequence 7, Appli
30	509.5	81.5	172	4	US-09-472-087-86	Sequence 86, Appl
31	507.5	81.2	120	4	US-09-424-840B-20	Sequence 20, Appl
32	502.5	80.4	244	3	US-08-918-148-79	Sequence 79, Appl
33	502.5	80.4	244	4	US-09-138-091A-77	Sequence 77, Appl
34	501	80.2	142	2	US-08-480-774A-2	Sequence 2, Appli
35	491	78.6	118	3	US-08-545-809A-142	Sequence 142, App
36	489.5	78.3	278	3	US-09-260-527-3	Sequence 3, Appli
37	488.5	78.2	139	4	US-09-471-276-837	Sequence 837, App
38	479.5	76.7	98	1	US-08-478-039-75	Sequence 75, Appl
39	479.5	76.7	98	1	US-08-476-349A-75	Sequence 75, Appl
40	479	76.6	118	3	US-08-545-809A-123	Sequence 123, App
41	476	76.0	119	2	US-08-652-816A-10	Sequence 10, Appl
42	475	76.0	155	4	US-09-471-276-888	Sequence 888, App
43	473	75.7	116	3	US-08-545-809A-140	Sequence 140, App
44	472	75.5	117	4	US-09-232-290-47	Sequence 47, Appl
45	470.5	75.3	150	4	US-09-582-337-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1  
US-09-025-769B-39  
; Sequence 39, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-025-769B-39

Query Match 86.9%; Score 543; DB 3; Length 119;  
Best Local Similarity 90.1%; Pred. No. 7e-47;  
Matches 109; Conservative 3; Mismatches 3; Indels 6; Gaps 3;

```
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYTHWSWIRQHPGKGLEWIGYIYSGSTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISS--YYMSWIRQPPGKGLEWIGYIYSGSTN 58
QY 61 YNPISLSRVITISVDTSKNQFSLKSSVTAADTAIVYCAR--GGDGY---KYWGQGLTVTVS 116
Db 59 YNPISLSRVITISVDTSKNQFSLKSSVTAADTAIVYCARWGGDGFYAMDYWGQGLTVTVS 118
QY 117 $ 117
Db 119 $ 119

RESULT 2
US-09-025-769B-65
; Sequence 65, Application US/09025769B
; Patent No. 630064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-65

Query Match 86.9%; Score 543; DB 3; Length 119;
Best Local Similarity 90.1%; Pred. No. 7e-47;
Matches 109; Conservative 3; Mismatches 3; Indels 6; Gaps 3;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYTHWSWIRQHPGKGLEWIGYIYSGSTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISS--YYMSWIRQPPGKGLEWIGYIYSGSTN 58
QY 61 YNPISLSRVITISVDTSKNQFSLKSSVTAADTAIVYCAR--GGDGY---KYWGQGLTVTVS 116
Db 59 YNPISLSRVITISVDTSKNQFSLKSSVTAADTAIVYCARWGGDGFYAMDYWGQGLTVTVS 118
QY 117 $ 117
Db 119 $ 119

RESULT 4
US-09-490-070A-65
; Sequence 65, Application US/09490070A
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Db 119 $ 119

RESULT 3
US-09-490-070A-39
; Sequence 39, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-070A-39

Query Match 86.9%; Score 543; DB 4; Length 119;
Best Local Similarity 90.1%; Pred. No. 7e-47;
Matches 109; Conservative 3; Mismatches 3; Indels 6; Gaps 3;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYTHWSWIRQHPGKGLEWIGYIYSGSTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISS--YYMSWIRQPPGKGLEWIGYIYSGSTN 58
QY 61 YNPISLSRVITISVDTSKNQFSLKSSVTAADTAIVYCAR--GGDGY---KYWGQGLTVTVS 116
Db 59 YNPISLSRVITISVDTSKNQFSLKSSVTAADTAIVYCARWGGDGFYAMDYWGQGLTVTVS 118
QY 117 $ 117
Db 119 $ 119

RESULT 4
US-09-490-070A-65
; Sequence 65, Application US/09490070A
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; STATE: New York
; COUNTRY: USA
; ZIP: 10021
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9090
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-153-65

Query Match 86.9%; Score 543; DB 4; Length 119;
Best Local Similarity 90.1%; Pred. No. 7e-47;
Matches 109; Conservative 3; Mismatches 3; Indels 6; Gaps 3;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYHWSWIRQHPGKLEWIGIYYSGSIY 60
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISS--YYMSWIRQPPGKLEWIGIYYSGSTN 58
QY 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAIVYCAR-GGDGY--KYWGQGTILVTVS 116
DB 59 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAIVYCARWGDDGFYAMDYWGQGTILVTVS 118
QY 117 S 117
DB 119 S 119

RESULT 7
US-09-490-324-39
; Sequence 39, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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;
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-324-39

Query Match 86.9%; Score 543; DB 4; Length 119;
Best Local Similarity 90.1%; Pred. No. 7e-47;
Matches 109; Conservative 3; Mismatches 3; Indels 6; Gaps 3;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYHWSWIRQHPGKLEWIGIYYSGSIY 60
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISS--YYMSWIRQPPGKLEWIGIYYSGSTN 58
QY 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAIVYCAR-GGDGY--KYWGQGTILVTVS 116
DB 59 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAIVYCARWGDDGFYAMDYWGQGTILVTVS 118
QY 117 S 117
DB 119 S 119

RESULT 8
US-09-490-324-65
; Sequence 65, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
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;; FILING DATE: 18-FEB-1998  
;; APPLICATION NUMBER: EP 95 11 3021.0  
;; FILING DATE: 18-AUG-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: James F. Haley, Jr., Esq.  
;; REGISTRATION NUMBER: 27,794  
;; REFERENCE/DOCKET NUMBER: MORPHO/5  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212)596-9000  
;; TELEFAX: (212)596-9090  
;; INFORMATION FOR SEQ ID NO: 65:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 119 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 65:  
US-09-490-324-65  
  
Query Match 86.9%; Score 543; DB 4; Length 119;  
Best Local Similarity 90.1%; Pred. No. 7e-47;  
Matches 109; Conservative 3; Mismatches 3; Indels 6; Gaps 3;  
  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPKGLGWIGYIYSGSTY 60  
Db |||||  
1 QVQLQESGPGLVKPSQTLSTCTVSGGSISS--YYSWIRQHPKGLGWIGYIYSGSTN 58  
QY 61 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAVYYCAR--GGDGY---KYMGGQGLTVTVSS 116  
Db |||||  
59 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAVYYCARWGGDGYFYAMDYWGQGLTVTVSS 118  
  
QY 117 S 117  
Db 119 S 119  
  
RESULT 9  
US-08-360-125-5  
; Sequence 5, Application US/08360125  
; Patent No. 5767246  
; GENERAL INFORMATION:  
; APPLICANT: Saiko HOSOKAWA  
; APPLICANT: Toshiaki TAGAWA  
; APPLICANT: Yoko HIRAKAWA  
; APPLICANT: No. 5767246ihiko ITO  
; APPLICANT: Kazuhiro NAGAIKE  
; TITLE OF INVENTION: Human Monoclonal Antibody  
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
; TITLE OF INVENTION: Cell Membrane  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/360,125  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/905,534  
; FILING DATE: June 29, 1992  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.

;; REGISTRATION NUMBER: 33,367  
;; REFERENCE/DOCKET NUMBER:  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-8850  
;; TELEFAX:  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 119 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; HYPOTHETICAL:  
;; ANTI-SENSE:  
;; FRAGMENT TYPE:  
;; ORIGINAL SOURCE:  
;; ORGANISM:  
;; STRAIN:  
;; INDIVIDUAL ISOLATE:  
;; DEVELOPMENTAL STAGE:  
;; HAPLOTYPE:  
;; TISSUE TYPE:  
;; CELL TYPE: Hybridoma producing human  
;; CELL TYPE: antibody GAH  
;; CELL LINE:  
;; ORGANELLER:  
;; IMMEDIATE SOURCE:  
;; LIBRARY:  
;; CLONE:  
;; POSITION IN GENOME:  
;; CHROMOSOME/SEGMENT:  
;; MAP POSITION:  
;; UNITS:  
;; FEATURE:  
;; NAME/KEY:  
;; LOCATION:  
;; IDENTIFICATION METHOD:  
;; OTHER INFORMATION:  
;; PUBLICATION INFORMATION:  
;; AUTHORS:  
;; TITLE:  
;; JOURNAL:  
;; VOLUME:  
;; ISSUE:  
;; PAGES:  
;; DATE:  
;; DOCUMENT NUMBER:  
;; FILING DATE:  
;; PUBLICATION DATE:  
;; RELEVANT RESIDUES IN SEQ ID NO:  
US-08-360-125-5  
  
Query Match 85.6%; Score 535; DB 1; Length 119;  
Best Local Similarity 86.6%; Pred. No. 4.4e-46;  
Matches 103; Conservative 7; Mismatches 7; Indels 2; Gaps 1;  
  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPKGLGWIGYIYSGSTY 60  
Db |||||  
1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSCGFYNNWIRQHPKGLGWIGYIYSGSTY 60  
QY 61 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAVYYCARGG--DGKYMGGQGLTVTVSS 117  
Db |||||  
61 YNPSLKSRTVISLDTSKSQFSLKSLTADTAVYYCARSTRLRGADYWGQGLTVTVSS 119  
  
RESULT 10  
US-08-450-578-5  
; Sequence 5, Application US/08450578  
; Patent No. 5837845  
; GENERAL INFORMATION:  
; APPLICANT: Saiko HOSOKAWA  
; APPLICANT: Toshiaki TAGAWA

APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 5837845Ihiko ITO  
APPLICANT: Kazuhiro NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
TITLE OF INVENTION: Cell Membrane  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,578  
FILING DATE: May 25, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human  
CELL TYPE: antibody GAH  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:

JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-450-578-5  
Query Match 85.6%; Score 535; DB 2; Length 119;  
Best Local Similarity 86.6%; Pred. No. 4.4e-46;  
Matches 103; Conservative 7; Mismatches 7; Indels 2; Gaps 1;  
QY 1 QVQLQESGPGLVKPSQTLSTLTCTVSGGSISSGTYHMSWIRQHPGKLEWIGIYYSGSY 60  
Db 1 QVQLQESGPGLVKPSQTLSTLTCTVSGGSISSGTYHMSWIRQHPGKLEWIGIYYSGSY 60  
QY 61 YNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVVYCARGG--DGKYWGQGTLTVTSS 117  
Db 61 YNP SLKSRVTISLDTSKSQFSLKLSLTAADTAVVYCARSTRLRGADYWGQGTMTVTSS 119  
RESULT 11  
US-09-017-628-5  
Sequence 5, Application US/09017628  
Patent No. 5990287  
GENERAL INFORMATION:  
APPLICANT: HOSOKAWA, Saiko  
APPLICANT: TAGAWA, Toshiaki  
APPLICANT: HIRAKAWA, Yoko  
APPLICANT: ITO, No. 5990287ihiko  
APPLICANT: NAGAIKE, Kazuhiro  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO  
TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE  
FILE REFERENCE: 177/527361KH  
CURRENT APPLICATION NUMBER: US/09/017,628  
CURRENT FILING DATE: 1998-02-02  
EARLIER APPLICATION NUMBER: 08/360,125  
EARLIER FILING DATE: 1994-12-20  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 119  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Hybridoma producing human antibody GAH  
US-09-017-628-5  
Query Match 85.6%; Score 535; DB 2; Length 119;  
Best Local Similarity 86.6%; Pred. No. 4.4e-46;  
Matches 103; Conservative 7; Mismatches 7; Indels 2; Gaps 1;  
QY 1 QVQLQESGPGLVKPSQTLSTLTCTVSGGSISSGTYHMSWIRQHPGKLEWIGIYYSGSY 60  
Db 1 QVQLQESGPGLVKPSQTLSTLTCTVSGGSISSGTYHMSWIRQHPGKLEWIGIYYSGSY 60  
QY 61 YNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVVYCARGG--DGKYWGQGTLTVTSS 117  
Db 61 YNP SLKSRVTISLDTSKSQFSLKLSLTAADTAVVYCARSTRLRGADYWGQGTMTVTSS 119  
RESULT 12  
US-09-014-880-5  
Sequence 5, Application US/09014880  
Patent No. 5990297  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA et al.  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY  
TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE  
NUMBER OF SEQUENCES: 42



; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
; STREET: 2033 K Street, N.W., #800  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/014,880  
; FILING DATE: January 28, 1998  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/450,578  
; FILING DATE: May 25, 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/360,125  
; FILING DATE: December 20, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/905,534  
; FILING DATE: June 29, 1992  
; NAME: Warren M. Cheek, Jr.  
; ATTORNEY/AGENT INFORMATION:  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-721-8200  
; TELEFAX: 202-721-8250  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; CELL TYPE: Hybridoma producing human  
; CELL TYPE: antibody GAH  
; US-09-014-880-5

Query Match 85.6%; Score 535; DB 2; Length 119;  
Best Local Similarity 86.6%; Fred. No. 4.4e-46;  
Matches 103; Conservative 7; Mismatches 7; Indels 2; Gaps 1;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYHWSWIRHPGKLEWIGYIYSGSTY 60  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYHWSWIRHPGKLEWIGYIYSGSTY 60

Qy 61 YNPSLKSRVTISVTSKRNQPSKLKLSVTAADTAIVYCARGG--DGYKYWGQGTLLTVSS 117  
Db 61 YNPSLKSRVTISLDTSKSQPSLKLSSLTAADTAIVYCARSTRLRGADYWGQGTWTVSS 119

RESULT 13  
US-08-450-363-5  
; Sequence 5, Application US/08450363  
; Patent No. 6436434  
; GENERAL INFORMATION:  
; APPLICANT: Saiko HOSOKAWA  
; APPLICANT: Toshiaki TAGAWA  
; APPLICANT: Yoko HIRAKAWA  
; APPLICANT: No. 6436434hiho ITO  
; APPLICANT: Kazuhiro NAGAIKE  
; TITLE OF INVENTION: Human Monoclonal Antibody  
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
; TITLE OF INVENTION: Cell Membrane  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/450,363  
; FILING DATE: May 25, 1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/360,125  
; FILING DATE: December 20, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/905,534  
; FILING DATE: June 29, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL:  
; ANTI-SENSE:  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM:  
; STRAIN:  
; INDIVIDUAL ISOLATE:  
; DEVELOPMENTAL STAGE:  
; HAPLOTYPE:  
; TISSUE TYPE:  
; CELL TYPE: Hybridoma producing human  
; CELL TYPE: antibody GAH  
; CELL LINE:  
; ORGANELLE:  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE:  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT:  
; MAP POSITION:  
; UNITS:  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
; PUBLICATION INFORMATION:  
; AUTHORS:  
; TITLE:  
; JOURNAL:  
; VOLUME:  
; ISSUE:  
; PAGES:  
; DATE:  
; DOCUMENT NUMBER:  
; FILING DATE:  
; PUBLICATION DATE:



COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/360,125  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:

INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human antibody 1-3-1  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:

US-08-360-125-11

Query Match 85.2%; Score 532.5; DB 1; Length 122;  
Best Local Similarity 86.1%; Pred. No. 8e-46;  
Matches 105; Conservative 4; Mismatches 8; Indels 5; Gaps 2;

Qy 1 QVQLQESGPGLVKPSQTL:SLTCTVSGGSISSGTYHMSWIROHPKGLIEWICVYYSGSTY 60  
Db 1 QVQLQESGPGLVKPSQTL:SLTCTVSGGSISSGTYHMSWIROHPKGLIEWICVYYSGSTY 60  
Qy 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGG-DGYKY----WGQGTLLTV 115  
Db 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGG-DGYKY----WGQGTLLTV 120  
Qy 116 SS 117  
Db 121 SS 122

Search completed: November 9, 2005, 11:46:37  
Job time : 19.1805 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2005, 11:40:37 ; Search time 65 Seconds  
(without alignments)  
753.137 Million cell updates/sec

Title: US-10-660-357A-5

Perfect score: 625

Sequence: 1 QVQLQSGPGLVKPSQTL...ARGGDGYKYGQGLTVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	625	100.0	117	14 US-10-330-613-5	Sequence 5, Appli
2	625	100.0	117	14 US-10-330-530-5	Sequence 5, Appli
3	625	100.0	117	16 US-10-660-357-5	Sequence 5, Appli
4	604	96.6	117	14 US-10-330-613-33	Sequence 33, Appli
5	604	96.6	117	14 US-10-330-530-33	Sequence 33, Appli
6	604	96.6	117	16 US-10-660-357-33	Sequence 33, Appli
7	587	93.9	117	14 US-10-330-613-13	Sequence 13, Appli
8	587	93.9	117	14 US-10-330-530-13	Sequence 13, Appli
9	587	93.9	117	16 US-10-660-357-13	Sequence 13, Appli
10	571.5	91.4	118	15 US-10-309-762-138	Sequence 138, Appli
11	571	91.4	123	15 US-10-309-762-10	Sequence 10, Appli

12	567.5	90.8	120	15 US-10-309-762-13	Sequence 13, Appli
13	567.5	90.8	120	15 US-10-309-762-144	Sequence 144, Appli
14	565.5	90.5	125	17 US-10-805-177-53	Sequence 53, Appli
15	564.5	90.3	122	18 US-10-984-960A-20	Sequence 20, Appli
16	564.5	90.3	149	17 US-10-910-901-22	Sequence 22, Appli
17	559.5	89.5	121	15 US-10-308-817-137	Sequence 137, Appli
18	559.5	89.5	121	15 US-10-453-698-137	Sequence 137, Appli
19	559.5	89.5	122	18 US-10-984-960A-56	Sequence 56, Appli
20	559	89.4	119	15 US-10-309-762-140	Sequence 140, Appli
21	556.5	89.0	120	17 US-10-706-689-40	Sequence 40, Appli
22	556.5	89.0	120	18 US-10-988-360-40	Sequence 40, Appli
23	556.5	89.0	124	15 US-10-309-762-75	Sequence 75, Appli
24	556.5	89.0	143	15 US-10-309-762-96	Sequence 96, Appli
25	555.5	88.9	110	15 US-10-309-762-74	Sequence 74, Appli
26	555.5	88.9	122	15 US-10-309-762-147	Sequence 147, Appli
27	555	88.8	121	15 US-10-309-762-151	Sequence 151, Appli
28	555	88.8	123	15 US-10-309-762-9	Sequence 9, Appli
29	553	88.5	125	15 US-10-309-762-8	Sequence 8, Appli
30	553	88.5	125	15 US-10-309-762-16	Sequence 16, Appli
31	552.5	88.4	122	15 US-10-309-762-15	Sequence 15, Appli
32	552	88.3	125	15 US-10-309-762-11	Sequence 11, Appli
33	552	88.3	129	16 US-10-312-316-48	Sequence 48, Appli
34	552	88.3	148	17 US-10-893-576-31	Sequence 31, Appli
35	552	88.3	480	17 US-10-910-901-6	Sequence 6, Appli
36	551	88.2	123	15 US-10-309-762-12	Sequence 12, Appli
37	551	88.2	142	17 US-10-893-576-37	Sequence 37, Appli
38	550.5	88.1	110	17 US-10-727-155-272	Sequence 272, Appli
39	550.5	88.1	136	20 US-11-131-648-15	Sequence 15, Appli
40	550.5	88.1	136	20 US-11-131-648-39	Sequence 39, Appli
41	550	88.0	121	15 US-10-309-762-152	Sequence 152, Appli
42	550	88.0	253	10 US-09-880-748-1619	Sequence 1619, Ap
43	550	88.0	253	15 US-10-293-418-1619	Sequence 1619, Ap
44	549.5	87.9	252	10 US-09-880-748-1994	Sequence 1994, Ap
45	549.5	87.9	252	15 US-10-293-418-1994	Sequence 1994, Ap

#### ALIGNMENTS

RESULT 1  
US-10-330-613-5  
; Sequence 5, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; PRIOR FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-5

Query Match 100.0%; Score 625; DB 14; Length 117;  
Best Local Similarity 100.0%; Pred. No. 1.7e-47;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSGPLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKLEWIGYIYSGSTY 60  
Db 1 QVQLQSGPLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKLEWIGYIYSGSTY 60  
QY 61 YNPPLSKSRVTISVDTSKNQFSLKLSVTAADTAVYVCARGDGYKYGQGLTVTVSS 117  
Db 61 YNPPLSKSRVTISVDTSKNQFSLKLSVTAADTAVYVCARGDGYKYGQGLTVTVSS 117

RESULT 2

```
US-10-330-530-5
; Sequence 5, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-5

Query Match      100.0%; Score 625; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-47;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYHWSWIRQHPGKGLEWIGYIYSGSTY 60
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYHWSWIRQHPGKGLEWIGYIYSGSTY 60

QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYKYWGQGLTVVSS 117
DB 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYKYWGQGLTVVSS 117

RESULT 3
US-10-660-357-5
; Sequence 5, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-5

Query Match      100.0%; Score 625; DB 16; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-47;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYHWSWIRQHPGKGLEWIGYIYSGSTY 60
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYHWSWIRQHPGKGLEWIGYIYSGSTY 60

QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYKYWGQGLTVVSS 117
DB 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYKYWGQGLTVVSS 117

RESULT 4
US-10-330-613-33
; Sequence 33, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-33

Query Match      96.6%; Score 604; DB 14; Length 117;
Best Local Similarity 94.0%; Pred. No. 1.2e-45;
Matches 110; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYHWSWIRQHPGKGLEWIGYIYSGSTY 60
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYHWSWIRQHPGKGLEWIGYIYSGSTY 60

QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYKYWGQGLTVVSS 117
DB 61 HNPPLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYKYWGQGLTVVSS 117

RESULT 5
US-10-330-530-33
; Sequence 33, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-33

Query Match      96.6%; Score 604; DB 14; Length 117;
Best Local Similarity 94.0%; Pred. No. 1.2e-45;
Matches 110; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYHWSWIRQHPGKGLEWIGYIYSGSTY 60
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYHWSWIRQHPGKGLEWIGYIYSGSTY 60

QY 61 YNPPLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYKYWGQGLTVVSS 117
DB 61 HNPPLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYKYWGQGLTVVSS 117

RESULT 6
US-10-660-357-33
; Sequence 33, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-33

Query Match      96.6%; Score 604; DB 14; Length 117;
Best Local Similarity 94.0%; Pred. No. 1.2e-45;
Matches 110; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYHWSWIRQHPGKGLEWIGYIYSGSTY 60
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYHWSWIRQHPGKGLEWIGYIYSGSTY 60

QY 61 YNPPLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYKYWGQGLTVVSS 117
DB 61 HNPPLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYKYWGQGLTVVSS 117
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; PRIOR FILING DATE: 2002-12-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-660-357-33

Query Match 96.6%; Score 604; DB 16; Length 117;  
Best Local Similarity 94.0%; Pred. No. 1.2e-45;  
Matches 110; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60  
QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYTCARGDGYKYWGQGLTVTVSS 117  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 HNPSLKSRITISVDTSKNQFSLKSSVTAADTAIVYTCARGDGYKYWGQGLTVTVSS 117

RESULT 7  
US-10-330-613-13  
; Sequence 13, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-13

Query Match 93.9%; Score 587; DB 14; Length 117;  
Best Local Similarity 94.0%; Pred. No. 3.8e-44;  
Matches 110; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60  
QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYTCARGDGYKYWGQGLTVTVSS 117  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYTCARGDGYKYWGQGLTVTVSS 117

RESULT 8  
US-10-330-530-13  
; Sequence 13, Application US/10330530  
; Publication No. US20030152514A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES  
; FILE REFERENCE: ABGENIX.031A  
; CURRENT APPLICATION NUMBER: US/10/330,530  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: US 60/346414  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo Sapiens

US-10-330-530-13

Query Match 93.9%; Score 587; DB 14; Length 117;  
Best Local Similarity 94.0%; Pred. No. 3.8e-44;  
Matches 110; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60  
QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYTCARGDGYKYWGQGLTVTVSS 117  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYTCARGDGYKYWGQGLTVTVSS 117

RESULT 9  
US-10-660-357-13  
; Sequence 13, Application US/10660357  
; Publication No. US20040115205A1  
; GENERAL INFORMATION:  
; APPLICANT: Bar-Eli, Menashe  
; APPLICANT: Green, Lary L.  
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18  
; FILE REFERENCE: ABGENIX.030C1  
; CURRENT APPLICATION NUMBER: US/10/660,357  
; CURRENT FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 10/330,580  
; PRIOR FILING DATE: 2002-12-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-660-357-13

Query Match 93.9%; Score 587; DB 16; Length 117;  
Best Local Similarity 94.0%; Pred. No. 3.8e-44;  
Matches 110; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60  
QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYTCARGDGYKYWGQGLTVTVSS 117  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYTCARGDGYKYWGQGLTVTVSS 117

RESULT 10  
US-10-309-762-138  
; Sequence 138, Application US/10309762  
; Publication No. US20040018198A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; APPLICANT: Foltz, Ian  
; APPLICANT: Handa, Masahisa  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
; FILE REFERENCE: ABGENIX.027A  
; CURRENT APPLICATION NUMBER: US/10/309,762  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/337275  
; PRIOR FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 138  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-309-762-138

```
Query Match          91.4%; Score 571.5; DB 15; Length 118;
Best Local Similarity 94.1%; Pred. No. 8.8e-43;
Matches 111; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYHWSWIRQHPGKGLEWIGYIYSGSTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYHWSWIRQHPGKGLEWIGYIYSGSTY 60

QY 61 YNPSLKSRVTISVDTSKNQFSLKSLSSVTAADTAVYYCAR--GGDGYKYWGQGLTLTVSS 117
Db 61 YNPSLKSRVTISVDTSKNQFSLKSLSSVTAADTAVYYCARYGSGSDYWGQGLTLTVSS 118

RESULT 11
US-10-309-762-10
; Sequence 10, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-10

Query Match          91.4%; Score 571; DB 15; Length 123;
Best Local Similarity 90.2%; Pred. No. 1e-42;
Matches 111; Conservative 1; Mismatches 5; Indels 6; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYHWSWIRQHPGKGLEWIGYIYSGSTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYHWSWIRQHPGKGLEWIGYIYSGSTY 60

QY 61 YNPSLKSRVTISVDTSKNQFSLKSLSSVTAADTAVYYCARGGDGY-----KYWGQGLTLTV 114
Db 61 YNPSLKSRVTISVDTSKNQFSLKSLSSVTAADTAVYYCARAGKYGSGSYLDYWGQGLTLTV 120

QY 115 VSS 117
Db 121 VSS 123

RESULT 12
US-10-309-762-13
; Sequence 13, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
```

```
; SEQ ID NO 13
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-13

Query Match          90.8%; Score 567.5; DB 15; Length 120;
Best Local Similarity 91.0%; Pred. No. 2e-42; 2; Mismatches 2; Indels 7; Gaps 2;
Matches 111; Conservative 2; Mismatches 2; Indels 7; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYHWSWIRQHPGKGLEWIGYIYSGSTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYHWSWIRQHPGKGLEWIGYIYSGSTY 60

QY 61 YNPSLKSRVTISVDTSKNQFSLKSLSSVTAADTAVYYCARGGDGYKY-----WGQGLTLTV 115
Db 61 YNPSLKSRVTISVDTSKNQFSLKSLSSVTAADTAVYYCAR--DGYNWYFDLWGRGTLTV 118

QY 116 SS 117
Db 119 SS 120

RESULT 13
US-10-309-762-144
; Sequence 144, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-144

Query Match          90.8%; Score 567.5; DB 15; Length 120;
Best Local Similarity 91.0%; Pred. No. 2e-42; 2; Mismatches 2; Indels 7; Gaps 2;
Matches 111; Conservative 2; Mismatches 2; Indels 7; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYHWSWIRQHPGKGLEWIGYIYSGSTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYHWSWIRQHPGKGLEWIGYIYSGSTY 60

QY 61 YNPSLKSRVTISVDTSKNQFSLKSLSSVTAADTAVYYCARGGDGYKY-----WGQGLTLTV 115
Db 61 YNPSLKSRVTISVDTSKNQFSLKSLSSVTAADTAVYYCAR--DGYNWYFDLWGRGTLTV 118

QY 116 SS 117
Db 119 SS 120

RESULT 14
US-10-805-177-53
; Sequence 53, Application US/10805177
; Publication No. US2005008449A1
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Chen, Francine
; APPLICANT: Bezabeh, Binyam
; APPLICANT: Foltz, Ian
```



```
; APPLICANT: Tse, Kam Fai
; APPLICANT: Jeffers, Michael
; APPLICANT: Mesri, Mehdi
; APPLICANT: Starling, Gary
; APPLICANT: Mezes, Peter
; APPLICANT: Khrantsov, Nikolai
; TITLE OF INVENTION: ANTIBODIES AGAINST T CELL IMMUNOGLOBULIN
; FILE REFERENCE: ABXCUR.006A
; CURRENT APPLICATION NUMBER: US/10/805,177
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/456,652
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-805-177-53
```

```
Query Match          90.5%; Score 565.5; DB 17; Length 125;
Best Local Similarity 87.9%; Pred. No. 3.2e-42;
Matches 109; Conservative 3; Mismatches 5; Indels 7; Gaps 1;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60

Qy 61 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAVYVCARGD-----DGKYWGQGLTV 113
Db 61 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAVYVCARNNNSSWYNNFDYWGQGLTV 120

Qy 114 TVSS 117
Db 121 TVSS 124
```

```
RESULT 15
US-10-984-960A-20
; Sequence 20, Application US/10984960A
; Publication No. US20050142137A1
; GENERAL INFORMATION:
; APPLICANT: Gallo, Michael
; APPLICANT: Chui, Daniel
; APPLICANT: Zhong, Haihong
; APPLICANT: Ara, Gulshan
; APPLICANT: LaRoche, William J.
; TITLE OF INVENTION: ANTIBODIES AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR
; FILE REFERENCE: Cura 970
; CURRENT APPLICATION NUMBER: US/10/984,960A
; CURRENT FILING DATE: 2004-11-08
; PRIOR APPLICATION NUMBER: 60/518,275
; PRIOR FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 20
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-984-960A-20
```

```
Query Match          90.3%; Score 564.5; DB 18; Length 122;
Best Local Similarity 89.3%; Pred. No. 3.8e-42;
Matches 109; Conservative 4; Mismatches 4; Indels 5; Gaps 1;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTY 60

Qy 61 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAVYVCARGD-----GYKYWGQGLTV 115
Db 61 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAVFYCAREGEYDEGGFDYWGQGLTV 120
```

Qy 116 SS 117  
Db 121 SS 122

Search completed: November 9, 2005, 12:42:58  
Job time : 66 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 12:25:58 ; Search time 12.609 Seconds  
(without alignments)  
892.802 Million cell updates/sec

Title: US-10-660-357A-5

Perfect score: 625  
Sequence: 1 QVQLQSGGPGLVKPSOTLSL.....ARGGDGYKYGQGLTVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	536	85.8	147	2 S13519	Ig heavy chain V r
2	527	84.3	140	2 I37782	Ig variable region
3	523	83.7	130	2 S31590	Ig heavy chain V r
4	522	83.5	116	2 S37456	Ig mu chain - huma
5	519	83.0	135	2 S78051	Ig heavy chain pre
6	516	82.6	121	2 S44113	Ig heavy chain V r
7	511.5	81.8	130	2 S30534	Ig heavy chain V r
8	511	81.8	99	2 S26801	Ig heavy chain V r
9	511	81.8	155	2 S31511	Ig heavy chain - h
10	509	81.4	155	2 S31512	Ig heavy chain - h
11	503.5	80.6	139	2 S31586	Ig heavy chain V r
12	503	80.5	128	2 S31514	Ig heavy chain - h
13	502	80.3	99	2 S26803	Ig heavy chain V r
14	497	79.5	99	2 S26802	Ig heavy chain V r
15	496.5	79.4	129	2 S44114	Ig heavy chain V r
16	491.5	78.6	122	2 S69912	Ig heavy chain V r
17	491	78.6	118	2 A26340	Ig V-D-J region (N
18	489	78.2	123	2 S30530	Ig heavy chain pre
19	489	78.2	146	2 S09711	Ig heavy chain V r
20	487.5	78.0	137	2 S31676	Ig heavy chain V r
21	487	77.9	146	2 S09710	Ig heavy chain V r
22	482	77.1	139	2 S31696	Ig heavy chain V r
23	480.5	76.9	145	2 S78055	Ig heavy chain pre
24	480	76.8	105	2 S44125	Ig lambda chain v
25	479	76.6	99	2 S12418	Ig heavy chain V r
26	479	76.6	140	2 A49045	Ig heavy chain V r
27	478.5	76.6	137	2 S31585	Ig heavy chain V r
28	476	76.2	99	2 S26807	Ig heavy chain V r
29	476	76.2	135	2 S31604	Ig heavy chain V r

30 475 76.0 127 2 S19668 Ig heavy chain V r  
31 474.5 75.9 140 2 S78052 Ig heavy chain pre  
32 474 75.8 97 2 S26906 Ig heavy chain V r  
33 473 75.7 99 2 S12412 Ig heavy chain V r  
34 473 75.7 116 2 B26340 Ig heavy chain pre  
35 472.5 75.6 118 2 S20780 Ig heavy chain V r  
36 472 75.5 97 2 S12416 Ig heavy chain V r  
37 471.5 75.4 110 2 S44110 Ig heavy chain V-D  
38 471.5 75.4 117 2 E34964 Ig heavy chain pre  
39 471 75.4 99 2 S26899 Ig heavy chain V r  
40 471 75.4 120 2 P70370 Ig mu chain precu  
41 470 75.2 99 2 S26800 Ig heavy chain V r  
42 470 75.2 124 2 S31684 Ig heavy chain V r  
43 468 74.9 140 2 A24770 hypothetical hybri  
44 465.5 74.5 118 2 S24443 Ig heavy chain V r  
45 465 74.4 97 2 P10118 Ig heavy chain V-I

ALIGNMENTS

RESULT 1

S13519  
Ig heavy chain V region precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S13519  
R;Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.  
Nucleic Acids Res. 19, 673, 1991  
A;Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked  
A;Reference number: S13519; MUID:91187691; PMID:2011536  
A;Accession: S13519  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-147 <MOR>  
A;Cross-references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;41-125/Domain: immunoglobulin homology <IMM>

Query Match 85.8%; Score 536; DB 2; Length 147;  
Best Local Similarity 86.0%; Pred. No. 7e-40;  
Matches 104; Conservative 6; Mismatches 7; Indels 4; Gaps 1;  
  
QY 1 QVQLQSGGPGLVKPSOTLSLCTVSGGSISSTGYHMSWIRQHPGKLEWIGYIYSGSTY 60  
Db 27 QQLQLQSGGPGLVKPSOTLSLCTVSGGSISSTGYHMSWIRQHPGKLEWIGYIYSGSTY 86  
  
QY 61 YNPGLSKSRVTISVDTSKNQFSLKLSSTVTAADTAVYYCARPLLFGLFDYWGQGLTVTVS 116  
Db 87 YNPGLSKSRVTISVDTSKNQFSLKLSSTVTAADTAVYYCARPLLFGLFDYWGQGLTVTVS 146  
  
QY 117 S 117  
Db 147 S 147

RESULT 2

I37782  
Ig variable region (VDJ) (clone T23-9) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999  
C;Accession: I37782; S25476  
R;Demaïson, C.; Chastagne, P.; These, J.; Zouali, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994  
A;Title: Somatic diversification in the heavy chain variable region genes expressed by  
A;Reference number: A36876; MUID:94119917; PMID:8290556  
A;Accession: I37782  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-140 <RES>  
A;Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583  
C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;46-128/Domain: immunoglobulin homology <IMM>

Query Match 84.3%; Score 527; DB 2; Length 140;  
Best Local Similarity 86.2%; Pred. No. 4.1e-39;  
Matches 106; Conservative 3; Mismatches 6; Indels 8; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHNSWIRQHPGKLEWIGYIYSGSY 60  
DB 20 QVQLQESGPGLVKPSQTLSTCTVSGSISST--YYMSWIRQPPGKLEWIGYIYSGSTN 77  
QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYICARGD-----GDGKYWGQGLT 114  
DB 78 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYICARHNSSWYGRFYDWGQGLT 137

QY 115 VSS 117  
|||  
DB 138 VSS 140

#### RESULT 3

S31690  
Ig heavy chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S31690  
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.  
submitted to the EMBL Data Library, June 1992  
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A;Reference number: S31585  
A;Accession: S31690  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-130 <CUI>  
A;Cross-references: EMBL:Z14199; NID:g30984; PIDN:CAA78568.1; PID:g30985  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;20-102/Domain: immunoglobulin homology <IMM>

Query Match 83.7%; Score 523; DB 2; Length 130;  
Best Local Similarity 82.7%; Pred. No. 8.4e-39;  
Matches 105; Conservative 3; Mismatches 7; Indels 12; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHNSWIRQHPGKLEWIGYIYSGSY 60  
DB 6 QVQLQESGPGLVKPSQTLSTCTVSGSISST--YYMSWIRQPPGKLEWIGYIYSGSTN 63  
QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYICARGD-----GKYWGQG 110  
DB 64 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYICARGSSVLLWFGELLYYFDWGG 123

QY 111 TLTVSS 117  
|||  
DB 124 TLTVSS 130

#### RESULT 4

S37456  
Ig mu chain - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S37456  
R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.  
submitted to the EMBL Data Library, September 1993  
A;Description: Cloning and analysis of human IGM anti-Thyroglobulin autoantibodies from  
A;Reference number: S37453  
A;Accession: S37456  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-116 <MCI>  
A;Cross-references: EMBL:X75024; NID:g404313; PIDN:CAA52932.1; PID:g758095  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;6-90/Domain: immunoglobulin homology <IMM>

Query Match 83.5%; Score 522; DB 2; Length 116;  
Best Local Similarity 87.1%; Pred. No. 9.1e-39;  
Matches 101; Conservative 2; Mismatches 5; Indels 8; Gaps 1;

QY 10 GLVKPSQTLSTCTVSGSISSTGYHNSWIRQHPGKLEWIGYIYSGSYNPSPSKSRV 69  
DB 1 GLVKPSQTLSTCTVSGSISSTGYHNSWIRQHPGKLEWIGYIYSGSYNPSPSKSRV 60  
QY 70 TISVDTSKNQFSLKSSVTAADTAVYICARGDGDGKY-----WGQGLT 117  
DB 61 TISVDTSKNQFSLKSSVTAADTAVYICARGSYGYYYMDVWGKGT 116

#### RESULT 5

S78051  
Ig heavy chain precursor V-D-J region (clone mAB 61VH) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 19-Nov-1997 #sequence\_revision 05-Dec-1997 #text\_change 23-Jul-1999  
C;Accession: S78051; S23716  
R;Harindranath, N.  
submitted to the EMBL Data Library, August 1990  
A;Reference number: S78051  
A;Accession: S78051  
A;Molecule type: mRNA  
A;Residues: 1-135 <HAR>  
A;Cross-references: EMBL:X54437; NID:g37814; PIDN:CAA38306.1; PID:g930117  
R;Harindranath, N.; Goldfarb, I.S.; Ikenatsu, H.; Burastero, S.E.; Wilder, R.L.; Norkin  
Int. Immunol. 3, 865-875, 1991  
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and  
patient.  
A;Reference number: S23716; MUID:920311262; PMID:1718404  
A;Accession: S23716  
A;Molecule type: mRNA  
A;Residues: 13-111 <HAW>  
A;Cross-references: EMBL:X54437  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;1-13/Domain: signal sequence (fragment) #status predicted <SIG>  
F;14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>  
F;27-111/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 519; DB 2; Length 135;  
Best Local Similarity 82.1%; Pred. No. 1.9e-38;  
Matches 101; Conservative 7; Mismatches 9; Indels 6; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHNSWIRQHPGKLEWIGYIYSGSY 60  
DB 13 QVQLQESGPGLVKPSQTLSTCTVSGSISRGSHYWGIRQPPGKLEWIGSYIYSGNTY 72  
QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYICARGG-----DGKYWGQGLT 114  
DB 73 FNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYICARLPDDYTLDGMDVWGQGT 132

QY 115 VSS 117  
|||  
DB 133 VSS 135

#### RESULT 6

S44113  
Ig heavy chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
C;Accession: S44113  
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
submitted to the EMBL Data Library, March 1994  
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable  
A;Reference number: S44105  
A;Accession: S44113  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-121 <HAW>



A:Molecule type: mRNA  
A:Residues: 1-155 <CHA>  
A:Cross-references: EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PID:g33083  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:47-129/Domain: immunoglobulin homology <IMM>

Query Match 81.4%; Score 509; DB 2; Length 155;  
Best Local Similarity 80.8%; Pred. No. 1.7e-37;  
Matches 101; Conservative 5; Mismatches 9; Indels 10; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGKGLWIGYIYSGSTY 60  
DB 33 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGKGLWIGYIYSGSAT 90  
QY 61 YNPFLKSRVTISVDTSKNQFSLKSSVTAADTAIVYCARGGD-----GYKYGQGTLL 112  
DB 91 YNPFLKSRVTISVDTSKNQFSLKSSVTAADTAIVYCARGGISSWYVYGMVDWGQGT 150  
QY 113 VTSS 117  
DB 151 VTSS 155

RESULT 11  
S31586  
Ig heavy chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S31586  
R:Quisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.  
Submitted to the EMBL Data Library, June 1992  
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A:Reference number: S31585  
A:Accession: S31586  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-139 <CUI>  
A:Cross-references: EMBL:Z14196; NID:g30978; PIDN:CAA78565.1; PID:g30979  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 80.6%; Score 503.5; DB 2; Length 139;  
Best Local Similarity 83.6%; Pred. No. 4.5e-37;  
Matches 102; Conservative 5; Mismatches 8; Indels 7; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGKGLWIGYIYSGSTY 60  
DB 20 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGKGLWIGRIYTSSTN 77  
QY 61 YNPFLKSRVTISVDTSKNQFSLKSSVTAADTAIVYCARGGD-----YKYGQGTLLTV 115  
DB 78 YNPFLKSRVTISVDTSKNQFSLKSSVTAADTAIVYCARGGIGIRRGAPDIWQGTMTV 137  
QY 116 SS 117  
DB 138 SS 139

RESULT 12  
S31514  
Ig heavy chain - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S31514  
R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
Submitted to the EMBL Data Library, December 1992  
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto  
A:Reference number: S31509  
A:Accession: S31514  
A>Status: preliminary  
A:Molecule type: mRNA

A:Residues: 1-128 <CHA>  
A:Cross-references: EMBL:X69862; NID:g33086; PIDN:CAA49496.1; PID:g33087  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:22-106/Domain: immunoglobulin homology <IMM>

Query Match 80.5%; Score 503; DB 2; Length 128;  
Best Local Similarity 80.2%; Pred. No. 4.6e-37;  
Matches 97; Conservative 9; Mismatches 11; Indels 4; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGKGLWIGYIYSGSTY 60  
DB 8 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGMALEWIAHIFSGSTY 67  
QY 61 YNPFLKSRVTISVDTSKNQFSLKSSVTAADTAIVYCARGGDGYKY----WGQGTLLTVTS 116  
DB 68 YNPFLKSRVTISVDTSKNQFSLKSSVTAADTAIVYCARGYNFYGFDPWGQGTLLTVTS 127  
QY 117 S 117  
DB 128 S 128

RESULT 13  
S26803  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S26803  
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.  
Eur. J. Immunol. 22, 1075-1082, 1992  
A:Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.  
A:Reference number: S26800; MUID:92201299; PMID:1348029  
A:Accession: S26803  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-99 <WEN>  
A:Cross-references: EMBL:Z14238; NID:g37710; PIDN:CAA78607.1; PID:g1335374  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 502; DB 2; Length 99;  
Best Local Similarity 97.0%; Pred. No. 4.2e-37;  
Matches 96; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGKGLWIGYIYSGSTY 60  
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGKGLWIGYIYSGSTY 60  
QY 61 YNPFLKSRVTISVDTSKNQFSLKSSVTAADTAIVYCAR 99  
DB 61 YNPFLKSRVTISVDTSKNQFSLKSSVTAADTAIVYCAR 99

RESULT 14  
S26802  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S26802  
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.  
Eur. J. Immunol. 22, 1075-1082, 1992  
A:Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.  
A:Reference number: S26800; MUID:92201299; PMID:1348029  
A:Accession: S26802  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-99 <WEN>  
A:Cross-references: EMBL:Z14239; NID:g37708; PIDN:CAA78608.1; PID:g1335373  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-99/Domain: immunoglobulin homology <IMM>

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Query Match
Best Local Similarity 79.5%; Score 497; DB 2; Length 99;
Matches 95; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGILVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGIYYSGSTY 60
Db 1 QVQLQESGPGILVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGIYYSGSTY 60
Qy 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCAR 99
Db 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCAR 99

RESULT 15
S44114
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44114
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
A;Reference number: S44105
A;Accession: S44114
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-129 <HAW>
A;Cross-references: EMBL:Z31579; NID:9472968; PIDN:CAA83451.1; PID:9940525
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity 79.4%; Score 496.5; DB 2; Length 129;
Matches 100; Conservative 6; Mismatches 10; Indels 9; Gaps 3;

Qy 1 QVQLQESGPGILVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGIYYSGSTY 60
Db 1 QVQLQESGPGILVKPSGTLSTCAVSGGSISSSNW-NSWVRQPPGKGLEWIGEYHSGSTN 59
Qy 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCAR-----GGDG-YKYWGQGTLL 112
Db 60 YNPFKSRVTISADTSKNQFSLKNSVTAADTAVYCARNYDFWSGGDGFYWGQGTLL 119
Qy 113 VTYSS 117
Db 120 VTYSS 124
```

Search completed: November 9, 2005, 13:08:01  
Job time : 12.609 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:46:52 ; Search time 60.406 Seconds  
(without alignments)  
991.843 Million cell updates/sec

Title: US-10-660-357A-5

Perfect score: 625

Sequence: 1 QVQLQESGPGLVKPSQTLSL.....ARGGDGKYWGQGLTVTSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	551	88.2	476	2 Q6GMX1	Q6gm1 homo sapien
2	519.5	83.1	478	2 Q72379	Q72379 homo sapien
3	500.5	80.1	465	2 Q6GMX6	Q6gm6 homo sapien
4	500	80.0	119	2 Q9UL73	Q9ul73 homo sapien
5	497.5	79.6	477	2 Q6GMX7	Q6gm7 homo sapien
6	489.5	78.3	150	2 Q95973	Q95973 homo sapien
7	488.5	78.2	496	2 Q96KX8	Q96kx8 homo sapien
8	488.5	78.2	576	2 Q6P418	Q6p418 homo sapien
9	486.5	77.8	620	2 Q96EY0	Q96ey0 homo sapien
10	478.5	76.6	130	2 Q812D7	Q81z47 homo sapien
11	477	76.3	492	2 Q72374	Q72374 homo sapien
12	474	75.8	139	2 Q86SX2	Q86sx2 homo sapien
13	453	72.5	129	1 HV2F_HUMAN	P01824 homo sapien
14	445	71.2	478	2 Q6NYH3	Q6nyh3 homo sapien
15	434	69.4	595	2 Q8WUX4	Q8wux4 homo sapien
16	434	69.4	597	2 Q6GMX5	Q6gm5 homo sapien
17	434	69.4	597	2 Q9BU10	Q9bul0 homo sapien
18	434	69.4	625	2 Q96AA6	Q96aa6 homo sapien
19	429.5	68.7	136	2 Q6LBQ5	Q6lbq5 mus musculus
20	429.5	68.7	146	1 HV2I_HUMAN	P06331 homo sapien
21	428	68.5	597	2 Q9BQ58	Q9bqb8 homo sapien
22	425.5	68.1	473	2 Q8TC53	Q8tc53 homo sapien
23	425	68.0	479	2 Q9NM22	Q9nm22 mus musculus
24	413.5	66.2	122	2 Q9UL75	Q9ul75 homo sapien
25	413	66.1	137	1 HV46_MOUSE	P01822 mus musculus
26	410	65.6	262	2 Q65Z11	Q65z11 mus musculus
27	404	64.6	116	2 Q723Y6	Q723y6 homo sapien
28	403	64.5	113	1 HV47_MOUSE	P01823 mus musculus
29	403	64.5	117	1 HV2G_HUMAN	P01825 homo sapien
30	401	64.2	476	2 Q6MZX7	Q6mzx7 homo sapien
31	387	61.9	117	1 HV62_MOUSE	P18533 mus musculus

32	380.5	60.9	116	1 HV61_MOUSE	P18532 mus musculus
33	379.5	60.7	116	1 HV60_MOUSE	P18531 mus musculus
34	356	57.0	121	2 Q9UL96	Q9ul96 homo sapien
35	352.5	56.4	118	2 Q811U5	Q811u5 mus musculus
36	351.5	56.2	482	2 Q91X92	Q91x92 mus musculus
37	350	56.0	144	1 HV43_MOUSE	P01819 mus musculus
38	345.5	55.3	135	1 HV02_XENLA	P20957 xenopus lae
39	343.5	55.0	121	2 Q99NG4	Q99ng4 mus musculus
40	330	52.8	118	2 Q9UL74	Q9ul74 homo sapien
41	330	52.8	119	1 HV2C_HUMAN	P01816 homo sapien
42	330	52.8	466	2 Q6IN78	Q6in78 homo sapien
43	326.5	52.2	606	2 Q6GMX2	Q6gm2 homo sapien
44	325	52.0	116	2 Q9UL93	Q9ul93 homo sapien
45	324.5	51.9	147	2 Q9Y509	Q9y509 homo sapien

#### ALIGNMENTS

RESULT 1  
Q6GMX1 PRELIMINARY; PRT; 476 AA.  
AC Q6GMX1;  
DT 05-JUL-2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DE Hypothetical protein.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426030999;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Vallalón D.S., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Faney J., Helton E., Kettman M., Madan A., Young A.C., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
EMBL; BC073773; AAH73773.1; -  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00047; ig; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.

```

KW  Hypothetical protein.
SQ  SEQUENCE 476 AA; 52286 MW; 622AABASC62DDE9D CRC64;

Query Match      88.2%; Score 551; DB 2; Length 476;
Best Local Similarity 82.7%; Pred. No. 3.8e-46;
Matches 105; Conservative 7; Mismatches 5; Indels 10; Gaps 1;

QY  1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYTHWSWIRQHPKGLIEWIGYIYSGSTY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  20 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYTHWSWIRQHPKGLIEWIGYIYSGSTY 79
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY  61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAATVAVYCARGVGWSFRSFAIDGNFNIWQ 110
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  80 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAATVAVYCARGVGWSFRSFAIDGNFNIWQ 139
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY  111 TLTVSS 117
    |||||
Db  140 TMTVSS 146
    |||||

RESULT 2
QY  Q7Z379 PRELIMINARY; PRT; 478 AA.
AC  Q7Z379;
DT  01-OCT-2003 (TrEMBLrel. 25, Created)
DT  01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE  Hypothetical protein DKFZp686K04218 (Fragment).
GN  Name=DKFZp686K04218;
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  TISSUE=Human rectum tumor.
RC  Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA  Fobo G., Han M., Wiemann S.;
RL  Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BX538066; CAD97996.1; -.
DR  HSSP; P01820; 1G7J.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003597; Ig-cl.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF07654; C1-set; 2.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS00835; IG_LIKE; 4.
DR  PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW  Hypothetical protein.
FT  NON_TER 1
SQ  SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;

Query Match      83.1%; Score 519.5; DB 2; Length 478;
Best Local Similarity 80.8%; Pred. No. 5e-43;
Matches 97; Conservative 12; Mismatches 8; Indels 3; Gaps 1;

QY  1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYTHWSWIRQHPKGLIEWIGYIYSGSTY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  19 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYTHWSWIRQHPKGLIEWIGYIYSGSTY 78
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY  61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAATVAVYCARGVGWSFRSFAIDGNFNIWQ 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  79 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAATVAVYCARGVGWSFRSFAIDGNFNIWQ 138
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
QY  Q6GMX6 PRELIMINARY; PRT; 465 AA.
AC  Q6GMX6;
DT  05-JUL-2004 (TrEMBLrel. 27, Created)
DT  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT  05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

```

```

DE  Hypothetical protein.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Primary B-Cells;
RX  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA  Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA  Jones S.J., Marra M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length human
RT  and mouse cDNA sequences.";
RN  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP  SEQUENCE FROM N.A.
RC  TISSUE=Primary B-Cells;
RA  Strausberg R.;
RL  Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC073766; AAH73766.1; -.
DR  InterPro; IPR003599; Ig.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003597; Ig-cl.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF07654; C1-set; 3.
DR  Pfam; PF00047; Ig; 4.
DR  SMART; SM00409; IGV; 2.
DR  SMART; SM00407; IGV; 3.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS00835; IG_LIKE; 4.
DR  PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW  Hypothetical protein.
SQ  SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match      80.1%; Score 500.5; DB 2; Length 465;
Best Local Similarity 86.4%; Pred. No. 3.7e-41;
Matches 102; Conservative 3; Mismatches 10; Indels 3; Gaps 2;

QY  1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYTHWSWIRQHPKGLIEWIGYIYSGSTY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  20 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYTHWSWIRQHPKGLIEWIGYIYSGSTY 77
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY  61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAATVAVYCARGVGWSFRSFAIDGNFNIWQ 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  78 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAATVAVYCARGVGWSFRSFAIDGNFNIWQ 135
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
QY  Q9UL73 PRELIMINARY; PRT; 119 AA.
ID  Q9UL73;
AC  Q9UL73;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE  Myosin-reactive immunoglobulin heavy chain variable region
DE  (Fragment).
OS  Homo sapiens (Human).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
 RX You X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 fetus.";  
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
 DR EMBL; AF035041; AAD56277.1; -.  
 DR PIR; PH0876; PH0876.  
 DR PIR; S12416; S12416.  
 DR HSSP; P01820; 1G7J.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON TER 1  
 FT NON TER 119  
 SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;  
 Query Match 80.0%; Score 500; DB 2; Length 119;  
 Best Local Similarity 82.6%; Pred. No. 9.9e-42;  
 Matches 100; Conservative 6; Mismatches 9; Indels 6; Gaps 2;  
 QY 1 QVQLQESGPGLVKPSQTLSTCTCTVSGGSISSGTYHWSWIRQHPKGLIEWIGYIYSGSTY 60  
 DB 1 QVQLQESGPGLVKPSQTLSTCTCTVSGGSISSGTYHWSWIRQHPKGLIEWIGYIYSGSTN 58  
 QY 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYVCAR---GGDGYKYGQGLTVTS 116  
 DB 59 YTPSLKSRVVISVDTSKNQFSLKLSVTAADTAVYFCARLSNWPYDFYFWGQGLTVTS 118  
 QY 117 S 117  
 DB 119 S 119  
 RESULT 5  
 Q6GMX7 PRELIMINARY; PRT; 477 AA.  
 ID Q6GMX7  
 AC Q6GMX7;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073765; AAH73765.1; -.  
 DR InterPro; IPR003599; Ig-like.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 2.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00409; IG; 4.  
 DR SMART; SM00407; IGV; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CFF85 CRC64;  
 Query Match 79.6%; Score 497.5; DB 2; Length 477;  
 Best Local Similarity 81.7%; Pred. No. 7.6e-41;  
 Matches 98; Conservative 8; Mismatches 9; Indels 5; Gaps 2;  
 QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPKGLIEWIGYIYSGSTY 60  
 DB 20 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPKGLIEWIGYIYSGSTT 77  
 QY 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYVCARGD---GKYWGQGLTVTVSS 117  
 DB 78 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYVCARGSSWDFADYWGQGLTVTVSS 137  
 RESULT 6  
 Q95973 PRELIMINARY; PRT; 150 AA.  
 ID Q95973  
 AC Q95973;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE VH4 heavy chain variable region precursor (Fragment).  
 GN Name=IGH;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF103795; AAC79084.1; -.  
 DR PIR; S31673; S31673.  
 DR HSSP; P01820; IG7J.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Signal.  
 FT SIGNAL 1 19 Potential.  
 FT CHAIN 20 >150 VH4 heavy chain variable region.  
 FT NON TER 150  
 FT NON TER 150  
 SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;  
 Query Match 78.3%; Score 489.5; DB 2; Length 150;  
 Best Local Similarity 80.5%; Pred. No. 1.4e-40;  
 Matches 95; Conservative 10; Mismatches 12; Indels 1; Gaps 1;  
 QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPKGLIEWIGYIYSGSTY 60



Db  
85 YNPSELKSRVTNMSVDTSKNQFSLKSSVTAADTAATVYCASQPWELPTVGLFYWGQSTLVT 144

DB	85	YNP	SLK
QY	116	SS	117
DB	145	SS	146

RESULT 10

[illegible]

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RP	SEQUENCE FROM N.A.	
JR	Jang Y.-J., Chung J., Park J.-Y.;	
RL	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AY145445; AAAG4329.1; -.	
DR	HSSP; P01820; 1G7J.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR003596; Ig_v.	
DR	SMART; SM00406; IGV; 1.	
DR	PROSITE; PS50835; IG_Like; 1.	
FT	NON_TER	1
FT	NON_TER	130
SQ	SEQUENCE 130 AA; 13901 MW;	036131FC6EC1551E CRC64;

Query Match	76.6%;	Score 478.5;	DB 2;	Length 130;
Best Local Similarity	74.6%;	Pred. No. 1.5e-39;		
Matches 97: Conservative	9;	Mismatches 11;	Indels 13;	Gaps 3

[illegible]

QY 60 ---YYNPSLKSRVTISVDTSKNQFSLKLSSTAAADTAVYYCA---RGDGY---KYW 107

61 SGSPYAPSLRSRV

61 SGSPYAPSLRSRVIIIVDTSKNQLSLRLSSVTAADTAVYYCASPTHCSSGGCYAFFQHW 120

QY 108 GGGELVTVSS 117  
||| |||||  
Db 121 GGGELVTVSS 130

DBb 121 GQGFLVTVSS 130

RESULT 11  
C72374

RESULT 11  
Q7Z374  
ID Q7Z374  
PRELIMINARY: PRT: 492 AA

Q72374	PRELIMINARY;	PRT;	492 AA.
ID Q72374			
AC Q72374;			

AC Q7Z374;  
DT 01-OCT-2003 (TREMBLrel. 25, Created)

DT	01-OCT-2003	(TREMBLrel. 25, Created)
DT	01-OCT-2003	(TREMBLrel. 25, Last sequence update)
DT	01 MAY 2004	(TREMBLrel. 26, Updated)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hymothetical protein DKEZ0686C02218 (Fragment)

DE Hypothetical protein DKFZp686C02218 (Fragment).  
GN Name=DKFZp686C02218;  
UI-MAK-2004 (1:EMBLrel. 26, last annotation update)

OS Homo sapiens (Human).  
 GN Name=DKFZp686C02218;  
 OS Homo sapiens (Homo sapiens) (fragment).

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
CY NCBI TaxID:9606.

CA  
RN  
[1]  
RP

RP 'SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;

RA Fobo G., Han M., Wiemann S.;  
RA Bloecker H., Boecher M., Mewes H.W., Weill B., Amid C., Osanger A.,  
PI. Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases

FOBO G., HAN M., WIEMANN S.;  
 RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: BX538077; CAD98001.1; -;  
 DR

DR HSSP; P01820; 1G7J.  
DR InterPro; IPR007110; Ig-like.

```
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760FOCA74B CRC64;

Query Match 76.3%; Score 477; DB 2; Length 492;
Best Local Similarity 75.8%; Pred. No. 8.4e-39;
Matches 91; Conservative 13; Mismatches 13; Indels 4; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGKGLEWIGYIYSGSTY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 32 QQLQESGPGLVKPSQTLSTCTVSGSVSNRYWGWIRQPPGKGLEWIGSIYNYNTY 91
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 YNPSLKSRVTISVDTSKNQFSLKSLSVTAADTAVYVCARGDG---YKYGQGLTVTVS 116
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 92 YPSLKSRLTIFVDTSKNHFSRLTSVTAADTAVYVCRRVVEGPGWGFDPWGQGLTVTVS 151
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 117 S 117
Db 152 S 152

RESULT 12
Q84SX2 PRELIMINARY; PRT; 139 AA.
AC Q86SX2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Full-length cDNA clone CS0DL004YM19 of B cells (Ramos cell line) of
DE Homo sapiens (human) (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Li W.B., Gruber C., Jessee J., Polayes D.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX248300; CAD62627.1; -.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;

Query Match 75.8%; Score 474; DB 2; Length 139;
Best Local Similarity 93.9%; Pred. No. 4.4e-39;
Matches 93; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGKGLEWIGYIYSGSTY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 33 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGKGLEWIGYIYSGSTN 90
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 YNPSLKSRVTISVDTSKNQFSLKSLSVTAADTAVYVCAR 99
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 91 YNPSLKSRVTISVDTSKNQFSLKSLSVTAADTAVYVCAR 129
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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RESULT 13
HV2F HUMAN STANDARD; PRT; 129 AA.
ID P01824;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-II region WAH.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=8222235; PubMed=6806818;
RX Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;
RT "Complete amino acid sequence of the delta heavy chain of human
RT immunoglobulin D.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
CC -!- MISCELLANEOUS: This chain was isolated from an IgD myeloma
CC protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02099; D2HUWA.
DR HSSP; P01820; IG7J.
DR GlycoSuiteDB; P01824; -.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 113
   Ig-like.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Query Match 72.5%; Score 453; DB 1; Length 129;
Best Local Similarity 67.4%; Pred. No. 4.9e-37;
Matches 87; Conservative 11; Mismatches 19; Indels 12; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISSTGYHWSWIRQHPGKGLEWIGYIYSGSTY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 RLQLQESGPGLVKPSQTLSTCTVSGGPIRRTGYWGWIRQPPGKLEWIGGYVTGSIY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 YNPSLKSRVTISVDTSKNQFSLKSLSVTAADTAVYVCARGG-----DGKYYWG 108
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 YNPSLGRVTISVDTISRNQFSLNLSMSAADTAVYVCARGNPPPYDGTGSDGIDVWG 120
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 109 QGTLTVTVSS 117
   :|||:|||||
Db 121 QGTLTVTVSS 129
   :|||:|||||

RESULT 14
Q6NYH3 PRELIMINARY; PRT; 478 AA.
AC Q6NYH3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC066594; AA66594.1; -.
DR HSSP; P01820; IA7N.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00406; IG; 1.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 478 AA; 51856 MW; 5F8B98F60F077256 CRC64;

Query Match 71.2%; Score 445; DB 2; Length 478;
Best Local Similarity 71.1%; Pred. No. 1.2e-35;
Matches 86; Conservative 17; Mismatches 12; Indels 6; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYTHMSWIRQHPGKGLEWIGYIYSGSTY 60
Db 20 QVDLQSSGPGLVKPSQTLSTCTVSGGSISSGYTHMSWIRQHPGKGLEWIGYIYSGSTL 77
QY 61 YNPSLKSRVTISVDTSKNQPSLKLSSVTAADTAIVYCARGGDG-----YKTWGGGTLVTVS 116
Db 78 YNPFSLSRVMTSVDTSKDQPSMKLTSVTAADTAIVYCARGYGKGRYFDLWGRGVPVTWS 137
QY 117 S 117
Db 138 S 138

RESULT 15
Q8WUX4 PRELIMINARY; PRT; 595 AA.
AC Q8WUX4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019235; AAH19235.2; -.
DR PIR; G34964; G34964.
DR HSSP; P01861; IADO.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 595 AA; 65290 MW; 0D4B50776545714E CRC64;

Query Match 69.4%; Score 434; DB 2; Length 595;
Best Local Similarity 71.7%; Pred. No. 1.9e-34;
Matches 91; Conservative 5; Mismatches 19; Indels 12; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGYTHMSWIRQHPGKGLEWIGYIYSGSTY 60
Db 27 QVQLQMGAGLLKPSQTLSTCTVSGGSISSGYTHMSWIRQHPGKGLEWIGIYHSGSTN 84
QY 61 YNPSLKSRVTISVDTSKNQPSLKLSSVTAADTAIVYCAR-----GGDGKYYWGGQ 110
Db 85 YNPSLKSRVTISVDTSKNQPSLKLSSVTAADTAIVYCARVITRASPGTDGRYNDVWGGQ 144
QY 111 TLTVSS 117
Db 145 TTVTVSS 151

Search completed: November 9, 2005, 13:05:47
Job time : 61.406 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model  
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(without alignments)  
627.306 Million cell updates/sec

Title: US-10-660-357A-9  
Perfect score: 650  
Sequence: 1 QVQLQESGPGLVKPSSETLSL.....WLLPDAFDIWGQGTMTVTS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_16Dec04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	650	100.0	121	7	Adc99780 Anti-huma
2	650	100.0	121	7	Add05384 Anti-MUC1
3	650	100.0	121	7	Adf09822 Human ant
4	643	98.9	121	7	Adc99772 Anti-huma
5	643	98.9	121	7	Adc99788 Anti-huma
6	643	98.9	121	7	Add05376 Anti-MUC1
7	643	98.9	121	7	Add05392 Anti-MUC1
8	643	98.9	121	7	Adf09814 Human ant
9	643	98.9	121	7	Adf09830 Human ant
10	598	92.0	121	7	Adc99808 Anti-huma
11	598	92.0	121	7	Add05412 Anti-MUC1
12	598	92.0	121	7	Adf09850 Human ant
13	566.5	87.2	243	8	Ado58076 S9 cell d
14	548	84.3	121	5	Abg92884 Human imm
15	546.5	84.1	121	5	Abb07171 ebvHigM M
16	546.5	84.1	121	8	Adi26658 Human ant
17	546.5	84.1	122	7	Adp03887 Murine-ex
18	546.5	84.1	122	7	Adp03884 Murine-ex
19	545.5	83.9	122	7	Adp03885 Murine-ex
20	545.5	83.9	122	7	Adp03889 Murine-ex
21	541	83.2	119	2	Aaw27554 Human Ab
22	541	83.2	119	6	Abj18676 Antibody
23	540.5	83.2	118	8	Adp22272 Human ant
24	540	83.1	123	6	Ada89258 Human ant
25	539.5	83.0	122	7	Adp03931 Murine-ex

26	537.5	82.7	120	7	ADP03864	Adp03864 Murine-ex
27	537.5	82.7	120	7	ADP03862	Adp03862 Murine-ex
28	537.5	82.7	121	7	ADP03984	Adp03984 Murine-ex
29	537	82.6	119	7	ADP03973	Adp03973 Murine-ex
30	536.5	82.5	246	3	AAV15126	Asy15126 Anti-muri
31	536.5	82.5	246	3	AAV15126	Asy15126 Anti-muri
32	535.5	82.4	122	7	ADP03933	Adp03933 Murine-ex
33	534.5	82.2	124	7	ADP03886	Adp03886 Murine-ex
34	534.5	82.2	193	5	ABP43199	Abp43199 Human ova
35	533.5	82.1	128	8	ADS19313	Adsi9313 Heavy cha
36	532.5	81.9	120	2	AAW90287	Aaw90287 Human ant
37	532.5	81.9	126	5	ABG92888	Abg92888 Human imm
38	532	81.8	125	7	ADP03868	Adp03868 Murine-ex
39	532	81.8	125	7	ADP03876	Adp03876 Murine-ex
40	530.5	81.6	114	5	ABG97827	Abg97827 Human MPL
41	530.5	81.6	114	5	ABG35304	Abg35304 Thrombopo
42	530.5	81.6	133	5	ABG97829	Abg97829 Mouse 12E
43	530.5	81.6	133	5	ABG35331	Abg35331 Thrombopo
44	530.5	81.6	244	2	AAV06718	Asv06718 Antibody
45	530.5	81.6	244	8	ADO39737	Ado39737 Human C-m

ALIGNMENTS

RESULT 1

ADC99780

ID ADC99780 standard; protein; 121 AA.

XX AC ADC99780;

XX AC (first entry)

DT 01-JAN-2004

DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 9.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast; lung cancer; human.

XX Homo sapiens.

XX WO2003057838-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

PI Gudas J;

DR WPI; 2003-587113/55.

DR N-PSDB; ADC99782.

XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.

PS Claim 1; SEQ ID NO 9; 78pp; English.

CC The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the cell surface such as tumours, specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody

CC heavy chain protein of the invention.  
XX  
SQ Sequence 121 AA;  
Query Match 100.0%; Score 650; DB 7; Length 121;  
Best Local Similarity 100.0%; Pred. No. 1.5e-47;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKLEWIGYIYYTWTNNY 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKLEWIGYIYYTWTNNY 60  
QY 61 PSLSKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGQGTWVTVS 120  
Db 61 PSLSKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGQGTWVTVS 120  
QY 121 S 121  
Db 121 S 121  
RESULT 2  
ADD05384  
ID ADD05384 standard; protein; 121 AA.  
XX  
AC ADD05384;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 9.  
XX  
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.  
XX  
OS Homo sapiens.  
XX  
PN WQ2003057006-A2.  
XX  
PD 17-JUL-2003.  
XX  
PF 26-DEC-2002; 2002WO-US041582.  
XX  
PR 28-DEC-2001; 2001US-0346460P.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Gudas J, Bar-Eli M;  
XX  
DR WPI; 2003-577496/54.  
DR N-PSDB; ADD05386.  
XX  
PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
PT associated with melanoma, or increasing survival of an animal having a  
PT metastatic tumor.  
XX  
PS Claim 1; SEQ ID NO 9; 87pp; English.  
XX  
CC The invention relates to a novel monoclonal antibody used for inhibiting  
CC tumour growth in an animal. The tumour inhibition process comprises  
CC selecting an animal in need of treatment for a tumour, providing a  
CC monoclonal antibody comprising a heavy chain amino acid, where the  
CC antibody consists of any one of 10 fully defined sequences of 117-123  
CC amino acids given in the specification, and where the monoclonal antibody  
CC binds MUC18, and contacting the tumour with the antibody resulting in  
CC inhibited proliferation of the cells. The monoclonal antibody has  
CC cytostatic and can be used in the production of a vaccine. The monoclonal  
CC antibodies against the MUC18 antigen are useful for diagnosing and  
CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or  
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or  
CC increasing survival of an animal having a metastatic tumour. This  
CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
CC protein of the invention.

XX  
SQ Sequence 121 AA;  
Query Match 100.0%; Score 650; DB 7; Length 121;  
Best Local Similarity 100.0%; Pred. No. 1.5e-47;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKLEWIGYIYYTWTNNY 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKLEWIGYIYYTWTNNY 60  
QY 61 PSLSKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGQGTWVTVS 120  
Db 61 PSLSKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGQGTWVTVS 120  
QY 121 S 121  
Db 121 S 121  
RESULT 3  
ADF09822  
ID ADF09822 standard; protein; 121 AA.  
XX  
AC ADF09822;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Human anti-MUC18 monoclonal antibody heavy chain #3.  
XX  
KW cell proliferation inhibition; MUC18 tumour antigen;  
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
KW carcinoma; cancer; malignancy; heavy chain; human.  
XX  
OS Homo sapiens.  
XX  
PN WQ2003057837-A2.  
XX  
PD 17-JUL-2003.  
XX  
PF 26-DEC-2002; 2002WO-US041580.  
XX  
PR 28-DEC-2001; 2001US-0346414P.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Gudas J;  
XX  
DR WPI; 2003-598367/56.  
DR N-PSDB; ADF09824.  
XX  
PT Inhibiting cell proliferation associated with expression of MUC18 tumor  
PT antigen, involves incubating and inhibiting cell by administering anti-  
PT MUC18 monoclonal antibody.  
XX  
PS Claim 1; SEQ ID NO 9; 83pp; English.  
XX  
CC The invention comprises a method for inhibiting cell proliferation  
CC associated with expression of MUC18 tumour antigen. The method involves  
CC administering anti-MUC18 monoclonal antibody. The method of the invention  
CC is useful for inhibiting cell (e.g. melanoma or tumour cell)  
CC proliferation associated with the expression of MUC18 tumour antigen, the  
CC method is preferably useful for inhibiting tumour metastasis. The method  
CC is useful for inhibiting cell proliferation in patients with tumours,  
CC carcinomas, cancer and other malignancies. The present amino acid  
CC sequence represents a heavy chain from an MUC18 tumour antigen-specific  
CC monoclonal antibody.  
XX  
SQ Sequence 121 AA;  
Query Match 100.0%; Score 650; DB 7; Length 121;  
Best Local Similarity 100.0%; Pred. No. 1.5e-47;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 121 S 121  
Db 121 S 121

## RESULT 6

ADD05376  
ID ADD05376 standard; protein; 121 AA.

XX AC ADD05376;

XX DT 01-JAN-2004 (first entry)

XX DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 1.

XX KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;

XX KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.

XX OS Homo sapiens.

XX PN WO2003057006-A2.

XX PD 17-JUL-2003.

XX PF 26-DEC-2002; 2002WO-US041582.

XX PR 28-DEC-2001; 2001US-0346460P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J, Bar-Eli M;

XX DR WPI; 2003-577496/54.

XX DR N-PSDB; ADD05378.

XX PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and

XX PT treating tumors, inhibiting tumor growth, inhibiting cell invasion

XX PT associated with melanoma, or increasing survival of an animal having a

XX PT metastatic tumor.

XX PS Claim 1; SEQ ID NO 1; 87pp; English.

XX CC The invention relates to a novel monoclonal antibody used for inhibiting

XX CC tumour growth in an animal. The tumour inhibition process comprises

XX CC selecting an animal in need of treatment for a tumour, providing a

XX CC monoclonal antibody comprising a heavy chain amino acid, where the

XX CC antibody consists of any one of 10 fully defined sequences of 117-123

XX CC amino acids given in the specification, and where the monoclonal antibody

XX CC binds MUC18, and contacting the tumour with the antibody resulting in

XX CC inhibited proliferation of the cells. The monoclonal antibody has

XX CC cytotstatic and can be used in the production of a vaccine. The monoclonal

XX CC antibodies against the MUC18 antigen are useful for diagnosing and

XX CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or

XX CC tumour metastasis), inhibiting cell invasion associated with melanoma, or

XX CC increasing survival of an animal having a metastatic tumour. This

XX CC sequence represents an anti-MUC18 antibody heavy chain, variable region,

XX CC protein of the invention.

XX SQ Sequence 121 AA;

Query Match 98.9%; Score 643; DB 7; Length 121;

Best Local Similarity 98.3%; Pred. No. 5.8e-47;

Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVSWIRPPGKLEWIGYIYTTNTYN 60

Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVSWIRPPGKLEWIGYIYTTNTYN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGGTMTVTS 120

Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120

QY 121 S 121  
Db 121 S 121

## RESULT 7

ADD05392  
ID ADD05392 standard; protein; 121 AA.

XX AC ADD05392;

XX DT 01-JAN-2004 (first entry)

XX DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 17.

XX KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;

XX KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.

XX OS Homo sapiens.

XX PN WO2003057006-A2.

XX PD 17-JUL-2003.

XX PF 26-DEC-2002; 2002WO-US041582.

XX PR 28-DEC-2001; 2001US-0346460P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J, Bar-Eli M;

XX DR WPI; 2003-577496/54.

XX DR N-PSDB; ADD05394.

XX PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and

XX PT treating tumors, inhibiting tumor growth, inhibiting cell invasion

XX PT associated with melanoma, or increasing survival of an animal having a

XX PT metastatic tumor.

XX PS Claim 1; SEQ ID NO 17; 87pp; English.

XX CC The invention relates to a novel monoclonal antibody used for inhibiting

XX CC tumour growth in an animal. The tumour inhibition process comprises

XX CC selecting an animal in need of treatment for a tumour, providing a

XX CC monoclonal antibody comprising a heavy chain amino acid, where the

XX CC antibody consists of any one of 10 fully defined sequences of 117-123

XX CC amino acids given in the specification, and where the monoclonal antibody

XX CC binds MUC18, and contacting the tumour with the antibody resulting in

XX CC inhibited proliferation of the cells. The monoclonal antibody has

XX CC cytotstatic and can be used in the production of a vaccine. The monoclonal

XX CC antibodies against the MUC18 antigen are useful for diagnosing and

XX CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or

XX CC tumour metastasis), inhibiting cell invasion associated with melanoma, or

XX CC increasing survival of an animal having a metastatic tumour. This

XX CC sequence represents an anti-MUC18 antibody heavy chain, variable region,

XX CC protein of the invention.

XX SQ Sequence 121 AA;

Query Match 98.9%; Score 643; DB 7; Length 121;

Best Local Similarity 98.3%; Pred. No. 5.8e-47;

Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVSWIRPPGKLEWIGYIYTTNTYN 60

Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVSWIRPPGKLEWIGYIYTTNTYN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGGTMTVTS 120

Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120

QY 121 S 121

Db 121 S 121

RESULT 8  
ADF09814  
ID ADF09814 standard; protein; 121 AA.  
XX  
AC ADF09814;  
XX  
AC ADF09814;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Human anti-MUC18 monoclonal antibody heavy chain #1.  
XX  
KW cell proliferation inhibition; MUC18 tumour antigen;  
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
KW carcinoma; cancer; malignancy; heavy chain; human.  
XX  
OS Homo sapiens.  
XX  
PN W02003057837-A2.  
XX  
PD 17-JUL-2003.  
XX  
PF 26-DEC-2002; 2002WO-US041580.  
XX  
PR 28-DEC-2001; 2001US-0346414P.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Gudas J;  
XX  
DR WPI: 2003-598367/56.  
DR N-PSDB; ADF09816.  
XX  
PT Inhibiting cell proliferation associated with expression of MUC18 tumor  
PT antigen, involves incubating and inhibiting cell by administering anti-  
PT MUC18 monoclonal antibody.  
XX  
PS Claim 1; SEQ ID NO 1; 83pp; English.  
XX  
CC The invention comprises a method for inhibiting cell proliferation  
CC associated with expression of MUC18 tumour antigen. The method involves  
CC administering anti-MUC18 monoclonal antibody. The method of the invention  
CC is useful for inhibiting cell (e.g. melanoma or tumour cell)  
CC proliferation associated with the expression of MUC18 tumour antigen, the  
CC method is preferably useful for inhibiting tumour metastasis. The method  
CC is useful for inhibiting cell proliferation in patients with tumours,  
CC carcinomas, cancer and other malignancies. The present amino acid  
CC sequence represents a heavy chain from an MUC18 tumour antigen-specific  
CC monoclonal antibody.  
XX  
SQ Sequence 121 AA;  
Query Match 98.9%; Score 643; DB 7; Length 121;  
Best Local Similarity 98.3%; Pred. No. 5.8e-47;  
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIRPPGKLEWIGYIYVTTN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIRPPGKLEWIGYIYVTTN 60  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDWGGTMTVTS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDWGGTMTVTS 120  
QY 121 S 121  
Db 121 S 121

RESULT 9  
ADF09830  
ID ADF09830 standard; protein; 121 AA.  
XX  
AC ADF09830;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Human anti-MUC18 monoclonal antibody heavy chain #5.  
XX  
KW cell proliferation inhibition; MUC18 tumour antigen;  
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
KW carcinoma; cancer; malignancy; heavy chain; human.  
XX  
OS Homo sapiens.  
XX  
PN W02003057837-A2.  
XX  
PD 17-JUL-2003.  
XX  
PF 26-DEC-2002; 2002WO-US041580.  
XX  
PR 28-DEC-2001; 2001US-0346414P.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Gudas J;  
XX  
DR WPI: 2003-598367/56.  
DR N-PSDB; ADF09832.  
XX  
PT Inhibiting cell proliferation associated with expression of MUC18 tumor  
PT antigen, involves incubating and inhibiting cell by administering anti-  
PT MUC18 monoclonal antibody.  
XX  
PS Claim 1; SEQ ID NO 17; 83pp; English.  
XX  
CC The invention comprises a method for inhibiting cell proliferation  
CC associated with expression of MUC18 tumour antigen. The method involves  
CC administering anti-MUC18 monoclonal antibody. The method of the invention  
CC is useful for inhibiting cell (e.g. melanoma or tumour cell)  
CC proliferation associated with the expression of MUC18 tumour antigen, the  
CC method is preferably useful for inhibiting tumour metastasis. The method  
CC is useful for inhibiting cell proliferation in patients with tumours,  
CC carcinomas, cancer and other malignancies. The present amino acid  
CC sequence represents a heavy chain from an MUC18 tumour antigen-specific  
CC monoclonal antibody.  
XX  
SQ Sequence 121 AA;  
Query Match 98.9%; Score 643; DB 7; Length 121;  
Best Local Similarity 98.3%; Pred. No. 5.8e-47;  
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIRPPGKLEWIGYIYVTTN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIRPPGKLEWIGYIYVTTN 60  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDWGGTMTVTS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDWGGTMTVTS 120  
QY 121 S 121  
Db 121 S 121

RESULT 10  
ADC99808  
ID ADC99808 standard; protein; 121 AA.  
XX  
AC ADC99808;  
XX  
DT 01-JAN-2004 (first entry)  
XX

DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 37.  
 XX  
 KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
 KW cytotatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
 KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
 KW lung cancer; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003057838-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 26-DEC-2002; 2002WO-US041581.  
 XX  
 PR 28-DEC-2001; 2001US-0346299P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Gudas J;  
 XX  
 DR WPI; 2003-587113/55.  
 DR N-PSDB; ADC99810.  
 XX  
 XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
 PT or condition associated with expression of MUC18 in a patient, e.g.  
 PT tumors, cancers, and other malignancies.  
 PT  
 XX  
 PS Claim 1; SEQ ID NO 37; 78pp; English.  
 XX  
 CC The invention relates to a novel isolated monoclonal antibody comprising  
 CC a heavy or light chain amino acid or a heavy or light chain variable  
 CC domain where the antibody binds to MUC18. The monoclonal antibody of the  
 CC invention demonstrates cytostatic activity and may be useful for treating  
 CC a disease or condition associated with the expression of MUC18 on the  
 CC cell surface such as tumours, specifically melanoma, oesophageal,  
 CC pancreatic or colorectal tumours, carcinomas, particularly cervical  
 CC carcinomas and cervical intraepithelial neoplasia and cancers including  
 CC colorectal, breast or lung cancer, as well as other malignancies. The  
 CC current sequence is that of the anti-human MUC18 monoclonal antibody  
 CC heavy chain protein of the invention.  
 CC  
 XX  
 SQ Sequence 121 AA;  
 Query Match 92.0%; Score 598; DB 7; Length 121;  
 Best Local Similarity 90.9%; Pred. No. 3.8e-43;  
 Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISISSYVWSWIROPKGLWIGYIYYTWTN 60  
 Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISISSYVWSWIROPKGLWIGYIYYTWTN 60  
 QY 61 PSLSKSRVTISVDTSKNQFSLRLSVTAADTALYYCARDQGWLLPDAFDIWGGTMTVTS 120  
 Db 61 PSLSKSRVTISVDTSKNQFSLRLSVTAADTALYYCARDQGWLLPDAFDIWGGTMTVTS 120  
 QY 121 S 121  
 Db 121 S 121  
 RESULT 11  
 ADD05412  
 ID ADD05412 standard; protein; 121 AA.  
 XX  
 AC ADD05412;  
 XX  
 DT 01-JAN-2004 (first entry)  
 XX  
 DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 37.  
 XX  
 KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
 KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.

XX Homo sapiens.  
 XX  
 PN WO2003057006-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 26-DEC-2002; 2002WO-US041582.  
 XX  
 PR 28-DEC-2001; 2001US-0346460P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Gudas J, Bar-Eli M;  
 XX  
 DR WPI; 2003-577496/54.  
 DR N-PSDB; ADD05414.  
 XX  
 XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
 PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
 PT associated with melanoma, or increasing survival of an animal having a  
 PT metastatic tumor.  
 PT  
 XX  
 PS Claim 1; SEQ ID NO 37; 87pp; English.  
 XX  
 CC The invention relates to a novel monoclonal antibody used for inhibiting  
 CC tumor growth in an animal. The tumor inhibition process comprises  
 CC selecting an animal in need of treatment for a tumour, providing a  
 CC monoclonal antibody comprising a heavy chain amino acid, where the  
 CC antibody consists of any one of 10 fully defined sequences of 117-123  
 CC amino acids given in the specification, and where the monoclonal antibody  
 CC binds MUC18, and contacting the tumour with the antibody resulting in  
 CC inhibited proliferation of the cells. The monoclonal antibody has  
 CC cytostatic and can be used in the production of a vaccine. The monoclonal  
 CC antibodies against the MUC18 antigen are useful for diagnosing and  
 CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or  
 CC tumour metastasis), inhibiting cell invasion associated with melanoma, or  
 CC increasing survival of an animal having a metastatic tumour. This  
 CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
 CC protein of the invention.  
 CC  
 XX  
 SQ Sequence 121 AA;  
 Query Match 92.0%; Score 598; DB 7; Length 121;  
 Best Local Similarity 90.9%; Pred. No. 3.8e-43;  
 Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISISSYVWSWIROPKGLWIGYIYYTWTN 60  
 Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISISSYVWSWIROPKGLWIGYIYYTWTN 60  
 QY 61 PSLSKSRVTISVDTSKNQFSLRLSVTAADTALYYCARDQGWLLPDAFDIWGGTMTVTS 120  
 Db 61 PSLSKSRVTISVDTSKNQFSLRLSVTAADTALYYCARDQGWLLPDAFDIWGGTMTVTS 120  
 QY 121 S 121  
 Db 121 S 121  
 RESULT 12  
 ADF09850  
 ID ADF09850 standard; protein; 121 AA.  
 XX  
 AC ADF09850;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human anti-MUC18 monoclonal antibody heavy chain #10.  
 XX  
 KW cell proliferation inhibition; MUC18 tumour antigen;  
 KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
 KW carcinoma; cancer; malignancy; heavy chain; human.

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XX OS Homo sapiens.
XX PN WO2003057837-A2.
XX PD 17-JUL-2003.
XX PF 26-DEC-2002; 2002WO-US041580.
XX PR 28-DEC-2001; 2001US-0346414P.
XX PA (ABGE-) ABGENIX INC.
XX PI Gudas J;
XX PT WPI; 2003-598367/56.
XX DR N-PSDB; ADF09852.
XX PT Inhibiting cell proliferation associated with expression of MUC18 tumor
PT antigen, involves incubating and inhibiting cell by administering anti-
PT MUC18 monoclonal antibody.
XX PS Claim 1; SEQ ID NO 37; 83pp; English.
XX CC The invention comprises a method for inhibiting cell proliferation
CC associated with expression of MUC18 tumour antigen. The method involves
CC administering anti-MUC18 monoclonal antibody. The method of the invention
CC is useful for inhibiting cell (e.g. melanoma or tumour cell)
CC proliferation associated with the expression of MUC18 tumour antigen, the
CC method is preferably useful for inhibiting tumour metastasis. The method
CC is useful for inhibiting cell proliferation in patients with tumours,
CC carcinomas, cancer and other malignancies. The present amino acid
CC sequence represents a heavy chain from an MUC18 tumour antigen-specific
CC monoclonal antibody.
XX SQ Sequence 121 AA;
Query Match 92.0%; Score 598; DB 7; Length 121;
Best Local Similarity 90.9%; Pred. No. 3.8e-43;
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGISSTYYWSWIRQPPGKLEWIGYIYYTWTNYYN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGISSTYYWSWIRQPPGKLEWIGYIYYTWTNYYN 60
QY 61 PSLKSRVTISVDTSKNQPSRLSSVTAADTALYYCARDQGWLLPDAFDIWGGQTMVTVS 120
Db 61 PSLKSRVTISVDTSKNQPSRLSSVTAADTALYYCARDQGWLLPDAFDIWGGQTMVTVS 120
QY 121 S 121
Db 121 S 121
RESULT 13
AD058076
ID AD058076 standard; protein; 243 AA.
XX AC AD058076;
XX DT 12-AUG-2004 (first entry)
XX DE S9 cell derived human scFVVL-VH protein.
XX KW B cell; surface immunoglobulin; Ig; binding site; antigen; human CD28;
XX closed system; detection laser-beam; catcher tube;
XX electrochemical device; fluorescence activated cell sorter; FACS;
XX antibody variable region; human.
XX OS Homo sapiens.
XX PN WO2004044584-A1.
XX
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PD 27-MAY-2004.
XX 12-NOV-2003; 2003WO-EP012664.
XX PR 13-NOV-2002; 2002EP-00025335.
XX PA (MICR-) MICROMET AG.
XX PI Baeuerle P, Hoffmann P, Weinberger S, Kischel R;
XX WPI; 2004-449579/42.
XX DR N-PSDB; ADO58077.
XX PT Identifying a B cell carrying a surface immunoglobulin molecule having a
PT binding site for an antigen of interest, useful for constructing
PT therapeutic antibodies, comprises contacting a sample with the antigen
PT and a receptor.
XX PS Claim 22; SEQ ID NO 76; 156pp; English.
XX CC The invention relates to a novel method for identifying a B cell carrying
CC a surface immunoglobulin (Ig) molecule having a binding site for an
CC antigen of interest. The method comprises contacting a sample putatively
CC containing the B cell with the antigen of interest and with a receptor
CC specifically binding to the Ig molecule, and assessing the presence of
CC the detectable signal. The invention further comprises: an antibody
CC generated by the method above which is specific for human CD28 or
CC comprising an amino acid(s) sequence(s) given in the specification,
CC and/or are encoded by a nucleic acid sequence(s) also given in the
CC specification; and a device for assessing the presence of a detectable
CC signal defined above, where the device comprises a closed system for the
CC detection laser-beam and a catcher tube, and where the B cell of interest
CC can be collected as a single cell by means of an electrochemical device,
CC which is triggered by an electric signal generated by the fluorescence
CC activated cell sorter (FACS) device, where the electrochemical device
CC moves the nozzle of the steady catcher tube liquid stream for a
CC programmed time over a collecting tube, microtiter plate or other
CC container after a B cell is sorted. The method is useful for identifying
CC a B cell carrying a surface Ig molecule having a binding site for an
CC antigen of interest. The method is also useful for cloning of antibody
CC variable regions from the identified B cells, which may subsequently be
CC employed in the construction of proteins such as antibodies or its
CC fragments or derivatives useful in therapeutic approaches. The method is
CC useful as an alternative to phage display for the gain of antibodies or
CC its fragments. This sequence represents an S2 cell derived human
CC polypeptide of the invention.
XX SQ Sequence 243 AA;
Query Match 87.2%; Score 566.5; DB 8; Length 243;
Best Local Similarity 90.1%; Pred. No. 3.6e-40;
Matches 109; Conservative 6; Mismatches 5; Indels 1; Gaps 1;
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGISSTYYWSWIRQPPGKLEWIGYIYYTWTNYYN 60
Db 124 QVQLQESGPGLVKPSSETLSLTCTVSGSGISSTYYWSWIRQPPGKLEWIGYIYYTWTNYYN 183
QY 61 PSLKSRVTISVDTSKNQPSRLSSVTAADTALYYCARDQGWLLPDAFDIWGGQTMVTVS 120
Db 184 PSLKSRVTISVDTSKNQPSRLSSVTAADTALYYCARDQGWLLPDAFDIWGGQTMVTVS 242
QY 121 S 121
Db 243 S 243
RESULT 14
ABG92884
ID ABG92884 standard; protein; 121 AA.
XX AC ABG92884;
XX DT 19-NOV-2002 (first entry)
XX
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XX DE Human immunoglobulin variable light domain #1.
XX KW Immunoglobulin; variable heavy chain; variable light chain; human;
KW G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;
KW immunologic deficiency syndrome; blood protein disorder; nephritis;
KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;
KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;
KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;
KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;
KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;
KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;
KW lymphocytopenia.
XX OS Homo sapiens.
XX PN WO200264612-A2.
XX PD 22-AUG-2002.
XX PF 08-FEB-2002; 2002WO-US003634.
XX PR 09-FEB-2001; 2001US-00779880.
XX PR 09-FEB-2001; 2001WO-US004153.
XX PR 12-JUN-2001; 2001US-0297257P.
XX PR 08-AUG-2001; 2001US-0310458P.
XX PR 12-OCT-2001; 2001US-0328447P.
XX PR 21-DEC-2001; 2001US-0341725P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Roschke V, Rosen CA, Ruben SM;
XX WPI; 2002-643455/69.
XX N-PSDB; ABS68607.
XX New human G-protein Chemokine Receptor gene (HDGNR10) useful for
PT treating, preventing, ameliorating or monitoring diseases or disorders
PT associated with aberrant expression of HDGNR10 e.g. cancer.
XX Example 55; Fig 4; 562pp; English.
XX The invention describes an isolated polynucleotide encoding a first
CC antibody at least 95-100% identical to a second antibody consisting of an
CC amino acid sequence comprising at least one, two or three CDR regions of
CC a variable heavy (VH) or variable light (VL) domain of the antibody
CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,
CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9E6, XF27/28.7D5, XF27/28.18B5,
CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody
CC is useful treating, preventing, ameliorating, prognosing or monitoring
CC cancers or other diseases or disorders e.g. immunologic deficiency
CC syndromes such as blood protein disorders and ataxia telangiectasia,
CC inflammation associated disorders such as endotoxin lethality, nephritis
CC and inflammatory bowel disease, conditions associated with an increase in
CC certain haematopoietic cells such as histiocytosis, defective or aberrant
CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,
CC an infectious disease, an autoimmune disease such as Addison's disease,
CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative
CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or
CC poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma,
CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a
CC disease or disorder associated with aberrant expression of novel human G-
CC protein chemokine receptor (CCR5) HDGNR10. This is the amino acid
CC sequence of human immunoglobulin sequence associated with the antibodies
CC against HDGNR10
XX SQ Sequence 121 AA;
Query Match 84.3%; Score 548; DB 5; Length 121;
Best Local Similarity 86.0%; Pred. No. 6.6e-39;
Matches 104; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYFWSWIRQPGKGLDWIGRIYTSNGTNYN 60

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Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYFWSWIRQPGKGLDWIGRIYTSNGTNYN 60
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAALYYCARDQGWLLPDAFDIWGGTWTWTVS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAALYYCARDQGWLLPDAFDIWGGTWTWTVS 120
QY 121 S 121
Db 121 S 121
RESULT 15
ABB07171
ID ABB07171 standard; protein; 121 AA.
XX
AC ABB07171;
XX
DT 13-MAR-2002 (first entry)
XX
DE ebvHlgM MS119D10 heavy chain variable region sequence.
XX
KW Neuromodulatory; central nervous system; CNS; sHlgM22; LYM 22; AKOR4;
KW ebvHlgM MS119D10; ebv HlgM CB2BG8; CB2IE12; MS119E5; virucide;
KW antiparkinsonian; neuroprotective; neurotropic; vulnerary.
XX
OS Homo sapiens.
XX WO200185797-A1.
XX PN 15-NOV-2001.
XX PD 30-MAY-2000; 2000WO-US014902.
XX PF 10-MAY-2000; 2000US-00568351.
XX PR (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX Rodriguez M, Miller DJ, Pease LR;
XX WPI; 2002-066596/09.
XX N-PSDB; ABA94218.
XX Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting
PT neurite outgrowth, regeneration, remyelination and neuroprotection in
PT central nervous system, useful to treat post-infectious
PT encephalomyelitis.
XX Claim 23; Fig 19; 219pp; English.
XX The invention provides a neuromodulatory agent (I) capable of promoting
CC neurite outgrowth, regeneration, remyelination and neuroprotection in
CC central nervous system (CNS). (I) is capable of inducing remyelination,
CC promoting cellular proliferation of glial cells, and promoting Ca2+
CC signaling with oligodendrocytes. An humanised antibody to (I) can be
CC selected from antibody sHlgM22 (LYM 22), ebvHlgM MS119D10, ebv HlgM
CC CB2BG8, AKOR4, CB2IE12, CB2IE7 or MS119E5. (I) is useful for stimulating
CC remyelination of CNS axons, stimulating proliferation of glial cells in
CC CNS axons, or treating demyelinating disease of CNS in a mammal in need
CC of such therapy. (I) is capable of binding to structures and cells within
CC CNS. (I) is preferably useful for treating a demyelinating disease of CNS
CC of a mouse infected with Strain DA of Theiler's murine encephalomyelitis
CC (TMEV) or for treating a human being having multiple sclerosis, or a
CC human or domestic animal with a viral demyelinating disease, or a post-
CC neural disease of CNS. (I) is also useful for an in vitro method of
CC stimulating the proliferation of glial cells from mixed cell culture. (I)
CC is also useful for stimulating remyelination of CNS axons. The antibodies
CC are useful for preventing infection by a bacterium, virus or like
CC pathogen that causes demyelination or other neurodegenerative condition
CC in a subject. Methods where (I) is administered to a patient are useful
CC for treating multiple sclerosis, Parkinson's disease, Alzheimer's
CC disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating
CC disease, CNS diseases, and other conditions in the CNS where nerves are

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CC damaged as by trauma. The present sequence represents the ebvHigM MS119D10 heavy chain variable region amino acid sequence

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Sequence 121 AA;

Query Match	84.1%	Score 546.5;	DB 5;	Length 121;
Best Local Similarity	87.6%;	Pred. No. 8.8e-39;		
Matches 106;	Conservative	6;	Mismatches 8;	Indels 1; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVSWIRQPPGKGLEWIGIYYTWTWTNYN 60

D**b** 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGIYYSGSTNYN 60

Qy 61 PSLKSRVTISVDTSKNQFSLKSSVTAADTALYYCARDQGWLLPDAFDIWGGTMTVVS 120

D**b** 61 PSLKSRVTISVDTSKNQFSLKLSSTVAADTAVVYCARSQQQLV-YFYDYGQGGLVTVS 119

Qy 121 S 121

Db 120 S 120

Search completed: November 9, 2005, 12:55:25  
Job time : 75.6015 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2005, 11:29:55 ; Search time 18.802 Seconds  
(without alignments)  
480.403 Million cell updates/sec

Title: US-10-660-357A-9

Perfect score: 650

Sequence: 1 QVQLQSGPGLVKPSETLSL.....WLLPDAFDIWGQMTVTWSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	541	83.2	119	3	US-09-025-769B-39
2	541	83.2	119	3	US-09-025-769B-65
3	541	83.2	119	4	US-09-490-070A-39
4	541	83.2	119	4	US-09-490-070A-65
5	541	83.2	119	4	US-09-490-153-39
6	541	83.2	119	4	US-09-490-153-65
7	541	83.2	119	4	US-09-490-324-39
8	541	83.2	119	4	US-09-490-324-65
9	532.5	81.9	118	3	US-09-025-769B-25
10	532.5	81.9	118	4	US-09-490-070A-25
11	532.5	81.9	118	4	US-09-490-153-25
12	532.5	81.9	118	4	US-09-490-324-25
13	532.5	81.9	120	4	US-09-424-840B-20
14	530.5	81.6	244	3	US-08-918-148-79
15	530.5	81.6	244	4	US-09-138-091A-77
16	516.5	79.5	473	3	US-09-049-672A-4
17	503	77.4	142	2	US-08-480-774A-2
18	501	77.1	117	4	US-09-720-493-2
19	500.5	77.0	139	4	US-09-471-276-837
20	499.5	76.8	122	1	US-08-360-125-11
21	499.5	76.8	122	2	US-08-450-578-11
22	499.5	76.8	122	2	US-09-017-628-11
23	499.5	76.8	122	2	US-09-014-880-11
24	499.5	76.8	122	2	US-08-450-363-11
25	499.5	76.8	122	4	US-09-467-903-11
26	495.5	76.2	487	4	US-09-800-729-145
27	489	75.2	116	3	US-08-545-809A-140

28	486	74.8	119	1	US-08-360-125-5
29	486	74.8	119	2	US-08-450-578-5
30	486	74.8	119	2	US-09-017-628-5
31	486	74.8	119	2	US-09-014-880-5
32	486	74.8	119	4	US-08-450-363-5
33	486	74.8	119	4	US-09-467-903-5
34	485	73.9	119	2	US-08-652-816A-10
35	480.5	73.9	172	4	US-09-472-087-7
36	480.5	73.9	172	4	US-09-472-087-86
37	480	73.8	123	3	US-08-753-450-4
38	478	73.5	118	3	US-08-545-809A-142
39	477	73.4	472	3	US-08-793-450-8
40	473.5	72.8	139	4	US-09-203-768A-2
41	472	72.6	115	4	US-09-471-276-888
42	471.5	72.5	118	4	US-09-343-698-6
43	471.5	72.5	118	4	US-08-325-955-6
44	470.5	72.4	832	3	US-08-630-820-7
45	470.5	72.4	832	4	US-09-273-453-7

ALIGNMENTS

RESULT 1  
US-09-025-769B-39  
; Sequence 39, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-025-769B-39

Query Match 83.2%; Score 541; DB 3; Length 119;  
Best Local Similarity 86.8%; Pred. No. 5.2e-46;  
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;





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; STATE: New York
; COUNTRY: USA
; ZIP: 10021
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9090
; TELEFAX: (212)596-9090
;
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 65:
;
; US-09-490-153-65
;
; Query Match 83.2%; Score 541; DB 4; Length 119;
; Best Local Similarity 86.8%; Pred. No. 5.2e-46;
; Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;
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; QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMTIRPPGKLEWIGYIYVTWNTYN 60
; Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMTIRPPGKLEWIGYIYVTWNTYN 60
;
; QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGGTMTVTS 120
; Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGGTMTVTS 120
;
; QY 121 S 121
; Db 119 S 119
;
; RESULT 7
; US-09-490-324-39
; Sequence 39, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
;
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-AUG-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9090
; TELEFAX: (212)596-9090
;
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 65:
;
; US-09-490-324-39
;
; Query Match 83.2%; Score 541; DB 4; Length 119;
; Best Local Similarity 86.8%; Pred. No. 5.2e-46;
; Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;
;
; QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMTIRPPGKLEWIGYIYVTWNTYN 60
; Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMTIRPPGKLEWIGYIYVTWNTYN 60
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; QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGGTMTVTS 120
; Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGGTMTVTS 120
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; QY 121 S 121
; Db 119 S 119
;
; RESULT 8
; US-09-490-324-65
; Sequence 65, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
;
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
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; APPLICATION NUMBER: US/09/025,769
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; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
;   NAME: James F. Haley, Jr., Esq.
;   REGISTRATION NUMBER: 27,794
;   REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212)596-9000
;   TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 65:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 119 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-324-65

Query Match      83.2%; Score 541; DB 4; Length 119;
Best Local Similarity 86.8%; Pred. No. 5.2e-46;
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

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Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYMSWIRQPPGKLEWIGIYYTWTNYYN 60

Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGGTMTVTS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARWGGDGFY--AMDYWGQGTLTVTS 118

Qy 121 S 121
Db 119 S 119

RESULT 9
US-09-025-769B-25
; Sequence 25, Application US/09025769B
; Patent No. 630064
; GENERAL INFORMATION:
;   APPLICANT: Knappik, Achim
;   APPLICANT: Pack, Peter
;   APPLICANT: Ilag, Vic
;   APPLICANT: Ge, Liming
;   APPLICANT: Moroney, Simon
;   APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;   STREET: 1251 Avenue of the Americas
;   CITY: New York
;   STATE: New York
;   COUNTRY: USA
;   ZIP: 10021
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/025,769B
;   FILING DATE: 18-FEB-1998
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: EP 95 11 3021.0
;     FILING DATE: 18-AUG-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME: James F. Haley, Jr., Esq.
;     REGISTRATION NUMBER: 27,794
;     REFERENCE/DOCKET NUMBER: MORPHO/5
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (212)596-9000
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;
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 118 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-25

Query Match      81.9%; Score 532.5; DB 3; Length 118;
Best Local Similarity 85.1%; Pred. No. 3.5e-45;
Matches 103; Conservative 7; Mismatches 8; Indels 3; Gaps 1;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYMSWIRQPPGKLEWIGIYYTWTNYYN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYMSWIRQPPGKLEWIGIYYTWTNYYN 60

Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGGTMTVTS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARGGG---GGVFDYWGQGTLTVTS 117

Qy 121 S 121
Db 118 S 118

RESULT 10
US-09-490-070A-25
; Sequence 25, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
;   APPLICANT: Knappik, Achim
;   APPLICANT: Pack, Peter
;   APPLICANT: Ilag, Vic
;   APPLICANT: Ge, Liming
;   APPLICANT: Moroney, Simon
;   APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
;   White & McAuliffe
;   STREET: 1666 K Street, N.W., Suite 300
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: USA
;   ZIP: 20006
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/490,070A
;   FILING DATE: 24-Jan-2000
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: EP 95 11 3021.0
;     FILING DATE: 18-AUG-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Colin G. Sandercock, Esq.
;     REGISTRATION NUMBER: 31,298
;     REFERENCE/DOCKET NUMBER: 37629-0005
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (202) 912-2000
;       TELEFAX: (202) 912-2020
;   INFORMATION FOR SEQ ID NO: 25:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 118 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: <Unknown>
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
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Db 61 PSLKSRVTISVDTSKNQFSLKSSVTAADTAVYTCARGRG---GGVFDMGQGLVTVS 117  
121 S 121  
118 S 118

RESULT 13  
US-09-424-840B-20  
; Sequence 20, Application US/09424840B  
; Patent No. 6790338  
; GENERAL INFORMATION:  
; APPLICANT: Berchtold, Peter  
; APPLICANT: Escher, Robert F. A.  
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES  
; FILE REFERENCE: 100564-09049  
; CURRENT APPLICATION NUMBER: US/09/424, 840B  
; CURRENT FILING DATE: 1999-12-03  
; PRIOR APPLICATION NUMBER: DE 19820663.1  
; PRIOR FILING DATE: 1998-05-08  
; PRIOR APPLICATION NUMBER: DE 19755227.7  
; PRIOR FILING DATE: 1997-12-12  
; PRIOR APPLICATION NUMBER: DE 19723904.8  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 120  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-424-840B-20

Query Match 81.9%; Score 532.5; DB 4; Length 120;  
Best Local Similarity 84.4%; Pred. No. 3.6e-45;  
Matches 103; Conservative 6; Mismatches 10; Indels 3; Gaps 2;  
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Db 1 QVKLESGLVLPKPSSETLSLTCTVSGGSISSYYMSWIRQPPGKLEWIGIYYSGNTN 60  
Qy 61 PSLKSRVTISVDTSKNQFSLKSSVTAADTAVYTCARDQOQ-WLLPDAFDIWGGTMTV 119  
Db 61 PSLKSRVTISVDTSKNQFSLKSSVTAADTAVYTCARLNDGW--NDGFDIWGGTMTV 118  
Qy 120 SS 121  
Db 119 SS 120

RESULT 14  
US-08-918-148-79  
; Sequence 79, Application US/08918148A  
; Patent No. 6342220  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Camellia  
; APPLICANT: W.  
; APPLICANT: Carter, Paul J.  
; APPLICANT: Fendly, Brian M.  
; APPLICANT: Gurney, Austin L.  
; TITLE OF INVENTION: Agonist Antibodies  
; FILE REFERENCE: P0979  
; CURRENT APPLICATION NUMBER: US/08/918,148A  
; CURRENT FILING DATE: 1997-08-25  
; NUMBER OF SEQ ID NOS: 79  
; SEQ ID NO 79  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: artificial  
US-08-918-148-79

Query Match 81.6%; Score 530.5; DB 3; Length 244;  
Best Local Similarity 84.3%; Pred. No. 1.3e-44;

Matches 102; Conservative 10; Mismatches 2; Indels 7; Gaps 2;  
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Db 3 QVLOQSGPGLVKPSSETLSLTCTVSGGSISSYYMSWIRQPPGKLEWIGIYYSGSTN 62  
Qy 61 PSLKSRVTISVDTSKNQFSLKSSVTAADTAVYTCARDQOQWLLPDAFDIWGGTMTV 120  
Db 63 PSLKSRVTISVDTSKNQFSLKSSVTAADTAVYTCAR--GRY-----FDWGRGTMTV 115  
Qy 121 S 121  
Db 116 S 116

RESULT 15  
US-09-138-091A-77  
; Sequence 77, Application US/09138091A  
; Patent No. 6737249  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Camellia W.  
; APPLICANT: Carter, Paul J.  
; APPLICANT: Fendly, Brian M.  
; APPLICANT: Gurney, Austin L.  
; TITLE OF INVENTION: Agonist Antibodies  
; FILE REFERENCE: 9491-013-27  
; CURRENT APPLICATION NUMBER: US/09/138,091A  
; CURRENT FILING DATE: 1998-08-21  
; PRIOR APPLICATION NUMBER: US 60/056,736  
; PRIOR FILING DATE: 1997-08-22  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 77  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: single chain antibody (scFv) fragments  
US-09-138-091A-77

Query Match 81.6%; Score 530.5; DB 4; Length 244;  
Best Local Similarity 84.3%; Pred. No. 1.3e-44;  
Matches 102; Conservative 10; Mismatches 2; Indels 7; Gaps 2;  
Qy 1 QVLOESGPGLVKPSSETLSLTCTVSGGSISSYYMSWIRQPPGKLEWIGIYYTWTN 60  
Db 3 QVLOQSGPGLVKPSSETLSLTCTVSGGSISSYYMSWIRQPPGKLEWIGIYYSGSTN 62  
Qy 61 PSLKSRVTISVDTSKNQFSLKSSVTAADTAVYTCARDQOQWLLPDAFDIWGGTMTV 120  
Db 63 PSLKSRVTISVDTSKNQFSLKSSVTAADTAVYTCAR--GRY-----FDWGRGTMTV 115  
Qy 121 S 121  
Db 116 S 116

Search completed: November 9, 2005, 11:46:37  
Job time: 18.802 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:40:37 ; Search time 67.2222 Seconds  
(without alignments)  
753.137 Million cell updates/sec

Title: US-10-660-357A-9  
Perfect score: 650  
Sequence: 1 QVQLQESGPGLVKPSSTLSL.....WLLPDAFDIGQGTWMTVSS 121

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues  
Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep:\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
- 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	650	100.0	121	14 US-10-330-613-9	Sequence 9, Appli
2	650	100.0	121	14 US-10-330-530-9	Sequence 9, Appli
3	650	100.0	121	16 US-10-660-357-9	Sequence 9, Appli
4	643	98.9	121	14 US-10-330-613-1	Sequence 1, Appli
5	643	98.9	121	14 US-10-330-613-17	Sequence 17, Appli
6	643	98.9	121	14 US-10-330-530-1	Sequence 1, Appli
7	643	98.9	121	14 US-10-330-530-17	Sequence 17, Appli
8	643	98.9	121	16 US-10-660-357-1	Sequence 1, Appli
9	643	98.9	121	16 US-10-660-357-17	Sequence 17, Appli
10	598	92.0	121	14 US-10-330-613-37	Sequence 37, Appli
11	598	92.0	121	14 US-10-330-530-37	Sequence 37, Appli

12	598	92.0	121	16 US-10-660-357-37	Sequence 37, Appli
13	554.5	85.3	118	15 US-10-292-088-142	Sequence 142, App
14	550.5	84.7	118	15 US-10-292-088-109	Sequence 109, App
15	548	84.3	121	14 US-10-067-800-60	Sequence 60, Appl
16	548	84.3	121	18 US-10-994-678-60	Sequence 60, Appl
17	546.5	84.1	121	14 US-10-010-729-11	Sequence 11, Appl
18	546.5	84.1	122	15 US-10-309-762-24	Sequence 24, Appl
19	546.5	84.1	122	15 US-10-309-762-27	Sequence 27, Appl
20	546	84.0	119	17 US-10-937-596-23	Sequence 23, Appl
21	545.5	83.9	122	15 US-10-309-762-25	Sequence 25, Appl
22	545.5	83.9	122	15 US-10-309-762-29	Sequence 29, Appl
23	541	83.2	119	14 US-10-125-687-5	Sequence 5, Appli
24	541	83.2	119	18 US-10-996-191-5	Sequence 5, Appli
25	540.5	83.2	118	17 US-10-727-155-178	Sequence 178, App
26	540	83.1	123	15 US-10-371-942-102	Sequence 102, App
27	539.5	83.0	122	15 US-10-309-762-71	Sequence 71, Appl
28	539.5	83.0	141	15 US-10-309-762-90	Sequence 90, Appl
29	537.5	82.7	120	15 US-10-309-762-4	Sequence 4, Appli
30	537.5	82.7	121	15 US-10-309-762-102	Sequence 102, App
31	537.5	82.7	121	15 US-10-309-762-154	Sequence 154, App
32	537	82.6	119	15 US-10-309-762-143	Sequence 143, App
33	537	82.6	125	15 US-10-309-762-11	Sequence 11, Appl
34	537	82.6	142	17 US-10-893-576-37	Sequence 37, Appl
35	535.5	82.4	122	15 US-10-309-762-73	Sequence 73, Appl
36	535.5	82.4	141	15 US-10-309-762-94	Sequence 94, Appl
37	534.5	82.2	116	18 US-10-822-306A-5	Sequence 5, Appli
38	534.5	82.2	124	15 US-10-309-762-26	Sequence 26, Appl
39	534.5	82.2	193	15 US-10-264-049-4331	Sequence 4331, Ap
40	533.5	82.1	118	17 US-10-706-689-10	Sequence 10, Appl
41	533.5	82.1	118	18 US-10-988-360-10	Sequence 10, Appl
42	533.5	82.1	128	15 US-10-173-551-24	Sequence 24, Appl
43	532.5	81.9	120	16 US-10-844-424-20	Sequence 20, Appl
44	532.5	81.9	121	17 US-10-805-177-56	Sequence 56, Appl
45	532.5	81.9	126	14 US-10-067-800-68	Sequence 68, Appl

ALIGNMENTS

RESULT 1  
US-10-330-613-9  
; Sequence 9, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-9

Query Match	100.0%;	Score 650;	DB 14;	Length 121;
Best Local Similarity	100.0%;	Pred. No. 3.5e-49;		
Matches 121;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	QVQLQESGPGLVKPSSTLSLTCTVSGGSISSYWSWIROP	PKGLEWIGYIYTTWNTYN	60
Db	1	QVQLQESGPGLVKPSSTLSLTCTVSGGSISSYWSWIROP	PKGLEWIGYIYTTWNTYN	60
QY	61	PSLKSRTVTSVDTSKNQFSLRSSVTAADTALYYCARDQ	QWLLPDAFDIGQGTWMTVS	120
Db	61	PSLKSRTVTSVDTSKNQFSLRSSVTAADTALYYCARDQ	QWLLPDAFDIGQGTWMTVS	120
QY	121	\$	121	

Db 121 S 121

RESULT 2

US-10-330-530-9

; Sequence 9, Application US/10330530

; Publication No. US20030152514A1

; GENERAL INFORMATION:

; APPLICANT: Gudas, Jean

; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES

; FILE REFERENCE: ABGENIX 031A

; CURRENT APPLICATION NUMBER: US/10/330,530

; CURRENT FILING DATE: 2002-12-26

; PRIOR APPLICATION NUMBER: US 60/346414

; PRIOR FILING DATE: 2001-12-18

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9

; LENGTH: 121

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-330-530-9

Query Match 100.0%; Score 650; DB 14; Length 121;

Best Local Similarity 100.0%; Pred. No. 3.5e-49;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTN 60

Db 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTN 60

QY 61 PSLSKRVITISVDTSKNQPSLRSLSSVTAADTALYYCARDQGWLLPDADFIMGQGTWTV 120

Db 61 PSLSKRVITISVDTSKNQPSLRSLSSVTAADTALYYCARDQGWLLPDADFIMGQGTWTV 120

QY 121 S 121

Db 121 S 121

RESULT 3

US-10-660-357-9

; Sequence 9, Application US/10660357

; Publication No. US20040115205A1

; GENERAL INFORMATION:

; APPLICANT: Bar-Eli, Menashe

; APPLICANT: Green, Larry L.

; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18

; FILE REFERENCE: ABGENIX 030C1

; CURRENT APPLICATION NUMBER: US/10/660,357

; CURRENT FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 10/330,580

; PRIOR FILING DATE: 2002-12-26

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9

; LENGTH: 121

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-660-357-9

Query Match 100.0%; Score 650; DB 16; Length 121;

Best Local Similarity 100.0%; Pred. No. 3.5e-49;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTN 60

Db 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTN 60

QY 61 PSLSKRVITISVDTSKNQPSLRSLSSVTAADTALYYCARDQGWLLPDADFIMGQGTWTV 120

Db 61 PSLSKRVITISVDTSKNQPSLRSLSSVTAADTALYYCARDQGWLLPDADFIMGQGTWTV 120

QY 121 S 121

Db 121 S 121

RESULT 4

US-10-330-613-1

; Sequence 1, Application US/10330613

; Publication No. US20030147809A1

; GENERAL INFORMATION:

; APPLICANT: Gudas, Jean

; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN

; FILE REFERENCE: ABGENIX 022A

; CURRENT APPLICATION NUMBER: US/10/330,613

; CURRENT FILING DATE: 2002-12-26

; PRIOR APPLICATION NUMBER: 60/346299

; PRIOR FILING DATE: 2001-12-18

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 121

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-330-613-1

Query Match 98.9%; Score 643; DB 14; Length 121;

Best Local Similarity 98.3%; Pred. No. 1.4e-48;

Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTN 60

Db 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTN 60

QY 61 PSLSKRVITISVDTSKNQPSLRSLSSVTAADTALYYCARDQGWLLPDADFIMGQGTWTV 120

Db 61 PSLSKRVITISVDTSKNQPSLRSLSSVTAADTALYYCARDQGWLLPDADFIMGQGTWTV 120

QY 121 S 121

Db 121 S 121

RESULT 5

US-10-330-613-17

; Sequence 17, Application US/10330613

; Publication No. US20030147809A1

; GENERAL INFORMATION:

; APPLICANT: Gudas, Jean

; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN

; FILE REFERENCE: ABGENIX 022A

; CURRENT APPLICATION NUMBER: US/10/330,613

; CURRENT FILING DATE: 2002-12-26

; PRIOR APPLICATION NUMBER: 60/346299

; PRIOR FILING DATE: 2001-12-18

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 17

; LENGTH: 121

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-330-613-17

Query Match 98.9%; Score 643; DB 14; Length 121;

Best Local Similarity 98.3%; Pred. No. 1.4e-48;

Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTN 60

Db 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTN 60

QY 61 PSLSKRVITISVDTSKNQPSLRSLSSVTAADTALYYCARDQGWLLPDADFIMGQGTWTV 120

Db 61 PSLSKRVITISVDTSKNQPSLRSLSSVTAADTALYYCARDQGWLLPDADFIMGQGTWTV 120

QY 121 S 121

Db 121 S 121

Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
QY 121 S 121  
Db 121 S 121

## RESULT 6

US-10-330-530-1  
; Sequence 1, Application US/10330530  
; Publication No. US20030152514A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES  
; FILE REFERENCE: ABGENIX.031A  
; CURRENT APPLICATION NUMBER: US/10/330,530  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: US 60/346414  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-530-1

Query Match 98.9%; Score 643; DB 14; Length 121;  
Best Local Similarity 98.3%; Pred. No. 1.4e-48;  
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSGPGLVFPSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGIYYTWTNYN 60  
Db 1 QVQLQSGPGLVFPSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGIYYTWTNYN 60  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
QY 121 S 121  
Db 121 S 121

## RESULT 7

US-10-330-530-17  
; Sequence 17, Application US/10330530  
; Publication No. US20030152514A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES  
; FILE REFERENCE: ABGENIX.031A  
; CURRENT APPLICATION NUMBER: US/10/330,530  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: US 60/346414  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-530-17

Query Match 98.9%; Score 643; DB 14; Length 121;  
Best Local Similarity 98.3%; Pred. No. 1.4e-48;  
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSGPGLVFPSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGIYYTWTNYN 60  
Db 1 QVQLQSGPGLVFPSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGIYYTWTNYN 60  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120

Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
QY 121 S 121  
Db 121 S 121

## RESULT 8

US-10-660-357-1  
; Sequence 1, Application US/10660357  
; Publication No. US20040115205A1  
; GENERAL INFORMATION:  
; APPLICANT: Bar-Eli, Menashe  
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18  
; TITLE OF INVENTION: ANTIGEN  
; FILE REFERENCE: ABGENIX.030C1  
; CURRENT APPLICATION NUMBER: US/10/660,357  
; CURRENT FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 10/330,580  
; PRIOR FILING DATE: 2002-12-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-660-357-1

Query Match 98.9%; Score 643; DB 16; Length 121;  
Best Local Similarity 98.3%; Pred. No. 1.4e-48;  
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSGPGLVFPSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGIYYTWTNYN 60  
Db 1 QVQLQSGPGLVFPSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGIYYTWTNYN 60  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
QY 121 S 121  
Db 121 S 121

## RESULT 9

US-10-660-357-17  
; Sequence 17, Application US/10660357  
; Publication No. US20040115205A1  
; GENERAL INFORMATION:  
; APPLICANT: Bar-Eli, Menashe  
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18  
; TITLE OF INVENTION: ANTIGEN  
; FILE REFERENCE: ABGENIX.030C1  
; CURRENT APPLICATION NUMBER: US/10/660,357  
; CURRENT FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 10/330,580  
; PRIOR FILING DATE: 2002-12-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-660-357-17

Query Match 98.9%; Score 643; DB 16; Length 121;  
Best Local Similarity 98.3%; Pred. No. 1.4e-48;  
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy	1	QVQLQESGPGLVKPKSETLSLTCTVSGGSISSYYMSWITROPCKGLEWIGIYYTWTNIN	60
Db	1	QVQLQESGPGLVKPKSETLSLTCTVSGGSISSYYMSWITROPCKGLEWIGIYYTWTNIN	60
Qy	61	PSLKSRTVISVTSKNQFSRLRSVTAADTALYYCARDQGWLLPDAFDIWGGTMTVTS	120
Db	61	PSLKSRTVISVTSKNQFSRLRSVTAADTALYYCARDQGWLLPDAFDIWGGTMTVTS	120
Qy	121	\$ 121	
Db	121	\$ 121	

```

RESULT 10
US-10-330-613-37
; Sequence 37, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: AGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-37

```

Query Match	92.0%;	Score 598;	DB 14;	Length 121;
Best Local Similarity	90.9%;	Pred. No. 1.2e-44;		
Matches 110; Conservative	7;	Mismatches 4;	Indels 0;	Gaps 0;

[illegible]

```

RESULT 11
US-10-330-530-37
; Sequence 37, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: AGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-37

```

Query Match 92.0%; Score 598; DB 14; Length 121;  
Best Local Similarity 90.9%; Pred. No. 1.2e-44;  
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy	1	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYMSWIRQPPCKGLEWIGYIYTTWTTNN	60
Db	1	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYMSWIRQPPCKGLEWIGYIYTTGNTYN	60
Qy	61	PSLSKRVTVISVDTSKNPFSLRLSVTAADTALYYCARDQGWLLPDAFDIWQGGTMTVTS	120
Db	61	PSLSKRVTVISVDTSKNPFSLKLSNVTAAATVAYYCARDPGQWLVPDAFDIWQGGTMTVS	120
Qy	121	S 121	
Db	121	S 121	

```

RESULT 12
US-10-660-357-37
; Sequence 37, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-37

```

```

Query Match          92.0%;   Score 598;   DB 16;   Length 121;
Best Local Similarity 90.9%;   Pred. No. 1.2e-44;
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0

```

Qy	1	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYMSWIRQPPCKGLEWIGYIYYTWTN	60
		QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYMSWIRQPPCKGLEWIGYIYYTWTN	60
Qy	61	PSLKSRTVISVDTSKNQPSLRLSSVTAADTALYYCARDQGWLLPDAFDIWCQGTWTVS	120
		PSLKSRTVISVDTSKNQPSLRLSSVTAADTALYYCARDQGWLLPDAFDIWCQGTWTVS	120
Qy	121	S 121	
		S 121	

```

RESULT 13
US-10-292-088-142
; Sequence 142, Application US/10292088
; Publication No. US2003021100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAMH
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 142
; LENGTH: 118

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; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/341,725
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-60

Query Match      84.3%; Score 548; DB 14; Length 121;
Best Local Similarity 86.0%; Pred. No. 2.8e-40;
Matches 104; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy      1 QVQLQSGPGLVKPSETSLTCTVSGSGSISSYYTWSWIROPKGLGWIGYIYYTWTN 60
Db      1 QVQLQSGPGLVKPSETSLTCTVSGSGSISSYYTWSWIROPKGLGWIGRIYTS 60

Qy      61 PSLSKRVTTISVDFTSKNQFSLRLSSVTAADTALVYCARDGOWMLLPDAFD 120
Db      61 PSLSKRVTTISVDFTSKNRFSLKSSVTAADTAVIYCARDRGSSWYPDAFD 120

Qy      121 S 121
Db      121 S 121

Search completed: November 9, 2005, 12:42:58
Job time : 67.2222 secs

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Query Match      84.7%;   Scred 550.5;   DB 15;   Length 118;
Best Local Similarity 87.6%;   Pred. No. 1.7e-40;
Matches 106;   Conservative 5;   Mismatches 7;   Indels 3;   Gaps 1;

QY      1  QVQLQESGPGGLVFPSETLSLTCTVSGGSISSYYMSWIRQPPGKLEWIGYIYYTWTNYYN 60
Db      1  QVQLQESGPGGLVFPSETLSLTCTVSGGSISSYYMSWIRQPPGKLEWIGYIYYSGSTNYYN 60

QY      61  PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGGWLLPDAFDIWGQGTMTVTS 120
Db      61  PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDYGG---NSYFDYWGQGTMTVTS 117

QY      121  S 121
Db      118  S 118

RESULT 15
US-10-067-800-60
; Sequence 60, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.1150001
; CURRENT APPLICATION NUMBER: US/10/067.800

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 12:25:58 ; Search time 13.0401 Seconds  
(without alignments)  
892.802 Million cell updates/sec

Title: US-10-660-357A-9

Perfect score: 650

Sequence: 1 QVQLQSGPGLVKPSETLSL.....WLLPDAFDIWGQGMVTVS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- PIR\_79:\*
- 1: pir1:\*
- 2: pir2:\*
- 3: pir3:\*
- 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	544	83.7	140	2 I37782	Ig variable region
2	534	82.2	130	2 S31690	Ig heavy chain V r
3	532	81.8	155	2 S31512	Ig heavy chain - h
4	529	81.4	155	2 S31511	Ig heavy chain - h
5	527.5	81.2	139	2 S31586	Ig heavy chain V r
6	519.5	79.9	130	2 S30534	Ig heavy chain V r
7	513.5	79.0	137	2 S31676	Ig heavy chain V r
8	510.5	78.5	118	2 S20780	Ig heavy chain V r
9	506	77.8	147	2 S13519	Ig heavy chain V r
10	499.5	76.8	140	2 S78052	Ig heavy chain pre
11	496	76.3	135	2 S78051	Ig heavy chain pre
12	491	75.5	105	2 S44125	Ig lambda chain V
13	490	75.4	97	2 S26906	Ig heavy chain V r
14	490	75.4	146	2 S09711	Ig heavy chain V r
15	489	75.2	116	2 B26340	Ig heavy chain pre
16	487	74.9	97	2 S12416	Ig heavy chain V r
17	487	74.9	121	2 S44113	Ig heavy chain V r
18	486	74.8	140	2 A49045	Ig heavy chain V r
19	482	74.2	139	2 S31696	Ig heavy chain V r
20	478	73.5	118	2 A26340	Ig heavy chain pre
21	475.5	73.2	129	2 S44114	Ig heavy chain V r
22	475	73.1	123	2 S30530	Ig heavy chain V r
23	474.5	73.0	126	2 S47010	Ig heavy chain V4
24	474.5	73.0	145	2 S78055	Ig heavy chain pre
25	469.5	72.2	118	2 S24443	Ig heavy chain V r
26	468	72.0	99	2 S26802	Ig heavy chain V r
27	468	72.0	99	2 S26803	Ig heavy chain V r
28	468	72.0	220	2 A49444	Ig gamma-1 heavy c
29	467	71.8	97	2 PH0876	Ig heavy chain V r

30	466	71.7	99	2 S12412	Ig heavy chain V r
31	463	71.2	143	2 B49028	Ig heavy chain V-I
32	461	70.9	97	2 S26804	Ig heavy chain V r
33	461	70.9	116	2 S18557	Ig heavy chain V r
34	460.5	70.8	122	2 D41287	Ig heavy chain V-I
35	459	70.6	99	2 S26801	Ig heavy chain V r
36	459	70.6	134	2 S54906	Ig heavy chain V r
37	459	70.6	146	2 S09710	Ig heavy chain V r
38	456.5	70.2	110	2 S44110	Ig heavy chain V-D
39	455.5	70.1	146	1 G1HUH2	Ig heavy chain pre
40	455	70.0	99	2 S12418	Ig heavy chain V r
41	453	69.7	140	2 A24770	Ig heavy chain V r
42	452	69.5	109	2 PH1673	hypothetical hybri
43	452	69.5	135	2 S31604	Ig heavy chain V r
44	450	69.2	115	2 S57464	Ig heavy chain V-J
45	449.5	69.2	231	2 B23746	Ig Fab region IV-J

ALIGNMENTS

RESULT 1

I37782

Ig variable region (VDJ) (clone T23-9) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999

C;Accession: I37782; S25476

R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.

Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994

A;Title: Somatic diversification in the heavy chain variable region genes expressed by

A;Reference number: A36876; MUID:94119917; PMID:8290556

A;Accession: I37782

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-140 <RES>

A;Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;46-128/Domain: immunoglobulin homology <IMM>

Query Match	83.7%	Score	544;	DB	2;	Length	140;
Best Local Similarity	86.0%	Pred. No.	6.4e-42;				
Matches	104;	Conservative	5;	Mismatches	12;	Indels	0;
Gaps	0;						
Qy	1	QVQLQSGPGLVKPSETLSL	CTVSGGSISSYVSWIRQPPGKLEWIGYIYTTWTN	YN	60		
Db	20	QVQLQSGPGLVKPSETLSL	CTVSGGSISSYVSWIRQPPGKLEWIGYIYSGSTN	YN	79		
Qy	61	PSLKSRTISVDTSKNQFSLRLSSVTAADTALYYCAR	DQGWLLPDAFDIWGQGMVTVS	120			
Db	80	PSLKSRTISVDTSKNQFSLRLSSVTAADTAVYYCAR	HNSSSWVGRYFDYWGQGLTVTS	139			
Qy	121	S 121					
Db	140	S 140					

RESULT 2

S31690

Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C;Accession: S31690

R;Quisnier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.

submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate from the

A;Reference number: S31585

A;Accession: S31690

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-130 <CUI>

A;Cross-references: EMBL:Z14199; NID:g30984; PIDN:CAA78568.1; PID:g30985

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;20-102/Domain: immunoglobulin homology <IMM>

Query Match 82.2%; Score 534; DB 2; Length 130;  
Best Local Similarity 84.0%; Pred. No. 4.7e-41;  
Matches 105; Conservative 5; Mismatches 11; Indels 4; Gaps 1;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIROPKGLGWIGYIYYTWTN 60  
Db 6 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIROPKGLGWIGYIYYTWTN 65  
  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWL- -LPDAFDIWGQGTW 116  
Db 66 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARGSSVLLWFGEILYYFDWVGQGT 125  
  
QY 117 VTVSS 121  
Db 126 VTVSS 130

RESULT 3  
S31512  
Ig heavy chain - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S31512  
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto  
A:Reference number: S31509  
A:Accession: S31512  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-155 <CHA>  
A:Cross-references: EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PID:g33083  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;47-129/Domain: immunoglobulin homology <IMM>

Query Match 81.8%; Score 532; DB 2; Length 155;  
Best Local Similarity 82.1%; Pred. No. 8.5e-41;  
Matches 101; Conservative 7; Mismatches 13; Indels 2; Gaps 1;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIROPKGLGWIGYIYYTWTN 60  
Db 33 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIROPKGLGWIGYIYYTWTN 92  
  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWL- -QWLLPDAFDIWGQGTW 118  
Db 93 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARGGSISSYYVYGGMDVWGQGTW 152  
  
QY 119 VSS 121  
Db 153 VSS 155

RESULT 4  
S31511  
Ig heavy chain - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S31511  
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto  
A:Reference number: S31509  
A:Accession: S31511  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-155 <CHA>  
A:Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID:g33095  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;47-129/Domain: immunoglobulin homology <IMM>

Query Match 81.4%; Score 529; DB 2; Length 155;  
Best Local Similarity 82.9%; Pred. No. 1.6e-40;  
Matches 102; Conservative 5; Mismatches 14; Indels 2; Gaps 1;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIROPKGLGWIGYIYYTWTN 60  
Db 33 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIROPKGLGWIGYIYYTWTN 92  
  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWL- -QWLLPDAFDIWGQGTW 118  
Db 93 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARGGSISSYYVYGGMDVWGQGTW 152  
  
QY 119 VSS 121  
Db 153 VSS 155

RESULT 5  
S31586  
Ig heavy chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S31586  
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.  
submitted to the EMBL Data Library, June 1992  
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A:Reference number: S31585  
A:Accession: S31586  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-139 <CUU>  
A:Cross-references: EMBL:Z14196; NID:g30978; PIDN:CAA78565.1; PID:g30979  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 527.5; DB 2; Length 139;  
Best Local Similarity 86.0%; Pred. No. 1.9e-40;  
Matches 104; Conservative 6; Mismatches 10; Indels 1; Gaps 1;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIROPKGLGWIGYIYYTWTN 60  
Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWWSWIROPKGLGWIGYIYYTWTN 79  
  
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWL- -QWLLPDAFDIWGQGTW 120  
Db 80 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARG-GLGIRRGAFDIWGQGTW 138  
  
QY 121 S 121  
Db 139 S 139

RESULT 6  
S30534  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Aug-1996  
C:Accession: S30534  
R;Mariette, X.  
submitted to the EMBL Data Library, October 1992  
A:Reference number: S30520  
A:Accession: S30534  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-130 <MAR>  
A:Cross-references: EMBL:Z18320  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;15-99/Domain: immunoglobulin homology <IMM>  
  
Query Match 79.9%; Score 519.5; DB 2; Length 130;

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Best Local Similarity 81.5%; Pred. No. 9.4e-40;
Matches 106; Conservative 6; Mismatches 9; Indels 9; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYSWIRQPPGKLEWIGYIYYTWTN 58
Db 1 QVQLQESGPGLVKPSQTLSTLTCTVSGGSISSGYSWIRQPPGKLEWIGRIYTSNSTN 60

QY 59 YNPGLSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGO-WL-----LPDAFDIW 111
Db 61 YNPGLSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDKGGFWSGYYTRNSRAAFDIW 120

QY 112 GQGTMTVTSS 121
Db 121 GQGTMTVTSS 130

RESULT 7
S31676
Ig heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31676
R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
Submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31676
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-137 <CUI>
A/Cross-references: EMBL:Z14102; NID:g31031; PIDN:CAA78551.1; PID:g31032
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 513.5; DB 2; Length 137;
Best Local Similarity 83.5%; Pred. No. 3.4e-39;
Matches 101; Conservative 6; Mismatches 11; Indels 3; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYSWIRQPPGKLEWIGYIYYTWTN 60
Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYSWIRQPPGKLEWIGRIYTSNSTN 79

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGO-WL-----LPDAFDIW 120
Db 80 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDAP--LTYGMDVWGQGTMTVTS 136

QY 121 S 121
Db 137 S 137

RESULT 8
S20780
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C/Accession: S20780
R/Mortari, F.; Wang, J.; Schroeder, H.W.
Submitted to the EMBL Data Library, April 1992
A/Description: Analysis of human cord blood Ig heavy chain Iga and Igg repertoire.
A/Reference number: S20764
A/Accession: S20780
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-118 <MOR>
A/Cross-references: EMBL:Z11958; NID:g33893; PIDN:CAA78015.1; PID:g33894
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 78.5%; Score 510.5; DB 2; Length 118;
Best Local Similarity 81.0%; Pred. No. 5.4e-39;
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Matches 98; Conservative 11; Mismatches 9; Indels 3; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYSWIRQPPGKLEWIGYIYYTWTN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSGYSWIRQPPGKLEWIAFIYRTGSHYN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGO-WL-----LPDAFDIW 120
Db 61 PSLKSRVTISVDTSKNQFSLKMTSVTAADTAVYSCARDGR---DGGFDIWGQGTMTVTS 117

QY 121 S 121
Db 118 S 118

RESULT 9
S13519
Ig heavy chain V region precursor - human
C/Species: Homo sapiens (man)
C/Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S13519
R/Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.
Nucleic Acids Res. 19, 673, 1991
A/Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked
A/Reference number: S13519; MUID:91187691; PMID:2011536
A/Accession: S13519
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-147 <MOR>
A/Cross-references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;41-125/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 506; DB 2; Length 147;
Best Local Similarity 82.1%; Pred. No. 1.7e-38;
Matches 101; Conservative 7; Mismatches 11; Indels 4; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSI--SSYYSWIRQPPGKLEWIGYIYYTWTN 58
Db 27 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSYWGWIRQPPGKLEWIGSIYSGSTY 86

QY 59 YNPGLSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGO-WL-----LPDAFDIW 118
Db 87 YNPGLSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARPL-LW-FGEELFDYWGGTTLVT 144

QY 119 VSS 121
Db 145 VSS 147

RESULT 10
S78052
Ig heavy chain precursor V-D-J region (clone mAb 63VH) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C/Accession: S78052; S23717
R/Harindranath, N.
Submitted to the EMBL Data Library, August 1990
A/Reference number: S78051
A/Accession: S78052
A/Molecule type: mRNA
A/Residues: 1-140 <HAR>
A/Cross-references: EMBL:X54441; NID:g37815; PIDN:CAA38308.1; PID:g930118
R/Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin
Int. Immunol. 3, 865-875, 1991
A/Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and
patient.
A/Reference number: S23716; MUID:92031262; PMID:1718404
A/Accession: S23717
A/Molecule type: mRNA
A/Residues: 15-111 <HAW>
A/Cross-references: EMBL:X54441
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Search completed: November 9, 2005, 13:08:02  
Job time : 14.0401 secs

RESULT 14  
S09711  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
C:Accession: S09711  
R:Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.  
Biochem. J. 268, 135-140, 1990  
A:Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of  
A:Reference number: S09710; MUID:90262535; PMID:2111699  
A:Accession: S09711  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-146 <HUG>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 75.4%; Score 490; DB 2; Length 146;  
Best Local Similarity 74.0%; Pred. No. 4.7e-37;  
Matches 97; Conservative 11; Mismatches 9; Indels 14; Gaps 3;  
  
Qy 1 QVQLQSGPGLVXPSETLSLTCTVSGGSISS--YYMSWIRQPPKGLGWIGIYYTWTN 58  
Db 20 QVQLQSGPGLVXPSETLSLTCTVSGGSSVSSGLYMSWIRQPPKGLGWIGIYYSGSTN 79  
  
Qy 59 YNPSLSKRVITISVDTSKNQSFSLSSVTAADTALYYCAR-----DQGWLLPDAFDI 110  
Db 80 YNPSLSKRVITISVDTSKNQSFSLKGLSVTAADTAVYYCARVLVSRGTSISQSYTNM---DV 135  
  
Qy 111 WGQGTWTVTVSS 121  
Db 136 WKGTTVTVTVSS 146

RESULT 15  
B26340  
Ig heavy chain precursor V-II region (71-4) - human  
C:Species: Homo sapiens (man)  
C:Date: 03-Jun-1988 #sequence\_revision 30-Jun-1991 #text\_change 23-Jul-1999  
C:Accession: B26340  
R:Kodaira, M.; Kinashi, T.; Umemura, I.; Matsuda, F.; Noma, T.; Ono, Y.; Honjo, T.  
J. Mol. Biol. 190, 529-541, 1986  
A:Title: Organization and evolution of variable region genes of the human immunoglobulin  
A:Reference number: A26340; MUID:87061007; PMID:3097326  
A:Accession: B26340  
A:Molecule type: DNA  
A:Residues: 1-116 <KOD>  
A:Cross-references: GB:X05711; NID:G33602; PIDN:CAA29183.1; PID:G296660  
A:Note: the authors translated the codon GAG for residue 25 as Gln  
C:Genetics: 16/1  
A:Introns: 16/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-116/Product: Ig heavy chain V region 71-4 #status predicted <MAT>  
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 75.2%; Score 489; DB 2; Length 116;  
Best Local Similarity 93.8%; Pred. No. 4.5e-37;  
Matches 91; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 QVQLQSGPGLVXPSETLSLTCTVSGGSISSYYMSWIRQPPKGLGWIGIYYTWTN 60  
Db 20 QVQLQSGPGLVXPSETLSLTCTVSGGSSVSSGLYMSWIRQPPKGLGWIGIYYSGSTN 79  
  
Qy 61 PSLKSRVITISVDTSKNQSFSLSSVTAADTALYYCAR 97  
Db 80 PSLKSRVITISVDTSKNQSFSLKGLSVTAADTAVYYCAR 116

CLASS 2000 10 2000 10 11

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:46:52 ; Search time 62.4712 Seconds  
(without alignments)  
991.843 Million cell updates/sec

Title: US-10-660-357A-9  
Perfect score: 650  
Sequence: 1 QVQLQESGPGLVKPSSTLSL.....WLLPDADFIMGGQMTVTSS 121

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_03:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	517	79.5	476	2	Q6GMX1	Q6gm1 homo sapien
2	516	79.4	119	2	Q9UL73	Q9ul73 homo sapien
3	509.5	78.4	465	2	Q6GMX6	Q6gm6 homo sapien
4	502.5	77.3	620	2	Q96EY0	Q96ey0 homo sapien
5	499.5	76.8	477	2	Q6GMX7	Q6gm7 homo sapien
6	496	76.3	139	2	Q86SX2	Q86sx2 homo sapien
7	494.5	76.1	478	2	Q72379	Q72379 homo sapien
8	478.5	73.6	150	2	Q95973	Q95973 homo sapien
9	473.5	72.8	576	2	Q6P418	Q6p418 homo sapien
10	473	72.8	492	2	Q72374	Q72374 homo sapien
11	461.5	71.0	496	2	Q96KX8	Q96kx8 homo sapien
12	455.5	70.1	146	1	HV21 HUMAN	P06331 homo sapien
13	453	69.7	478	2	Q6NYH3	Q6nyh3 homo sapien
14	452	69.5	595	2	Q8WUX4	Q8wux4 homo sapien
15	452	69.5	597	2	Q6GMX5	Q6gm5 homo sapien
16	452	69.5	597	2	Q9BU10	Q9bu10 homo sapien
17	452	69.5	625	2	Q96AA6	Q96aa6 homo sapien
18	450	69.2	597	2	Q9BQB8	Q9bqb8 homo sapien
19	446	68.6	129	1	HV2F HUMAN	P01824 homo sapien
20	439	67.5	117	1	HV2G HUMAN	P01825 homo sapien
21	436.5	67.2	130	2	Q81ZD7	Q81zd7 homo sapien
22	417.5	64.2	116	2	Q723V6	Q723v6 homo sapien
23	407.5	62.7	122	2	Q9UL75	Q9ul75 homo sapien
24	405	62.3	479	2	Q99M22	Q99m22 mus musculus
25	395	60.8	476	2	Q6MZK7	Q6mzx7 homo sapien
26	392.5	60.4	136	2	Q6LRQ5	Q6lbq5 mus musculus
27	392	60.3	137	1	HV45 MOUSE	P01822 mus musculus
28	387.5	59.6	473	2	Q8TC63	Q8tc63 homo sapien
29	378	58.2	113	1	HV47 MOUSE	P01823 mus musculus
30	375	57.7	262	2	Q65Z11	Q65z11 mus musculus
31	374.5	57.6	482	2	Q91X92	Q91x92 mus musculus

RESULT 1

ID	Q6GMX1	PRELIMINARY;	PRT;	476 AA.
AC	Q6GMX1;			
DT	05-JUL-2004 (Tremblrel. 27, Created)			
DT	05-JUL-2004 (Tremblrel. 27, Last sequence update)			
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Spleen;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Spleen;			
RC	Strausberg R.;			
RL	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC073773; AAH73773.1; -.			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003597; IG-cl.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; IG_v.			
DR	Pfam; PF07654; C1-set; 3.			
DR	Pfam; PF00047; ig; 4.			
DR	SMART; SM00409; IG; 2.			
DR	SMART; SM00407; IGcl; 3.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 4.			
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.			

P18531 mus musculus  
P18533 mus musculus  
P18532 mus musculus  
P01819 mus musculus  
Q99ng4 mus musculus  
P20957 xenopus lae  
Q811u5 mus musculus  
Q9ul74 homo sapien  
Q9ul96 homo sapien  
Q6pja4 homo sapien  
Q9ul91 homo sapien  
Q8wuk1 homo sapien  
Q6gmy2 homo sapien  
Q6in78 homo sapien

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KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match
Best Local Similarity 79.5%; Score 517; DB 2; Length 476;
Matches 102; Conservative 10; Mismatches 8; Indels 8; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISS--YYWSWIRPPGKGLEWIGYIYTTN 58
Db 20 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGIYYWSWIRPPGKGLEWIGYIYSGSY 79
|||||
QY 59 YNPILKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGW-----LLPDPFIWQ 113
Db 80 YNPILKSRVTISLDTSKNQFSLKXNSVTAADTAVYFCAR-AGVWGSRFSAIDGFNIWQ 138
|||||
QY 114 GTWMTVSS 121
Db 139 GTWMTVSS 146
|||||

RESULT 2
ID Q9UL73 PRELIMINARY; PRT; 119 AA.
AC Q9UL73;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.H., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035041; AAD56277.1; -.
DR PIR; PH0876; PH0876.
DR PIR; S12416; S12416.
DR HSP; P01820; IG7J.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13219 MW; 1BD86B6420EA0BE CRC64;

Query Match
Best Local Similarity 79.4%; Score 516; DB 2; Length 119;
Matches 100; Conservative 8; Mismatches 11; Indels 2; Gaps 2;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRPPGKGLEWIGYIYTTN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRPPGKGLEWIGYIYSGTNT 60
|||||
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDPFIWQGTWTVS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDPFIWQGTWTVS 120
|||||
QY 121 $ 121
Db 119 $ 119
|||||

RESULT 3
Q6GMX6 PRELIMINARY; PRT; 465 AA.
ID Q6GMX6
```

```
AC 06GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vayallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00407; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match
Best Local Similarity 78.4%; Score 509.5; DB 2; Length 465;
Matches 99; Conservative 8; Mismatches 9; Indels 5; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRPPGKGLEWIGYIYTTN 60
Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRPPGKGLEWIGRIYSGSTN 79
|||||
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDPFIWQGTWTVS 120
Db 80 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDPFIWQGTWTVS 120
|||||
QY 121 $ 121
Db 135 $ 135
|||||

RESULT 4
Q96EY0
```



Q96EY0 PRELIMINARY; PRT; 620 AA.  
 AC Q96EY0; 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE IGHM protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Primary B-Cells;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Besak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC011857; AAH11857.2; -  
 DR PIR: S15590; S15590.  
 DR HSP; P01820; I67J.  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig cl.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF07654; Cl-set; 4.  
 DR Pfam: SM00409; IG; 2.  
 DR SMART; SM00407; IGC1; 4.  
 DR SMART; SM00406; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 3.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 3.  
 SQ SEQUENCE 620 AA; 68125 MW; 990A1A4A6E8F27B CRC64;  
 Query Match 77.3%; Score 502.5; DB 2; Length 620;  
 Best Local Similarity 82.0%; Pred. No. 6.4e-42;  
 Matches 100; Conservative 6; Mismatches 13; Indels 3; Gaps 2;  
 QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVMSWIRQPPGKLEWIGYIYTTWTN 60  
 DB 27 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVMSWIRQPPGKLEWIGYIYTTWTN 86  
 QY 61 PSLSKRVITISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGGTMTV 119  
 DB 87 PSLSKRVITISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGGTMTV 144  
 QY 120 SS 121  
 DB 145 SS 146

RESULT 5

Q6GMX7 PRELIMINARY; PRT; 477 AA.  
 AC Q6GMX7; 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Primary B-Cells;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Besak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC073765; AAH73765.1; -  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig cl.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF07654; Cl-set; 2.  
 DR Pfam: SM00409; IG; 3.  
 DR SMART; SM00407; IGC1; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CFF85 CRC64;  
 Query Match 76.8%; Score 499.5; DB 2; Length 477;  
 Best Local Similarity 81.0%; Pred. No. 9.7e-42;  
 Matches 98; Conservative 8; Mismatches 12; Indels 3; Gaps 2;  
 QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVMSWIRQPPGKLEWIGYIYTTWTN 60  
 DB 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVMSWIRQPPGKLEWIGYIYTTWTN 79  
 QY 61 PSLSKRVITISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGGTMTV 120  
 DB 80 PSLSKRVITISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGGTMTV 136  
 QY 121 S 121  
 DB 137 S 137

```
RESULT 6
Q86SX2
ID Q86SX2 PRELIMINARY; PRT; 139 AA.
AC Q86SX2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Full-length cDNA clone CSODL004YM19 of B cells (Ramos cell line) of
DE Homo sapiens (human) (Fragment).
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Li W.B., Gruber C., Jessee J., Polayes D.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX248300; CAD62627.1; -.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;

Query Match 76.3%; Score 496; DB 2; Length 139;
Best Local Similarity 94.9%; Pred. No. 5.8e-42;
Matches 93; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGIYYTWTN 60
DB 33 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGIYYTWTN 92
QY 61 PSLSKSRVTISVDTSKNQFSLRLSVTAADTALYYCARD 98
DB 93 PSLSKSRVTISVDTSKNQFSLRLSVTAADTAVYYCARD 130

RESULT 7
Q7Z379
ID Q7Z379 PRELIMINARY; PRT; 478 AA.
AC Q7Z379;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686K04218 (Fragment).
GN Name=DKFZp686K04218;
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloecher H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538066; CAD97996.1; -.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.

ID Q86P418 PRELIMINARY; PRT; 576 AA.
AC Q86P418;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Full-length cDNA clone CSODL004YM19 of B cells (Ramos cell line) of
DE Homo sapiens (human) (Fragment).
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Li W.B., Gruber C., Jessee J., Polayes D.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX248300; CAD62627.1; -.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;

Query Match 76.3%; Score 496; DB 2; Length 139;
Best Local Similarity 94.9%; Pred. No. 5.8e-42;
Matches 93; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGIYYTWTN 60
DB 33 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGIYYTWTN 92
QY 61 PSLSKSRVTISVDTSKNQFSLRLSVTAADTALYYCARD 98
DB 93 PSLSKSRVTISVDTSKNQFSLRLSVTAADTAVYYCARD 130

RESULT 8
Q95973
ID Q95973 PRELIMINARY; PRT; 150 AA.
AC Q95973;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE VH4 heavy chain variable region precursor (Fragment).
GN Name=IGM;
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF103795; AAC79084.1; -.
DR PIR; S31673; S31673.
DR PIR; S78056; S78056.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW SIGNAL.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 >150 VH4 heavy chain variable region.
FT NON_TER 150 150
SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;

Query Match 73.6%; Score 478.5; DB 2; Length 150;
Best Local Similarity 78.9%; Pred. No. 3.6e-40;
Matches 97; Conservative 7; Mismatches 12; Indels 7; Gaps 2;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGIYYTWTN 58
DB 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGIYYTWTN 79
QY 59 YNPPLSKSRVTISVDTSKNQFSLRLSVTAADTALYYCARDQGGWLLPDAFDIWGQGTMT 118
DB 80 YNPPLSKSRVTISVDTSKNQFSLRLSVTAADTAVYYCAR-----LQMGAFDFWGHGTMVT 134
QY 119 VSS 121
DB 135 VSS 137

RESULT 9
Q6P418
ID Q6P418 PRELIMINARY; PRT; 576 AA.
AC Q6P418;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Full-length cDNA clone CSODL004YM19 of B cells (Ramos cell line) of
DE Homo sapiens (human) (Fragment).
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Li W.B., Gruber C., Jessee J., Polayes D.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX248300; CAD62627.1; -.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
```





DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 2.  
DR SMART; SM00409; IG; 4.  
DR SMART; SM00406; IGV; 1.  
DR SMART; SM00407; IGC1; 3.  
DR PROSITE; PS0835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein\_  
SQ SEQUENCE 478 AA; 51956 MW; 5F8B98F60F077256 CRC64;  
  
Query Match 69.7%; Score 453; DB 2; Length 478;  
Best Local Similarity 71.9%; Pred. No. 4.6e-37;  
Matches 87; Conservative 16; Mismatches 16; Indels 2; Gaps 1;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYKWSIRQPPGKLEWIGYIYYTWTNYN 60  
Db 20 QVDLQESGPGLVKPSSETLSLTCTSVSGDSIASYKWSIRKSPQGMWIGYIFHSGTLYN 79  
  
QY 61 PSLKSRVTISVDTSKQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWDGQWTVTS 120  
Db 80 PSLKSRVTISVDTSKQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWDGQWTVTS 137  
  
QY 121 S 121  
Db 138 S 138

RESULT 14  
Q8WUX4 PRELIMINARY; PRT; 595 AA.  
AC Q8WUX4  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Lymph;  
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Richards S., Wozny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Jones S.J., Marra M.A.;  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).  
[2]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Lymph;  
RC TISSUE=Lymph;  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC019235; AAH19235.2; -.  
DR PIR; G34964; G34964.

DR HSSP; P01861; IADQ.  
DR Pfam; PF07654; C1-set; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
KW Hypothetical protein\_  
SQ SEQUENCE 595 AA; 65290 MW; 0D4B50776545714E CRC64;  
  
Query Match 69.5%; Score 452; DB 2; Length 595;  
Best Local Similarity 69.8%; Pred. No. 7.4e-37;  
Matches 90; Conservative 10; Mismatches 17; Indels 12; Gaps 2;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYKWSIRQPPGKLEWIGYIYYTWTNYN 60  
Db 27 QVQLQEWAGALLKPSSETLSLTCTGVYGSFGYKWSIRQPPGKLEWIGIINHSNSTYN 86  
  
QY 61 PSLKSRVTISVDTSKQFSLRLSSVTAADTALYYCAR-----DQGWLLPDAFDIWDG 112  
Db 87 PSLKSRVTISVDTSKQFSLRLSSVTAADTALYYCARVITRASPTDGRY----GMDVWG 142  
  
QY 113 QGTWTVTVSS 121  
Db 143 QGTWTVTVSS 151  
  
RESULT 15  
Q6GMX5 PRELIMINARY; PRT; 597 AA.  
AC Q6GMX5  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Lymph;  
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Richards S., Wozny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Lymph;  
RC TISSUE=Lymph;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073767; AAH73767.1; -.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.

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DR InterPro: IPR003596; Ig_v.  
DR Pfam: PF07654; Cl-set; 4.  
DR Pfam: PF00047; Ig; 4.  
DR SMART: SM00409; IG; 2.  
DR SMART: SM00407; IGC1; 4.  
DR SMART: SM00406; IG; 1.  
DR PROSITE: PS50835; IG_LIKE; 5.  
DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.  
KW Hypothetical protein.  
SQ SEQUENCE 597 AA; 65304 MW; 2A1E75F6AED85230 CRC64;  
  
Query Match 69.5%; Score 452; DB 2; Length 597;  
Best Local Similarity 69.8%; Pred. No. 7.4e-37;  
Matches 90; Conservative 10; Mismatches 17; Indels 12; Gaps 2;  
  
Qy 1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTN 60  
Db 20 QVQLQWAGAGLLKPSETLSLTGCVYGGSFSGYWSWIRQPPGKGLEWIGEINHSGST 79  
Qy 61 PSLKSRVTISVDTSKNQPSLRLLSSVTAADTALYYCAR-----DQGWLLPDAFD 112  
Db 80 PSLKSRVTISVDTSKKQLSLKLSVNAADTAVYYCARVITRASPGTDGRY----GMDV 135  
Qy 113 QGTMTVTVSS 121  
Db 136 QGTMTVTVSS 144  
  
Search completed: November 9, 2005, 13:05:47  
Job time : 62.4712 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:43:32 ; Search time 72.1353 Seconds  
(without alignments)  
627.306 Million cell updates/sec

Title: US-10-660-357A-13

Perfect score: 624

Sequence: 1 QVQLQSGPGLVPSQTL...AREGDFYWGQTLTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	624	100.0	117	7 ADC99784	Adc99784 Anti-huma
2	624	100.0	117	7 Add05388	Add05388 Anti-MUC1
3	624	100.0	117	7 Adf09826	Adf09826 Human ant
4	587	94.1	117	7 ADC99776	Adc99776 Anti-huma
5	587	94.1	117	7 Add05380	Add05380 Anti-MUC1
6	587	94.1	117	7 Adf09818	Adf09818 Human ant
7	585.5	93.8	118	7 Adp03968	Adp03968 Murine-ex
8	579	92.8	123	7 Adp03870	Adp03870 Murine-ex
9	575.5	92.2	120	7 Adp03974	Adp03974 Murine-ex
10	575.5	92.2	120	7 Adp03873	Adp03873 Murine-ex
11	574.5	92.1	124	7 Adp03935	Adp03935 Murine-ex
12	572	91.7	125	7 Adp03868	Adp03868 Murine-ex
13	572	91.7	125	7 Adp03876	Adp03876 Murine-ex
14	571.5	91.6	121	7 Adj80377	Adj80377 Antibody
15	570.5	91.4	122	7 Adp03977	Adp03977 Murine-ex
16	570	91.3	121	7 Adp03981	Adp03981 Murine-ex
17	569	91.2	120	4 Aab62775	Aab62775 Human HIV
18	569	91.2	125	7 Adp03871	Adp03871 Murine-ex
19	568	91.0	117	7 Adc99804	Adc99804 Anti-huma
20	568	91.0	117	7 Add05408	Add05408 Anti-MUC1
21	568	91.0	117	7 Adf09845	Adf09845 Human ant
22	567	90.9	121	7 Adp03982	Adp03982 Murine-ex
23	567	90.9	122	4 Aab62765	Aab62765 Human HIV
24	566	90.7	119	7 Adp03970	Adp03970 Murine-ex
25	566	90.7	253	5 Abp45608	Abp45608 Human Bly

## ALIGNMENTS

## RESULT 1

ADC99784  
ID ADC99784 standard; protein; 117 AA.

XX AC  
XX ADC99784;

DT 01-JAN-2004 (first entry)

DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 13.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
KW lung cancer; human.

XX Homo sapiens.

XX WO2003057838-A2.

XX 17-JUL-2003.

PF 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

PI Gudas J;

DR WPI; 2003-587113/55.

DR N-PSDB; ADC99786.

PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
or condition associated with expression of MUC18 in a patient, e.g.  
tumors, cancers, and other malignancies.

PS Claim 1; SEQ ID NO 13; 78pp; English.

CC The invention relates to a novel isolated monoclonal antibody comprising  
a heavy or light chain amino acid or a heavy or light chain variable  
domain where the antibody binds to MUC18. The monoclonal antibody of the  
invention demonstrates cytostatic activity and may be useful for treating  
a disease or condition associated with the expression of MUC18 on the  
cell surface such as tumours, specifically melanoma, oesophageal,  
pancreatic or colorectal tumours, carcinomas, particularly cervical  
carcinomas and cervical intraepithelial neoplasia and cancers including  
colorectal, breast or lung cancer, as well as other malignancies. The  
current sequence is that of the anti-human MUC18 monoclonal antibody

Adg96435 Single ch  
Adk52356 Human ant  
Aab62745 Human HIV  
Adp03872 Murine-ex  
Adp03983 Murine-ex  
Aaw78433 Antibody  
Abb97976 Heavy cha  
Adg88414 Anti-Ob-R  
Adp03869 Murine-ex  
Adp03969 Murine-ex  
Adp22124 Human ant  
Adp22104 Human ant  
Adp22096 Human ant  
Adp03961 Murine-ex  
Adp03934 Murine-ex  
Adc99796 Anti-huma  
Adf05400 Anti-MUC1  
Adf09838 Human ant  
Adp03877 Murine-ex  
Adp03874 Murine-ex

26 566 90.7 253 7 ADG96435  
27 566 90.7 446 8 ADK52356  
28 565.5 90.6 123 4 AAB62745  
29 565 90.5 123 7 ADP03872  
30 565 90.5 125 7 ADP03983  
31 563 90.2 123 2 AAW78433  
32 563 90.2 123 5 ABB97976  
33 563 90.2 123 7 ADG88414  
34 563 90.2 123 7 ADP03869  
35 562.5 90.1 120 7 ADP03969  
36 562.5 90.1 128 8 ADP22124  
37 562.5 90.1 128 8 ADP22104  
38 562.5 90.1 128 8 ADP22096  
39 562 90.1 119 7 ADP03961  
40 561.5 90.0 110 7 ADP03934  
41 561 89.9 119 7 ADC99796  
42 561 89.9 119 7 ADD05400  
43 561 89.9 119 7 ADF09838  
44 559 89.6 123 7 ADP03877  
45 559 89.6 127 7 ADP03874

CC heavy chain protein of the invention.

XX Sequence 117 AA;

Query Match

Best Local Similarity 100.0%; Score 624; DB 7; Length 117;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYYWTWIRQHPGKLEWIGFIYSGSTY 60

Db 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYYWTWIRQHPGKLEWIGFIYSGSTY 60

QY 61 YNPISLKSRTVISVDTSKNQFSLKSSVTAADTAVYYCAREGDFYWGQGTILTVSS 117

Db 61 YNPISLKSRTVISVDTSKNQFSLKSSVTAADTAVYYCAREGDFYWGQGTILTVSS 117

RESULT 2

ADD05388

ID ADD05388 standard; protein; 117 AA.

XX AC

XX ADD05388;

DT 01-JAN-2004 (first entry)

XX DE

DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 13.

XX KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;

KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.

XX OS Homo sapiens.

XX PN WO2003057006-A2.

XX PD 17-JUL-2003.

XX PF 26-DEC-2002; 2002WO-US041582.

XX PR 28-DEC-2001; 2001US-0346460P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J, Bar-Eli M;

XX WPI; 2003-577496/54.

XX DR N-PSDB; ADD05390.

XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and

PT treating tumors, inhibiting tumor growth, inhibiting cell invasion

PT associated with melanoma, or increasing survival of an animal having a

PT metastatic tumor.

XX Claim 1; SEQ ID NO 13; 87pp; English.

XX The invention relates to a novel monoclonal antibody used for inhibiting

CC tumour growth in an animal. The tumour inhibition process comprises

CC selecting an animal in need of treatment for a tumour, providing a

CC monoclonal antibody comprising a heavy chain amino acid, where the

CC antibody consists of any one of 10 fully defined sequences of 117-123

CC amino acids given in the specification, and where the monoclonal antibody

CC binds MUC18, and contacting the tumour with the antibody resulting in

CC inhibited proliferation of the cells. The monoclonal antibody has

CC cytostatic and can be used in the production of a vaccine. The monoclonal

CC antibodies against the MUC18 antigen are useful for diagnosing and

CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or

CC tumour metastasis), inhibiting cell invasion associated with melanoma, or

CC increasing survival of an animal having a metastatic tumour. This

CC sequence represents an anti-MUC18 antibody heavy chain, variable region,

XX protein of the invention.

XX Sequence 117 AA;

Query Match 100.0%; Score 624; DB 7; Length 117;

Best Local Similarity 100.0%; Pred. No. 3.1e-48;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYYWTWIRQHPGKLEWIGFIYSGSTY 60

Db 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYYWTWIRQHPGKLEWIGFIYSGSTY 60

QY 61 YNPISLKSRTVISVDTSKNQFSLKSSVTAADTAVYYCAREGDFYWGQGTILTVSS 117

Db 61 YNPISLKSRTVISVDTSKNQFSLKSSVTAADTAVYYCAREGDFYWGQGTILTVSS 117

RESULT 3

ADF09826

ID ADF09826 standard; protein; 117 AA.

XX AC

XX ADF09826;

DT 12-FEB-2004 (first entry)

XX DE

DE Human anti-MUC18 monoclonal antibody heavy chain #4.

XX KW

KW cell proliferation inhibition; MUC18 tumour antigen;

KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;

KW carcinoma; cancer; malignancy; heavy chain; human.

XX OS Homo sapiens.

XX PN WO2003057837-A2.

XX PD 17-JUL-2003.

XX PF 26-DEC-2002; 2002WO-US041580.

XX PR 28-DEC-2001; 2001US-0346414P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J;

XX WPI; 2003-598367/56.

XX DR N-PSDB; ADF09828.

XX Inhibiting cell proliferation associated with expression of MUC18 tumor

PT antigen, involves incubating and inhibiting cell by administering anti-

PT MUC18 monoclonal antibody.

XX Claim 1; SEQ ID NO 13; 83pp; English.

XX The invention comprises a method for inhibiting cell proliferation

CC associated with expression of MUC18 tumour antigen. The method involves

CC administering anti-MUC18 monoclonal antibody. The method of the invention

CC is useful for inhibiting cell (e.g. melanoma or tumour cell)

CC proliferation associated with the expression of MUC18 tumour antigen, the

CC method is preferably useful for inhibiting tumour metastasis. The method

CC is useful for inhibiting cell proliferation in patients with tumours,

CC carcinomas, cancer and other malignancies. The present amino acid

CC sequence represents a heavy chain from an MUC18 tumour antigen-specific

CC monoclonal antibody.

XX Sequence 117 AA;

Query Match 100.0%; Score 624; DB 7; Length 117;

Best Local Similarity 100.0%; Pred. No. 3.1e-48;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYYWTWIRQHPGKLEWIGFIYSGSTY 60

Db 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYYWTWIRQHPGKLEWIGFIYSGSTY 60

QY 61 YNPISLKSRTVISVDTSKNQFSLKSSVTAADTAVYYCAREGDFYWGQGTILTVSS 117

Db 61 YNPISLKSRTVISVDTSKNQFSLKSSVTAADTAVYYCAREGDFYWGQGTILTVSS 117



RESULT 4  
 ADC99776  
 ID ADC99776 standard; protein; 117 AA.  
 XX  
 AC ADC99776;  
 XX  
 DT 01-JAN-2004 (first entry)  
 XX  
 DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 5.  
 XX  
 KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
 KW cytosolic; melanoma; oesophageal; pancreatic; colorectal tumour;  
 KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
 .XX lung cancer; human.  
 OS Homo sapiens.  
 XX  
 FN WO2003057838-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 26-DEC-2002; 2002WO-US041581.  
 XX  
 PR 28-DEC-2001; 2001US-0346299P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Gudas J;  
 XX  
 DR WPI; 2003-587113/55.  
 DR N-PSDB; ADC99776.  
 XX  
 PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
 PT or condition associated with expression of MUC18 in a patient, e.g.  
 PT tumors, cancers, and other malignancies.  
 XX  
 PS Claim 1; SEQ ID NO 5; 78pp; English.  
 XX  
 CC The invention relates to a novel isolated monoclonal antibody comprising  
 CC a heavy or light chain amino acid or a heavy or light chain variable  
 CC domain where the antibody binds to MUC18. The monoclonal antibody of the  
 CC invention demonstrates cytostatic activity and may be useful for treating  
 CC a disease or condition associated with the expression of MUC18 on the  
 CC cell surface such as tumours, specifically melanoma, oesophageal,  
 CC pancreatic or colorectal tumours, carcinomas, particularly cervical  
 CC carcinomas and cervical intraepithelial neoplasia and cancers including  
 CC colorectal, breast or lung cancer, as well as other malignancies. The  
 CC current sequence is that of the anti-human MUC18 monoclonal antibody  
 CC heavy chain protein of the invention.  
 XX  
 SQ Sequence 117 AA;  
 Query Match 94.1%; Score 587; DB 7; Length 117;  
 Best Local Similarity 94.0%; Pred. No. 6.4e-45;  
 Matches 110; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYWTWIRQHPKGLGWIGFTIYSGSTY 60  
 Db 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYWTWIRQHPKGLGWIGFTIYSGSTY 60  
 QY 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYVCAREGDGFDYWGQGLTVTVSS 117  
 Db 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYVCAREGDGFDYWGQGLTVTVSS 117  
 QY 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYVCAREGDGFDYWGQGLTVTVSS 117  
 Db 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYVCAREGDGFDYWGQGLTVTVSS 117  
 RESULT 5  
 ADD05380  
 ID ADD05380 standard; protein; 117 AA.  
 XX  
 AC ADD05380;  
 XX

01-JAN-2004 (first entry)  
 Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 5.  
 monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
 antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.  
 Homo sapiens.  
 WO2003057006-A2.  
 17-JUL-2003.  
 26-DEC-2002; 2002WO-US041582.  
 28-DEC-2001; 2001US-0346460P.  
 (ABGE-) ABGENIX INC.  
 Gudas J, Bar-Eli M;  
 WPI; 2003-577496/54.  
 N-PSDB; ADD05382.  
 Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
 treating tumors, inhibiting tumor growth, inhibiting cell invasion  
 associated with melanoma, or increasing survival of an animal having a  
 metastatic tumor.  
 Claim 1; SEQ ID NO 5; 87pp; English.  
 The invention relates to a novel monoclonal antibody used for inhibiting  
 tumor growth in an animal. The tumor inhibition process comprises  
 selecting an animal in need of treatment for a tumor, providing a  
 monoclonal antibody comprising a heavy chain amino acid, where the  
 antibody consists of any one of 10 fully defined sequences of 117-123  
 amino acids given in the specification, and where the monoclonal antibody  
 binds MUC18, and contacting the tumor with the antibody resulting in  
 inhibited proliferation of the cells. The monoclonal antibody has  
 cytostatic and can be used in the production of a vaccine. The monoclonal  
 antibodies against the MUC18 antigen are useful for diagnosing and  
 treating tumors, inhibiting tumor growth (e.g. melanoma, lung tumour or  
 tumour metastasis), inhibiting cell invasion associated with melanoma, or  
 increasing survival of an animal having a metastatic tumour. This  
 sequence represents an anti-MUC18 antibody heavy chain, variable region,  
 protein of the invention.  
 Sequence 117 AA;  
 Query Match 94.1%; Score 587; DB 7; Length 117;  
 Best Local Similarity 94.0%; Pred. No. 6.4e-45;  
 Matches 110; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYWTWIRQHPKGLGWIGFTIYSGSTY 60  
 Db 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYWTWIRQHPKGLGWIGFTIYSGSTY 60  
 QY 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYVCAREGDGFDYWGQGLTVTVSS 117  
 Db 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYVCAREGDGFDYWGQGLTVTVSS 117  
 RESULT 6  
 ADF09818  
 ID ADF09818 standard; protein; 117 AA.  
 XX  
 AC ADF09818;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human anti-MUC18 monoclonal antibody heavy chain #2.  
 XX  
 KW cell proliferation inhibition; MUC18 tumour antigen;

KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
KW carcinoma; cancer; malignancy; heavy chain; human.  
XX Homo sapiens.  
XX WO2003057837-A2.  
XX  
XX  
PD 17-JUL-2003.  
XX  
XX  
PF 26-DEC-2002; 2002WO-US041580.  
XX  
XX  
PR 28-DEC-2001; 2001US-0346414P.  
XX  
XX (ABGE-) ABGENIX INC.  
XX  
XX Gudas J;  
PI  
XX  
XX  
XX MPI; 2003-598367/56.  
DR N-PSDB; ADF09820.  
XX  
XX  
PT Inhibiting cell proliferation associated with expression of MUC18 tumor  
PT antigen, involves incubating and inhibiting cell by administering anti-  
PT MUC18 monoclonal antibody.  
XX  
XX Claim 1; SEQ ID NO 5; 83pp; English.  
XX  
XX The invention comprises a method for inhibiting cell proliferation  
CC associated with expression of MUC18 tumour antigen. The method involves  
CC administering anti-MUC18 monoclonal antibody. The method of the invention  
CC is useful for inhibiting cell (e.g. melanoma or tumour cell)  
CC proliferation associated with the expression of MUC18 tumour antigen, the  
CC method is preferably useful for inhibiting tumour metastasis. The method  
CC is useful for inhibiting cell proliferation in patients with tumours,  
CC carcinomas, cancer and other malignancies. The present amino acid  
CC sequence represents a heavy chain from an MUC18 tumour antigen-specific  
CC monoclonal antibody.  
XX  
XX Sequence 117 AA;  
SQ  
Query Match 94.1%; Score 587; DB 7; Length 117;  
Best Local Similarity 94.0%; Pred. No. 6.4e-45;  
Matches 110; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWIRQHPGKLEWIGIYYSGSY 60  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWIRQHPGKLEWIGIYYSGSY 60  
QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYVCAREGDFYWGQGLTVTVSS 117  
Db 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYVCAREGDFYWGQGLTVTVSS 117  
RESULT 7  
ADP03968  
ID ADP03968 standard; protein; 118 AA.  
XX  
XX  
AC ADP03968;  
XX  
XX 29-JUL-2004 (first entry)  
XX  
XX Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 138.  
DE  
XX  
KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
KW cytostatic; colorectal neoplasm; renal cell carcinoma;  
KW cervical intraepithelial squamous neoplasia;  
KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
KW gene therapy; murine; mouse; human; heavy chain variable domain.  
XX  
XX Unidentified.  
OS  
XX WO2003048328-A2.  
PN  
XX  
XX 12-JUN-2003.  
PD

XX  
PF 02-DEC-2002; 2002WO-US038550.  
XX  
XX  
PR 03-DEC-2001; 2001US-0337275P.  
XX  
XX (ABGE-) ABGENIX INC.  
XX  
XX  
PI Gudas J, Foltz I, Handa M, Gallo M;  
PI  
XX  
XX MPI; 2003-523295/49.  
DR  
XX  
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
XX  
XX Example 2; SEQ ID NO 138; 89pp; English.  
XX  
XX The invention relates to a novel isolated monoclonal antibody (mAb)  
CC comprising a heavy chain polypeptide and light chain polypeptide having a  
CC sequence chosen from one of 53 fully defined amino acid sequences given  
CC in the specification, where the antibody specifically binds carbonic  
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
CC demonstrates cytostatic activity and may be useful for treating a tumour,  
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.  
XX  
XX Sequence 118 AA;  
SQ  
Query Match 93.8%; Score 585.5; DB 7; Length 118;  
Best Local Similarity 94.9%; Pred. No. 8.8e-45;  
Matches 112; Conservative 2; Mismatches 3; Indels 1; Gaps 1;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWIRQHPGKLEWIGIYYSGSY 60  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWIRQHPGKLEWIGIYYSGSY 60  
QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYVCAR-EGDGFYWGQGLTVTVSS 117  
Db 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYVCARYGSGSDYWGQGLTVTVSS 118  
RESULT 8  
ADP03870  
ID ADP03870 standard; protein; 123 AA.  
XX  
XX  
AC ADP03870;  
XX  
XX 29-JUL-2004 (first entry)  
XX  
XX Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 10.  
DE  
XX  
KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
KW cytostatic; colorectal neoplasm; renal cell carcinoma;  
KW cervical intraepithelial squamous neoplasia;  
KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
KW gene therapy; murine; mouse; human; heavy chain variable domain.  
XX  
XX Unidentified.  
OS  
XX WO2003048328-A2.  
PN  
XX  
XX 12-JUN-2003.  
PD  
XX  
XX 02-DEC-2002; 2002WO-US038550.  
PF  
XX  
XX 03-DEC-2001; 2001US-0337275P.  
PR  
XX  
XX (ABGE-) ABGENIX INC.  
PA

XX PI Gudas J, Foltz I, Handa M, Gallo M;  
 XX WPI; 2003-523295/49.  
 XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
 XX PS Claim 1; SEQ ID NO 10; 89pp; English.  
 XX The invention relates to a novel isolated monoclonal antibody (mAb)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
 CC demonstrates cytostatic activity and may be useful for treating a tumour,  
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumour or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
 CC (heavy chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.  
 XX SQ Sequence 123 AA;  
 Query Match 92.8%; Score 579; DB 7; Length 123;  
 Best Local Similarity 90.2%; Pred. No. 3.5e-44;  
 Matches 111; Conservative 3; Mismatches 3; Indels 6; Gaps 1;  
 QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYYWTWIRQHPKGLGWIGFIYSGSY 60  
 DB 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYYWTWIRQHPKGLGWIGFIYSGSY 60  
 QY 61 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAVYYCAREGDG- - - - -DYWGQGLT 114  
 DB 61 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAVYYCAREGDG- - - - -DYWGQGLT 120  
 QY 115 VSS 117  
 DB 121 VSS 123  
 RESULT 9  
 ADP03974  
 ID ADP03974 standard; protein; 120 AA.  
 AC ADP03974;  
 XX 29-JUL-2004 (first entry)  
 XX Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 144.  
 XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KW cytostatic; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;  
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; heavy chain variable domain.  
 XX Unidentified.  
 OS  
 XX W02003048328-A2.  
 PN 12-JUN-2003.  
 PD 02-DEC-2002; 2002WO-US038550.  
 XX 03-DEC-2001; 2001US-0337275P.  
 XX (ABGE-) ABGENIX INC.  
 PA Gudas J, Foltz I, Handa M, Gallo M;  
 PI WPI; 2003-523295/49.  
 XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX WPI; 2003-523295/49.  
 XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
 XX PS Example 2; SEQ ID NO 144; 89pp; English.  
 XX The invention relates to a novel isolated monoclonal antibody (mAb)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
 CC demonstrates cytostatic activity and may be useful for treating a tumour,  
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumour or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
 CC (heavy chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.  
 XX SQ Sequence 120 AA;  
 Query Match 92.2%; Score 575.5; DB 7; Length 120;  
 Best Local Similarity 91.7%; Pred. No. 7e-44;  
 Matches 110; Conservative 4; Mismatches 3; Indels 3; Gaps 1;  
 QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYYWTWIRQHPKGLGWIGFIYSGSY 60  
 DB 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYYWTWIRQHPKGLGWIGFIYSGSY 60  
 QY 61 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAVYYCAREGDG- - - - -PDYWGQGLT 117  
 DB 61 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAVYYCAREGDG- - - - -PDYWGQGLT 120  
 RESULT 10  
 ADP03873  
 ID ADP03873 standard; protein; 120 AA.  
 XX AC ADP03873;  
 XX 29-JUL-2004 (first entry)  
 XX Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 13.  
 XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KW cytostatic; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;  
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; heavy chain variable domain.  
 XX Unidentified.  
 OS  
 XX W02003048328-A2.  
 PN 12-JUN-2003.  
 PD 02-DEC-2002; 2002WO-US038550.  
 XX 03-DEC-2001; 2001US-0337275P.  
 XX (ABGE-) ABGENIX INC.  
 PA Gudas J, Foltz I, Handa M, Gallo M;  
 PI WPI; 2003-523295/49.  
 XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX  
PS  
XX  
XX  
CC The invention relates to a novel isolated monoclonal antibody (mAb) comprising a heavy chain polypeptide and light chain polypeptide having a sequence chosen from one of 53 fully defined amino acid sequences given in the specification, where the antibody specifically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention demonstrates cytostatic activity and may be useful for treating a tumour, such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma, cervical intraepithelial squamous and glandular neoplasia, oesophageal tumour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody VH (heavy chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into a transgenic mouse strain.

XX  
SQ Sequence 120 AA;

Query Match 92.2%; Score 575.5; DB 7; Length 120;  
Best Local Similarity 91.7%; Pred. No. 7e-44;  
Matches 110; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYVWYWTIRQHPGKGLEWIGFTYYSGSY 60  
|||  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYVWYWTIRQHPGKGLEWIGFTYYSGSY 60  
|||

QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCAREGDG---FDYWGQGLTVSS 117  
|||  
Db 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCAREGDG---FDYWGQGLTVSS 120  
|||

RESULT 11  
ADP03935  
ID ADP03935 standard; protein; 124 AA.  
XX  
AC ADP03935;  
XX  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SRQ 75.  
XX  
KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
KW cytostatic; colorectal neoplasm; renal cell carcinoma;  
KW cervical intraepithelial squamous neoplasia;  
KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
KW gene therapy; murine; mouse; human; heavy chain variable domain.  
XX  
OS Unidentified.  
XX  
XX  
PN WO2003048328-A2.  
XX  
PD 12-JUN-2003.  
XX  
PF 02-DEC-2002; 2002WO-US038550.  
XX  
PR 03-DEC-2001; 2001US-0337275P.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Gudas J, Foltz I, Handa M, Gallo M;  
XX  
XX WPI; 2003-523295/49.  
XX  
PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g., colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical intraepithelial squamous and glandular neoplasia or esophageal tumors.  
XX  
PS Claim 1; SEQ ID NO 75; 89pp; English.  
XX  
CC The invention relates to a novel isolated monoclonal antibody (mAb) comprising a heavy chain polypeptide and light chain polypeptide having a sequence chosen from one of 53 fully defined amino acid sequences given

CC in the specification, where the antibody specifically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention demonstrates cytostatic activity and may be useful for treating a tumour, such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma, cervical intraepithelial squamous and glandular neoplasia, oesophageal tumour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody VH (heavy chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into a transgenic mouse strain.

XX  
SQ Sequence 124 AA;

Query Match 92.1%; Score 574.5; DB 7; Length 124;  
Best Local Similarity 89.5%; Pred. No. 8.9e-44;  
Matches 111; Conservative 3; Mismatches 3; Indels 7; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYVWYWTIRQHPGKGLEWIGFTYYSGSY 60  
|||  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYVWYWTIRQHPGKGLEWIGFTYYSGSY 60  
|||

QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCAREG-----DGFYWGQGLTV 113  
|||  
Db 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARENYDILTGFNWFDPWGQGLTV 120  
|||

QY 114 TVSS 117  
|||  
Db 121 TVSS 124  
|||

RESULT 12  
ADP03868  
ID ADP03868 standard; protein; 125 AA.  
XX  
AC ADP03868;  
XX  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 8.  
XX  
KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
KW cytostatic; colorectal neoplasm; renal cell carcinoma;  
KW cervical intraepithelial squamous neoplasia;  
KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
KW gene therapy; murine; mouse; human; heavy chain variable domain.  
XX  
OS Unidentified.  
XX  
XX  
PN WO2003048328-A2.  
XX  
PD 12-JUN-2003.  
XX  
PF 02-DEC-2002; 2002WO-US038550.  
XX  
PR 03-DEC-2001; 2001US-0337275P.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Gudas J, Foltz I, Handa M, Gallo M;  
XX  
XX WPI; 2003-523295/49.  
XX  
PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g., colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical intraepithelial squamous and glandular neoplasia or esophageal tumors.  
XX  
PS Claim 1; SEQ ID NO 8; 89pp; English.  
XX  
CC The invention relates to a novel isolated monoclonal antibody (mAb) comprising a heavy chain polypeptide and light chain polypeptide having a sequence chosen from one of 53 fully defined amino acid sequences given in the specification, where the antibody specifically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention

CC demonstrates cytostatic activity and may be useful for treating a tumour,  
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.  
XX  
SQ Sequence 125 AA;

Query Match 91.7%; Score 572; DB 7; Length 125;  
Best Local Similarity 88.0%; Pred. No. 1.5e-43;  
Matches 110; Conservative 2; Mismatches 5; Indels 8; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPKGLGLEWIGFIYSGSTY 60  
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPKGLGLEWIGFIYSGSTY 60  
QY 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARE-----GDGFYWGQGTLL 112  
DB 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARTYYDILTGYPDADFINGQGTM 120  
QY 113 VTVSS 117  
DB 121 VTVSS 125

RESULT 13  
ADP03876  
ID ADP03876 standard; protein; 125 AA.

XX ADP03876;

XX 29-JUL-2004 (first entry)

XX Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 16.  
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
XX cytostatic; colorectal neoplasm; renal cell carcinoma;  
XX cervical intraepithelial squamous neoplasia;  
XX cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
XX gene therapy; murine; mouse; human; heavy chain variable domain.  
XX

XX Unidentified.

XX WO2003048328-A2.

XX 12-JUN-2003.

XX 02-DEC-2002; 2002WO-US038550.

XX 03-DEC-2001; 2001US-0337275P.

XX (ABGE-) ABGENIX INC.

XX Gudas J, Foltz I, Handa M, Gallo M;

XX WPI; 2003-523295/49.

XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
XX colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
XX intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX Claim 1; SEQ ID NO 16; 89pp; English.

XX The invention relates to a novel isolated monoclonal antibody (mAb)  
XX comprising a heavy chain polypeptide and light chain polypeptide having a  
XX sequence chosen from one of 53 fully defined amino acid sequences given  
XX in the specification, where the antibody specifically binds carbonic  
XX anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
XX demonstrates cytostatic activity and may be useful for treating a tumour,  
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,

CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.  
XX  
SQ Sequence 125 AA;

Query Match 91.7%; Score 572; DB 7; Length 125;  
Best Local Similarity 88.0%; Pred. No. 1.5e-43;  
Matches 110; Conservative 2; Mismatches 5; Indels 8; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPKGLGLEWIGFIYSGSTY 60  
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPKGLGLEWIGFIYSGSTY 60  
QY 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARE-----GDGFYWGQGTLL 112  
DB 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARTYYDILTGYPDADFINGQGTM 120  
QY 113 VTVSS 117  
DB 121 VTVSS 125

RESULT 14

ADJ80377

ID ADJ80377 standard; protein; 121 AA.

XX ADJ80377;

XX 06-MAY-2004 (first entry)

XX Antibody variable heavy chain with homology to mouse anti-human antibody.

XX hybrid antibody; antibody; framework region; homology; immunogenicity.

XX Unidentified.

XX WO2003048321-A2.

XX 12-JUN-2003.

XX 03-DEC-2002; 2002WO-US038450.

XX 03-DEC-2001; 2001US-0336591P.

XX (ALEX-) ALEXION PHARM INC.

XX Rother R, Wu D;

XX WPI; 2003-513753/48.

XX Producing a hybrid antibody or hybrid antibody fragment by operatively  
XX linking the selected framework sequences to one or more complementarity  
XX determining regions of the initial antibody.

XX Example 1; SEQ ID NO 137; 77pp; English.

XX The invention relates to a method of producing a hybrid antibody or  
XX hybrid antibody fragment by: (i) providing an initial antibody having  
XX specificity for a target; (ii) determining the sequence of a variable  
XX region of the initial antibody; (iii) selecting a first component of the  
XX variable region consisting of FR1, FR2, FR3 and FR4; (iv) comparing the  
XX sequence of the first component to sequences contained in a reference  
XX database of antibody sequences or antibody fragment sequences from a  
XX target species; (v) selecting a sequence from an antibody in the database  
XX which demonstrates a high degree of homology to the first component; (vi)  
XX selecting a second component of the variable region which is different  
XX than the first component, the second component selected from the group  
XX consisting of FR1, FR2, FR3 and FR4; (vii) comparing the sequence of the  
XX second component to sequences contained in a reference database of

CC antibody sequences or antibody fragment sequences from the target species  
CC ; (viii) selecting a sequence from the database which demonstrates a high  
CC degree of homology to the second component and which is from a different  
CC antibody than the selected antibody; and (ix) operatively linking the  
CC selected framework sequences to one or more complementarity determining  
CC regions (CDRs) of the initial antibody to produce a hybrid antibody or  
CC hybrid antibody fragment. The method is useful for producing a hybrid  
CC antibody or hybrid antibody fragment (claimed). The antibody and  
CC fragments are useful for therapeutic and diagnostic purposes. The method  
CC uses entire framework regions from a single antibody variable heavy or  
CC variable light chain to receive the CDRs. This produces antibodies that  
CC are highly homologous and exhibit reduced immunogenicity while  
CC maintaining an optimum binding profile. This sequence represents an  
CC antibody variable heavy chain which has good homology to an initial  
CC murine anti-human mannose binding lectin antibody (ADJ80371). The  
CC sequence was used to generate a hybrid antibody of the invention.

XX  
SQ Sequence 121 AA;

Query Match 91.6%; Score 571.5; DB 7; Length 121;  
Best Local Similarity 90.9%; Pred. No. 1.6e-43;  
Matches 110; Conservative 1; Mismatches 5; Indels 5; Gaps 1;  
QY 2 VQLQESGPGLVKPSQTLTCTVSGGSISGGYVWIRQHPGKGLEWIGFYIYSGSTY 61  
DB 1 VQLQESGPGLVKPSQTLTCTVSGGSISGGYVWIRQHPGKGLEWIGFYIYSGSTY 60  
QY 62 NPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCAR-----EGDGFYWGQGTLLVTVS 116  
DB 61 NPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGLKWGSNHVFDYWGQGTLLVTVS 120  
QY 117 S 117  
DB 121 S 121

RESULT 15

ADP03977  
ID ADP03977 standard; protein; 122 AA.

AC ADP03977;

XX  
DT 29-JUL-2004 (first entry)

DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 147.

XX  
KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
KW cytotstatic; colorectal neoplasm; renal cell carcinoma;  
KW cervical intraepithelial squamous neoplasia;  
KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
KW gene therapy; murine; mouse; human; heavy chain variable domain.

XX Unidentified.

XX WO2003048328-A2.

XX 12-JUN-2003.

XX 02-DEC-2002; 2002WO-US038550.

XX 03-DEC-2001; 2001US-0337275P.

XX (ABGE-) ABGENIX INC.

XX Gudas J, Foltz I, Handa M, Gallo M;

XX WPI; 2003-523295/49.

XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.;  
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

PS Example 2; SEQ ID NO 147; 89pp; English.

XX The invention relates to a novel isolated monoclonal antibody (mAb)  
CC comprising a heavy chain polypeptide and light chain polypeptide having a  
CC sequence chosen from one of 53 fully defined amino acid sequences given  
CC in the specification, where the antibody specifically binds carbonic  
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
CC demonstrates cytostatic activity and may be useful for treating a tumour,  
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.

XX  
SQ Sequence 122 AA;

Query Match 91.4%; Score 570.5; DB 7; Length 122;  
Best Local Similarity 90.2%; Pred. No. 2e-43; Mismatches 5; Gaps 1;  
Matches 110; Conservative 2; Mismatches 5; Indels 5; Gaps 1;  
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DB 1 VQLQESGPGLVKPSQTLTCTVSGGSISGGYVWIRQHPGKGLEWIGFYIYSGSTY 60  
QY 61 YNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCAR-----EGDGFYWGQGTLLVTV 115  
DB 61 YNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCAR-----EGDGFYWGQGTLLVTV 120  
QY 116 SS 117  
DB 121 SS 122

Search completed: November 9, 2005, 12:55:25

Job time : 72.1353 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:29:55 ; Search time 18.1805 Seconds  
(without alignments)  
480.403 Million cell updates/sec

Title: US-10-660-357A-13  
Perfect score: 624  
Sequence: 1 QVQLQESGPGLVKPSQTL.....AREGDFYWGQGLTVTSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	550	88.1	119	1	US-08-360-125-5
2	550	88.1	119	2	US-08-450-578-5
3	550	88.1	119	2	US-09-017-628-5
4	550	88.1	119	2	US-09-014-880-5
5	550	88.1	119	4	US-08-450-363-5
6	550	88.1	119	4	US-09-467-903-5
7	543	87.0	119	3	US-09-025-769B-39
8	543	87.0	119	3	US-09-025-769B-65
9	543	87.0	119	4	US-09-490-070A-39
10	543	87.0	119	4	US-09-490-070A-65
11	543	87.0	119	4	US-09-490-153-39
12	543	87.0	119	4	US-09-490-153-65
13	543	87.0	119	4	US-09-490-324-39
14	543	87.0	119	4	US-09-490-324-65
15	542.5	86.9	473	3	US-09-049-672A-4
16	542.5	86.9	487	4	US-09-800-729-145
17	527.5	84.5	118	3	US-09-025-769B-25
18	527.5	84.5	118	4	US-09-490-070A-25
19	527.5	84.5	118	4	US-09-490-153-25
20	527.5	84.5	118	4	US-09-490-324-25
21	527.5	84.5	122	1	US-08-360-125-11
22	527.5	84.5	122	2	US-08-450-578-11
23	527.5	84.5	122	2	US-09-017-628-11
24	527.5	84.5	122	2	US-09-014-880-11
25	527.5	84.5	122	4	US-08-450-363-11
26	527.5	84.5	122	4	US-09-467-903-11
27	525.5	84.2	172	4	US-09-472-087-7

28	525.5	84.2	172	4	US-09-472-087-86	Sequence 86, Appli
29	524	84.0	117	4	US-09-720-493-2	Sequence 2, Appli
30	517	82.9	118	3	US-08-545-809A-116	Sequence 116, Appl
31	511.5	82.0	120	4	US-09-424-840B-20	Sequence 20, Appl
32	510.5	81.8	244	3	US-08-918-148-79	Sequence 79, Appl
33	510.5	81.8	244	4	US-09-138-091A-77	Sequence 77, Appl
34	500	80.1	155	4	US-09-471-276-888	Sequence 888, App
35	495.5	79.4	139	4	US-09-471-276-837	Sequence 837, App
36	495	79.3	142	2	US-08-480-774A-2	Sequence 2, Appli
37	488	78.2	118	3	US-08-545-809A-142	Sequence 142, App
38	482.5	77.3	278	3	US-09-260-527-3	Sequence 3, Appli
39	482	77.2	119	2	US-08-652-816A-10	Sequence 10, Appl
40	481.5	77.2	139	4	US-09-203-768A-2	Sequence 2, Appli
41	481	77.1	118	3	US-08-545-809A-123	Sequence 123, App
42	480.5	77.0	150	4	US-09-582-337-14	Sequence 14, Appl
43	478	76.6	123	3	US-08-793-450-4	Sequence 4, Appli
44	476.5	76.4	98	1	US-08-478-039-75	Sequence 75, Appl
45	476.5	76.4	98	1	US-08-476-349A-75	Sequence 75, Appl

ALIGNMENTS

RESULT 1  
US-08-360-125-5  
; Sequence 5, Application US/08360125  
; Patent No. 5767246  
; GENERAL INFORMATION:  
; APPLICANT: Saiko HOSOKAWA  
; APPLICANT: Toshiaki TAGAWA  
; APPLICANT: Yoko HIRAKAWA  
; APPLICANT: No. 5767246biko ITO  
; APPLICANT: Kazuhiro NAGAIKE  
; TITLE OF INVENTION: Human Monoclonal Antibody  
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
; TITLE OF INVENTION: Cell Membrane  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/360,125  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/905,534  
; FILING DATE: June 29, 1992  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

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;
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; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human
; CELL TYPE: antibody GAH
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
;
; US-08-360-125-5
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; Query Match 88.1%; Score 550; DB 1; Length 119;
; Best Local Similarity 88.2%; Pred. No. 1.3e-48;
; Matches 105; Conservative 6; Mismatches 6; Indels 2; Gaps 1;
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; QY 1 QVQLQSGGCLVKPSQTLSTCTVSGGSISSGGYYWYTWIRQHPGKGLEWIGFIYSGSY 60
; DB 1 QVQLQSGGCLVKPSQTLSTCTVSGGSISSCGFYNNWIRQHPGKLEWIGFIYSGSY 60
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; QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVVYCAREG--DGFYWGQGLTVTVSS 117
; DB 61 YNPSLKSRVTISLDTSKQFSLKSLSLTAADTAVVYCARSTRLRGADYWGQGTMTVTVSS 119
;
; RESULT 2
; US-08-450-578-5
; Sequence 5, Application US/08450578
; Patent No. 5837845
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: NO. 5837845hiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
;
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,578
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human
; CELL TYPE: antibody GAH
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
;
; US-08-450-578-5
;
; Query Match 88.1%; Score 550; DB 2; Length 119;
; Best Local Similarity 88.2%; Pred. No. 1.3e-48;
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ORGANELLE: <Unknown>  
IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: <Unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <Unknown>  
MAP POSITION: <Unknown>  
UNITS: <Unknown>  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-467-903-5

Query Match 88.1%; Score 550; DB 4; Length 119;  
Best Local Similarity 88.2%; Pred. No. 1.3e-48;  
Matches 105; Conservative 6; Mismatches 6; Indels 2; Gaps 1;  
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DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGVYWTWIRQHPGKGLWIGFIYSGSTY 60  
QY 61 YNPSLRSRVTSVDTSKNQFSLKLSVTAADTAVYYCAREG--DGFYWGQGTLLTVSS 117  
DB 61 YNPSLRSRVTSVDTSKNQFSLKLSVTAADTAVYYCARSLRGADYWGQGTLLTVSS 119

RESULT 7  
US-09-025-769B-39  
Sequence 39, Application US/09025769B  
Patent No. 6300064  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilag, Vic  
APPLICANT: Ge, Liming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids

NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-39

Query Match 87.0%; Score 543; DB 3; Length 119;  
Best Local Similarity 90.1%; Pred. No. 6.6e-48;  
Matches 109; Conservative 3; Mismatches 3; Indels 6; Gaps 3;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGVYWTWIRQHPGKGLWIGFIYSGSTY 60  
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGVYWTWIRQHPGKGLWIGFIYSGSTN 58  
QY 61 YNPSLRSRVTSVDTSKNQFSLKLSVTAADTAVYYCAR-EGDGF---DYWGQGTLLTVS 116  
DB 59 YNPSLRSRVTSVDTSKNQFSLKLSVTAADTAVYYCARWGSDGFYAMDYWGQGTLLTVS 118  
QY 117 S 117  
DB 119 S 119

RESULT 8  
US-09-025-769B-65  
Sequence 65, Application US/09025769B  
Patent No. 6300064  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilag, Vic  
APPLICANT: Ge, Liming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-65

Query Match      87.0%; Score 543; DB 3; Length 119;
Best Local Similarity 90.1%; Pred. No. 6.6e-48;
Matches 109; Conservative 3; Mismatches 3; Indels 6; Gaps 3

QY 1 QVQLQESGPGLVKPSQTLISLTCTVSGGSISSGGYYMTIRHPGKGLEWIGFIYYSGSY 60
Db 1 QVQLQESGPGLVKPSQTLISLTCTVSGGSISSGGYYMTIRHPGKGLEWIGFIYYSGSY 58
QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCAR-EGDGF---DYWGQGLTVTVS 116
Db 59 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARWGSGDGFVMDYWGQGLTVTVS 118
QY 117 S 117
Db 119 S 119

RESULT 9
US-09-490-070A-39
; Sequence 39, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-070A-39

Query Match      87.0%; Score 543; DB 4; Length 119;
Best Local Similarity 90.1%; Pred. No. 6.6e-48;

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Matches 109; Conservative 3; Mismatches 3; Indels 6; Gaps 3
Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYYWTWIRQHPCKGLEWIGFIYSGSTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYYWTWIRQHPCKGLEWIGFIYSGSTN 58
Qy 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCAR--EGDGF---DYWGQGTLTVTS 116
Db 59 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARWGSDGFYAMDYWGQGTLTVTS 118
Qy 117 S 117
Db 119 S 119

RESULT 10
US-09-490-070A-65
; Sequence 65, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-070A-65

Query Match 87.0%; Score 543; DB 4; Length 119;
Best Local Similarity 90.1%; Pred. No. 6.6e-48;
Matches 109; Conservative 3; Mismatches 3; Indels 6; Gaps 3;
Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYYWTWIRQHPCKGLEWIGFIYSGSTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYYWTWIRQHPCKGLEWIGFIYSGSTN 58
Qy 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCAR--EGDGF---DYWGQGTLTVTS 116
Db 59 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARWGSDGFYAMDYWGQGTLTVTS 118
Qy 117 S 117
Db 119 S 119

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Db 59 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARWGDDGFYAMDYWGQGLTVTS 118

Qy 117 S 117

Db 119 S 119

## RESULT 11

US-09-490-153-39

; Sequence 39, Application US/09490153

; Patent No. 6706484

; GENERAL INFORMATION:

APPLICANT: Knappik, Achim

PACK, Peter

Ilag, Vic

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,153

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 39:

US-09-490-153-39

Query Match

Best Local Similarity 87.08; Score 543; DB 4; Length 119;

Matches 109; Conservative 3; Mismatches 3; Indels 6; Gaps 3;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYVTWIRQHPGKGLIEWIGFIYSGSTY 60

Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYVTWIRQHPGKGLIEWIGFIYSGSTN 58

Qy 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCAR-EGDGF---DYWGQGLTVTS 116

Db 59 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARWGDDGFYAMDYWGQGLTVTS 118

Qy 117 S 117

Db 119 S 119

## RESULT 13

US-09-490-324-39

; Sequence 39, Application US/09490324

; Patent No. 6828422

; GENERAL INFORMATION:

APPLICANT: Knappik, Achim

## RESULT 12

US-09-490-153-65

; Sequence 65, Application US/09490153

; Patent No. 6706484

; GENERAL INFORMATION:

APPLICANT: Knappik, Achim

PACK, Peter

Ilag, Vic

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,153

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 65:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 65:

US-09-490-153-65

Query Match

Best Local Similarity 87.08; Score 543; DB 4; Length 119;

Matches 109; Conservative 3; Mismatches 3; Indels 6; Gaps 3;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYVTWIRQHPGKGLIEWIGFIYSGSTY 60

Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYVTWIRQHPGKGLIEWIGFIYSGSTN 58

Qy 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCAR-EGDGF---DYWGQGLTVTS 116

Db 59 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARWGDDGFYAMDYWGQGLTVTS 118

Qy 117 S 117

Db 119 S 119



Wed Nov 9 13:47:04 2005

STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/049,672A  
FILING DATE: HERewith  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Cerrone, Michael C  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0497 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 473 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: PANTUT01  
CLONE: 1513264  
US-09-049-672A-4

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Best Local Similarity 84.7%; Pred. No. 3.9e-47;  
Matches 105; Conservative 5; Mismatches 7; Indels 7; Gaps 1;  
  
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Db |||||  
Db 20 QVQLQESGPGLVKPSOTLSLTCTVSGGSISSGGYYWTWIRQHPKGLGWIGFIYYSGSTL 79  
QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARE-----GDGFYWGQGTLLV 113  
Db |||||  
Db 80 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARE-----GDGFYWGQGTLLV 139  
  
QY 114 TVSS 117  
Db |||||  
Db 140 TVSS 143

Search completed: November 9, 2005, 11:46:38  
Job time : 19.1805 secs

100-361760-1000



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:40:37 ; Search time 65 Seconds  
(without alignments)  
753.137 Million cell updates/sec

Title: US-10-660-357A-13  
Perfect score: 624  
Sequence: 1 QVQLQSGGGLVKKPSQTLSTLTCTVSGGSISSGGYYVTWIRQHPGKGLWIGFYISGSTY 60

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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2:	/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3:	/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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5:	/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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12:	/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13:	/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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19:	/cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
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22:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	624	100.0	117	14	US-10-330-613-13
2	624	100.0	117	14	US-10-330-530-13
3	624	100.0	117	16	US-10-660-357-13
4	587.5	94.2	122	18	US-10-984-960A-20
5	587	94.1	117	14	US-10-330-613-5
6	587	94.1	117	14	US-10-330-530-5
7	587	94.1	117	16	US-10-660-357-5
8	585.5	93.8	118	15	US-10-309-762-138
9	581.5	93.2	125	17	US-10-805-177-53
10	579	92.8	123	15	US-10-309-762-10
11	575.5	92.2	120	15	US-10-309-762-13

ALIGNMENTS	
RESULT 1	
US-10-330-613-13	
; Sequence 13, Application US/10330613	
; Publication No. US20030147809A1	
; GENERAL INFORMATION:	
; APPLICANT: Gudas Jean	
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN	
; FILE REFERENCE: ABGENIX.022A	
; CURRENT APPLICATION NUMBER: US/10/330,613	
; CURRENT FILING DATE: 2002-12-26	
; PRIOR APPLICATION NUMBER: 60/346299	
; PRIOR FILING DATE: 2001-12-18	
; NUMBER OF SEQ ID NOS: 40	
; SOFTWARE: FastSeq for Windows Version 4.0	
; SEQ ID NO 13	
; LENGTH: 117	
; TYPE: PRT	
; ORGANISM: Homo Sapiens	
US-10-330-613-13	
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Best Local Similarity 100.0%; Pred. No. 1e-47;	
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Db	1 QVQLQSGGGLVKKPSQTLSTLTCTVSGGSISSGGYYVTWIRQHPGKGLWIGFYISGSTY 60
QY	61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAIVYCAREGDGFYWGQGLTVVSS 117
Db	61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAIVYCAREGDGFYWGQGLTVVSS 117
RESULT 2	

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US-10-330-530-13
; Sequence 13, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-13

Query Match      100.0%; Score 624; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1e-47;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY 60

QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYVCAREGDFYWGQGLTVTVSS 117
Db 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYVCAREGDFYWGQGLTVTVSS 117

RESULT 3
US-10-660-357-13
; Sequence 13, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-13

Query Match      100.0%; Score 624; DB 16; Length 117;
Best Local Similarity 100.0%; Pred. No. 1e-47;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY 60

QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYVCAREGDFYWGQGLTVTVSS 117
Db 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYVCAREGDFYWGQGLTVTVSS 117

RESULT 4
US-10-984-960A-20
; Sequence 20, Application US/10984960A
; Publication No. US20050142137A1
; GENERAL INFORMATION:
; APPLICANT: Gallo, Michael
; APPLICANT: Chui, Daniel
; APPLICANT: Zhong, Haihong
; APPLICANT: Ara, Gulshan
; APPLICANT: LaRoche, William J.
; TITLE OF INVENTION: ANTIBODIES AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR
; FILE REFERENCE: Cura 970
; CURRENT APPLICATION NUMBER: US/10/984,960A
; CURRENT FILING DATE: 2004-11-08
; PRIOR APPLICATION NUMBER: 60/518,275
; PRIOR FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 20
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-984-960A-20

Query Match      94.2%; Score 587.5; DB 18; Length 122;
Best Local Similarity 91.8%; Pred. No. 1.9e-44;
Matches 112; Conservative 4; Mismatches 1; Indels 5; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGVSISSGGYYTWSWIRQHPGKGLEWIGFIYYSGSTY 60

QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYVCAREGDFYWGQGLTVTV 115
Db 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYVCAREGYYDEGGDFYWGQGLTVTV 120

QY 116 SS 117
Db 121 SS 122

RESULT 5
US-10-330-613-5
; Sequence 5, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-5

Query Match      94.1%; Score 587; DB 14; Length 117;
Best Local Similarity 94.0%; Pred. No. 2e-44;
Matches 110; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYHWSWIRQHPGKGLEWIGFIYYSGSTY 60

QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYVCAREGDFYWGQGLTVTVSS 117
Db 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAIVYVCARGDGYKYGQGLTVTVSS 117

RESULT 6
US-10-330-530-5
; Sequence 5, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
```

; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES  
; FILE REFERENCE: ABGENIX.031A  
; CURRENT APPLICATION NUMBER: US/10/330,530  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: US 60/346414  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-530-5

Query Match 94.1%; Score 587; DB 14; Length 117;  
Best Local Similarity 94.0%; Pred. No. 2e-44; Indels 0; Gaps 0;  
Matches 110; Conservative 4; Mismatches 3;  
Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGISGGYYTWTWIRQHPKGLGWIGFIYSGSY 60  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGISGGYYTWTWIRQHPKGLGWIGFIYSGSY 60  
Qy 61 YNPSLKSRTVISVDTSKNQFSLKSLSSVTAADTAVYYCAREGDFYWGQGLTVTVSS 117  
Db 61 YNPSLKSRTVISVDTSKNQFSLKSLSSVTAADTAVYYCAREGDFYWGQGLTVTVSS 117

## RESULT 7

US-10-660-357-5.  
; Sequence 5, Application US/10660357  
; Publication No. US20040115205A1  
; GENERAL INFORMATION:  
; APPLICANT: Bar-Eli, Menashe  
; APPLICANT: Green, Larry L.  
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18  
; FILE REFERENCE: ABGENIX.030C1  
; CURRENT APPLICATION NUMBER: US/10/660,357  
; CURRENT FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 10/330,580  
; PRIOR FILING DATE: 2002-12-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-660-357-5

Query Match 94.1%; Score 587; DB 16; Length 117;  
Best Local Similarity 94.0%; Pred. No. 2e-44; Indels 0; Gaps 0;  
Matches 110; Conservative 4; Mismatches 3;  
Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGISGGYYTWTWIRQHPKGLGWIGFIYSGSY 60  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGISGGYYTWTWIRQHPKGLGWIGFIYSGSY 60  
Qy 61 YNPSLKSRTVISVDTSKNQFSLKSLSSVTAADTAVYYCAREGDFYWGQGLTVTVSS 117  
Db 61 YNPSLKSRTVISVDTSKNQFSLKSLSSVTAADTAVYYCAREGDFYWGQGLTVTVSS 117

## RESULT 8

US-10-309-762-138  
; Sequence 138, Application US/10309762  
; Publication No. US20040018198A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; APPLICANT: Foltz, Ian  
; APPLICANT: Handa, Masahisa  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX

; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN  
; FILE REFERENCE: ABGENIX.027A  
; CURRENT APPLICATION NUMBER: US/10/309,762  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/337275  
; PRIOR FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 138  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-309-762-138

Query Match 93.8%; Score 585.5; DB 15; Length 118;  
Best Local Similarity 94.9%; Pred. No. 2.7e-44; Indels 1; Gaps 1;  
Matches 112; Conservative 2; Mismatches 3;  
Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGISGGYYTWTWIRQHPKGLGWIGFIYSGSY 60  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGISGGYYTWTWIRQHPKGLGWIGFIYSGSY 60  
Qy 61 YNPSLKSRTVISVDTSKNQFSLKSLSSVTAADTAVYYCAR-EGDGFYWGQGLTVTVSS 117  
Db 61 YNPSLKSRTVISVDTSKNQFSLKSLSSVTAADTAVYYCARYYGGSDYWGQGLTVTVSS 118

## RESULT 9

US-10-805-177-53  
; Sequence 53, Application US/10805177  
; Publication No. US2005008449A1  
; GENERAL INFORMATION:  
; APPLICANT: Landes, Gregory M.  
; APPLICANT: Chen, Francine  
; APPLICANT: Bezabeh, Biryam  
; APPLICANT: Foltz, Ian  
; APPLICANT: Tse, Kam Fai  
; APPLICANT: Jeffers, Michael  
; APPLICANT: Mesri, Mehdi  
; APPLICANT: Starling, Gary  
; APPLICANT: Mezes, Peter  
; APPLICANT: Khramtsov, Nikolai  
; TITLE OF INVENTION: ANTIBODIES AGAINST T CELL IMMUNOGLOBULIN  
; FILE REFERENCE: ABXCUR.006A  
; CURRENT APPLICATION NUMBER: US/10/805,177  
; CURRENT FILING DATE: 2004-03-19  
; PRIOR APPLICATION NUMBER: 60/456,652  
; PRIOR FILING DATE: 2003-03-19  
; NUMBER OF SEQ ID NOS: 141  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 53  
; LENGTH: 125  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-805-177-53

Query Match 93.2%; Score 581.5; DB 17; Length 125;  
Best Local Similarity 89.5%; Pred. No. 6.5e-44; Indels 7; Gaps 1;  
Matches 111; Conservative 3; Mismatches 3;  
Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGISGGYYTWTWIRQHPKGLGWIGFIYSGSY 60  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGISGGYYTWTWIRQHPKGLGWIGFIYSGSY 60  
Qy 61 YNPSLKSRTVISVDTSKNQFSLKSLSSVTAADTAVYYCAREG-----DGFYWGQGLTV 113  
Db 61 YNPSLKSRTVISVDTSKNQFSLKSLSSVTAADTAVYYCARNNNSSNNYNNFDYWGQGLTV 120  
Qy 114 TVSS 117  
Db 121 TVSS 124

```
RESULT 10
US-10-309-762-10
; Sequence 10, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 123
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-309-762-10
```

```
Query Match 92.8%; Score 579; DB 15; Length 123;
Best Local Similarity 90.2%; Pred. No. 1.1e-43;
Matches 111; Conservative 3; Mismatches 3; Indels 6; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYSGSY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWWSWIRQHPGKGLEWIGFIYSGSY 60

QY 61 YNPGLKSRVTISVDTSKNQFSLKSSVTAADTAVVYICAREGDG-----DYWGQGLTVT 114
Db 61 YNPGLKSRVTISVDTSKNQFSLKSSVTAADTAVVYICAREGYYWWSWIRQHPGKGLEWIGFIYSGSY 120

QY 115 VSS 117
Db 121 VSS 123
```

```
RESULT 11
US-10-309-762-13
; Sequence 13, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 120
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-309-762-13
```

```
Query Match 92.2%; Score 575.5; DB 15; Length 120;
Best Local Similarity 91.7%; Pred. No. 2.1e-43;
Matches 110; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYSGSY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWWSWIRQHPGKGLEWIGFIYSGSY 60
```

```
QY 61 YNPGLKSRVTISVDTSKNQFSLKSSVTAADTAVVYICAREGDG---FDYWGQGLTVTSS 117
Db 61 YNPGLKSRVTISVDTSKNQFSLKSSVTAADTAVVYICAREGYYWWSWIRQHPGKGLEWIGFIYSGSY 120

RESULT 12
US-10-309-762-144
; Sequence 144, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 120
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-309-762-144
```

```
Query Match 92.2%; Score 575.5; DB 15; Length 120;
Best Local Similarity 91.7%; Pred. No. 2.1e-43;
Matches 110; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYSGSY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWWSWIRQHPGKGLEWIGFIYSGSY 60

QY 61 YNPGLKSRVTISVDTSKNQFSLKSSVTAADTAVVYICAREGDG---FDYWGQGLTVTSS 117
Db 61 YNPGLKSRVTISVDTSKNQFSLKSSVTAADTAVVYICAREGYYWWSWIRQHPGKGLEWIGFIYSGSY 120
```

```
RESULT 13
US-10-984-960A-56
; Sequence 56, Application US/10984960A
; Publication No. US20050142137A1
; GENERAL INFORMATION:
; APPLICANT: Gallo, Michael
; APPLICANT: Chui, Daniel
; APPLICANT: Zhong, Haihong
; APPLICANT: Ara, Gulshan
; APPLICANT: LaRoche, William J.
; TITLE OF INVENTION: ANTIBODIES AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR
; FILE REFERENCE: Cura 970
; CURRENT APPLICATION NUMBER: US/10/984,960A
; PRIOR FILING DATE: 2004-11-08
; PRIOR APPLICATION NUMBER: 60/518,275
; PRIOR FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 56
; LENGTH: 122
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-984-960A-56
```

```
Query Match 92.1%; Score 574.5; DB 18; Length 122;
Best Local Similarity 89.3%; Pred. No. 2.6e-43;
Matches 109; Conservative 4; Mismatches 4; Indels 5; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYSGSY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWWSWIRQHPGKGLEWIGFIYSGSY 60
```

Db 1 QVOLQESGPGLVKPSQTLSTCTVSGGSIKSGDYNSWVRLQPGKGLEWIGYIYSGSTY 60  
QY 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCAREG-----GFDYWGQGTLLV 115  
Db 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCAREGYYDSGGFDYWGQGTLLV 120  
QY 116 SS 117  
Db 121 SS 122

RESULT 14  
US-10-309-762-75  
; Sequence 75, Application US/10309762  
; Publication No. US20040018198A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; APPLICANT: Foltz, Ian  
; APPLICANT: Handa, Masahisa  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
; FILE REFERENCE: AGENIX.027A  
; CURRENT APPLICATION NUMBER: US/10/309,762  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/337275  
; PRIOR FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 75  
; LENGTH: 124  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-309-762-75

Query Match 92.1%; Score 574.5; DB 15; Length 124;  
Best Local Similarity 89.5%; Pred. No. 2,7e-43;  
Matches 111; Conservative 3; Mismatches 3; Indels 7; Gaps 1;  
QY 1 QVOLQESGPGLVKPSQTLSTCTVSGGSIKSGDYNSWVRLQPGKGLEWIGYIYSGSTY 60  
Db 1 QVOLQESGPGLVKPSQTLSTCTVSGGSIKSGDYNSWVRLQPGKGLEWIGYIYSGSTY 60  
QY 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCAREG-----GFDYWGQGTLLV 113  
Db 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARENYDILITGFNWFDPWGQGTLLV 120  
QY 114 TVSS 117  
Db 121 TVSS 124

RESULT 15  
US-10-309-762-96  
; Sequence 96, Application US/10309762  
; Publication No. US20040018198A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; APPLICANT: Foltz, Ian  
; APPLICANT: Handa, Masahisa  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
; FILE REFERENCE: AGENIX.027A  
; CURRENT APPLICATION NUMBER: US/10/309,762  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/337275  
; PRIOR FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 96  
; LENGTH: 143  
; TYPE: PRT

; ORGANISM: Homo sapiens  
US-10-309-762-96  
Query Match 92.1%; Score 574.5; DB 15; Length 143;  
Best Local Similarity 89.5%; Pred. No. 3.1e-43;  
Matches 111; Conservative 3; Mismatches 3; Indels 7; Gaps 1;  
QY 1 QVOLQESGPGLVKPSQTLSTCTVSGGSIKSGDYNSWVRLQPGKGLEWIGYIYSGSTY 60  
Db 20 QVOLQESGPGLVKPSQTLSTCTVSGGSIKSGDYNSWVRLQPGKGLEWIGYIYSGSTY 79  
QY 61 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCAREG-----GFDYWGQGTLLV 113  
Db 80 YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARENYDILITGFNWFDPWGQGTLLV 139  
QY 114 TVSS 117  
Db 140 TVSS 143  
Search completed: November 9, 2005, 12:42:59  
Job time : 66 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 12:25:58 ; Search time 12.609 Seconds  
(without alignments)  
892.802 Million cell updates/sec

Title: US-10-660-357A-13

Perfect score: 624

Sequence: 1 QVQLQESGPGLVKPSQTL...AREGDFYWGQGLTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	549	88.0	147	2 S13519	Ig heavy chain V r
2	537	86.1	140	2 I37782	Ig variable region
3	530	84.9	135	2 S78051	Ig heavy chain pre
4	525	84.1	121	2 S44113	Ig heavy chain V r
5	524.5	84.1	130	2 S30534	Ig heavy chain V r
6	523	83.8	130	2 S31690	Ig heavy chain V r
7	518	83.0	128	2 S31514	Ig heavy chain - h
8	517	82.9	99	2 S26801	Ig heavy chain V r
9	517	82.9	116	2 S37456	Ig mu chain - huma
10	509	81.6	155	2 S31511	Ig heavy chain - h
11	507	81.2	146	2 S09710	Ig heavy chain V r
12	507	81.2	155	2 S31512	Ig heavy chain - h
13	506.5	81.2	139	2 S31586	Ig heavy chain V r
14	503.5	80.7	122	2 S69912	Ig V-D-J region (N
15	500	80.1	99	2 S26803	Ig heavy chain V r
16	499.5	80.0	137	2 S31676	Ig heavy chain V r
17	496.5	79.6	129	2 S44114	Ig heavy chain V r
18	495	79.3	99	2 S26802	Ig heavy chain V r
19	495	79.3	123	2 S30530	Ig heavy chain V r
20	494	79.2	146	2 S09711	Ig heavy chain V r
21	493.5	79.1	118	2 S20780	Ig heavy chain V r
22	488.5	78.3	145	2 S78055	Ig heavy chain pre
23	488	78.2	118	2 A26340	Ig heavy chain pre
24	488	78.2	140	2 A49045	Ig heavy chain pre
25	487	78.0	127	2 S19668	Ig heavy chain V r
26	486	77.9	99	2 S26807	Ig heavy chain V r
27	485.5	77.8	110	2 S44110	Ig heavy chain V-D
28	483.5	77.5	140	2 S78052	Ig heavy chain pre
29	483	77.4	139	2 S31696	Ig heavy chain V r

30	481	77.1	99	2 S12418	Ig heavy chain V r
31	480	76.9	109	2 PH1673	Ig heavy chain V r
32	478	76.6	135	2 S31504	Ig heavy chain V r
33	476.5	76.4	137	2 S31585	Ig heavy chain V r
34	472.5	75.7	126	2 S47010	Ig heavy chain V4.
35	472	75.6	97	2 S26906	Ig heavy chain V r
36	472	75.6	99	2 S26800	Ig heavy chain V r
37	472	75.6	105	2 S44125	Ig lambda chain V
38	472	75.6	124	2 S31684	Ig heavy chain V r
39	471.5	75.6	139	2 A41287	Ig heavy chain pre
40	471	75.5	99	2 S12412	Ig heavy chain V r
41	471	75.5	99	2 S26899	Ig heavy chain V r
42	471	75.5	116	2 B26340	Ig heavy chain pre
43	470	75.3	97	2 S12416	Ig heavy chain V r
44	470	75.3	120	2 PT0370	Ig mu chain precu
45	468.5	75.1	118	2 S24443	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S13519

Ig heavy chain V region precursor - human

C;Species: Homo sapiens (man)

C;Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C;Accession: S13519

R;Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.

Nucleic Acids Res. 19, 673, 1991

A;Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked A;Reference number: S13519; MUID:91187691; PMID:2011536

A;Accession: S13519

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-147 <MOR>

A;Cross-references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;41-125/Domain: immunoglobulin homology <IMM>

Query Match	88.0%	Score 549;	DB 2;	Length 147;
Best Local Similarity	88.4%	Pred. No. 7.3e-42;		
Matches 107;	Conservative	3;	Mismatches	7;
			Indels	4;
			Gaps	1;
Qy	1	QVQLQESGPGLVKPSQTL	SLTCTVSGSIS	SSGGYYVTWIRQHPGKLEWIGFIYSGSTY 60
Db	27	QLQLQESGPGLVKPS	ETSLTCTVSGSIS	SSGGYYGWI
Qy	61	YNPSLKSRTISVDTS	KNQFSLKLSVTA	ADTAVYICARE---GDGFDYWGQGLTVTS 116
Db	87	YNPSLKSRTISVDTS	KNQFSLKLSVTA	ADTAVYICARPLLWFGE
Qy	117	S	117	
Db	147	S	147	

RESULT 2

I37782

Ig variable region (VDJ) (clone T23-9) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999

C;Accession: I37782; S25476

R;Demaison, C.; Chaetagner, P.; Theze, J.; Zouali, M.

Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994

A;Title: Somatic diversification in the heavy chain variable region genes expressed by A;Reference number: A36876; MUID:94119917; PMID:8290556

A;Accession: I37782

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-140 <RES>

A;Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F:46-128/Domain: immunoglobulin homology <IMM>

Query Match 86.1%; Score 537; DB 2; Length 140;  
Best Local Similarity 87.9%; Pred. No. 8e-41;  
Matches 107; Conservative 3; Mismatches 5; Indels 8; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWWTWIRQHPGKLEWIGFIYSGSTY 60  
DB 20 QVQLQESGPGLVKPSQTLSTCTVSGGSISS--YYWSWIRQPPGKLEWIGFIYSGSTN 77

QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAATVAVYVCAREG-----GDGFDYWGQGLT 114  
DB 78 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAATVAVYCARHNSWSWGRFYDWGQGLT 137

QY 115 VSS 117  
DB 138 VSS 140

RESULT 3  
S78051

Ig heavy chain precursor V-D-J region (clone mAb 61VH) - human (fragment)

C:Species: Homo sapiens (man)  
C:Date: 19-Nov-1997 #sequence\_revision 05-Dec-1997 #text\_change 23-Jul-1999

C:Accession: S78051; S23716

R:Harindranath, N.

submitted to the EMBL Data Library, August 1990

A:Reference number: S78051

A:Accession: S78051

A:Molecule type: mRNA

A:Residues: 1-135 <HAR>

A:Cross-references: EMBL:X54437; NID:G37814; PIDN:CAA38306.1; PID:9930117

R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins  
Int. Immunol. 3, 865-875, 1991

A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h  
patient.

A:Reference number: S23716; MUID:92031262; PMID:1718404

A:Accession: S23716

A:Molecule type: mRNA

A:Residues: 13-111 <HAW>

A:Cross-references: EMBL:X54437

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:1-13/Domain: signal sequence (fragment) #status predicted <SIG>

F:14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>

F:27-111/Domain: immunoglobulin homology <IMM>

Query Match 84.9%; Score 530; DB 2; Length 135;  
Best Local Similarity 83.7%; Pred. No. 3.2e-40;  
Matches 103; Conservative 5; Mismatches 9; Indels 6; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWWTWIRQHPGKLEWIGFIYSGSTY 60  
DB 13 QLQLQESGPGLVKPSQTLSTCTVSGGSISSGGYWGWIWIRQPPGKLEWIGSIYSGNTY 72

QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAATVAVYVCAREG-----DGFDYWGQGLT 114  
DB 73 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAATVAVYCARLGGPDYTLDCGMVWGQGLT 132

QY 115 VSS 117  
DB 133 VSS 135

RESULT 4  
S44113

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001

C:Accession: S44113

R:Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.

submitted to the EMBL Data Library, March 1994

A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r

A:Reference number: S44105

A:Accession: S44113

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-121 <HAW>

A:Cross-references: EMBL:Z31389; NID:9472967; PIDN:CAA83264.1; PID:9940524

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 525; DB 2; Length 121;  
Best Local Similarity 84.3%; Pred. No. 8e-40;  
Matches 102; Conservative 3; Mismatches 12; Indels 4; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWWTWIRQHPGKLEWIGFIYSGSTY 60

DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGVISSSSYYWGWTRQPPGKLEWIGSIYSGSTY 60

QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAATVAVYVCAREG---FDYWGQGLT 116

DB 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAATVAVYVCAREG---FDYWGQGLT 120

QY 117 S 117

DB 121 S 121

RESULT 5  
S30534

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Aug-1996

C:Accession: S30534

R:Marlette, X.

submitted to the EMBL Data Library, October 1992

A:Reference number: S30520

A:Accession: S30534

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-130 <MAR>

A:Cross-references: EMBL:Z18320

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 524.5; DB 2; Length 130;

Best Local Similarity 80.8%; Pred. No. 9.6e-40;

Matches 105; Conservative 3; Mismatches 9; Indels 13; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWWTWIRQHPGKLEWIGFIYSGSTY 60

DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWWTWIRQHPGKLEWIGFIYSGSTN 60

QY 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAATVAVYVCAREG---FDYV 107

DB 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAATVAVYVCARDKGFWSGYTRNSRAFDIW 120

QY 108 GQGLT 117

DB 121 GQGLT 130

RESULT 6  
S31690

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C:Accession: S31690

R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31585

A:Accession: S31690



A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-130 <CUI>  
A;Cross-references: EMBL:Z14199; NID:g30984; PIDN:CAA78568.1; PID:g30985  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;20-102/Domain: immunoglobulin homology <IMM>

Query Match 83.8%; Score 523; DB 2; Length 130;  
Best Local Similarity 82.7%; Pred. No. 1.3e-39;  
Matches 105; Conservative 3; Mismatches 7; Indels 12; Gaps 2;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYWTWIRQHPKGLGWIGFIYSGSTY 60  
Db 6 QVQLQESGPGLVKPSQTLSTCTVSGGSISS--YYSWSRQPPKGLGWIGFIYSGSTN 63

Qy 61 YNPFLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCAREGD-----GFDYWGQG 110  
Db 64 YNPFLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGSVLLWFGELLYYFDYWGQG 123

Qy 111 TLVTVSS 117  
Db 124 TLVTVSS 130

RESULT 7  
S31514  
Ig heavy chain - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S31514  
submitted to the EMBL Data Library, December 1992  
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autoantibodies from  
A;Reference number: S31509  
A;Accession: S31514  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-128 <CHA>  
A;Cross-references: EMBL:X69862; NID:g33086; PIDN:CAA49496.1; PID:g33087  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;22-106/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 518; DB 2; Length 128;  
Best Local Similarity 82.6%; Pred. No. 3.5e-39;  
Matches 100; Conservative 7; Mismatches 10; Indels 4; Gaps 1;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYWTWIRQHPKGLGWIGFIYSGSTY 60  
Db 8 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGFYWSWIRQHPGMALEWIAHIVFSGSTY 67

Qy 61 YNPFLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCAR-----EGDGFYWGQGLTVTVSS 116  
Db 68 YNPFLKSRVTISVDTSKNQFSLRSTVTPADTAVYYCARFYNGFYGFDPWGQGLTVTVSS 127

Qy 117 S 117  
Db 128 S 128

RESULT 8  
S26801  
Ig heavy chain V region (DP-65) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 25-Oct-1996 #text\_change 20-Jun-2000  
C;Accession: S26801; S26900  
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.  
Eur. J. Immunol. 22, 1075-1082, 1992  
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.  
A;Reference number: S26800; MUID:92201299; PMID:1348029  
A;Accession: S26801  
A;Status: preliminary

A;Molecule type: DNA  
A;Residues: 1-99 <WEN>  
A;Cross-references: EMBL:Z14237; NID:g37706; PIDN:CAA78606.1; PID:g1335372  
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 82.9%; Score 517; DB 2; Length 99;  
Best Local Similarity 98.0%; Pred. No. 3.3e-39;  
Matches 97; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYWTWIRQHPKGLGWIGFIYSGSTY 60  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYWSWIRQHPKGLGWIGFIYSGSTY 60

Qy 61 YNPFLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCAR 99  
Db 61 YNPFLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCAR 99

RESULT 9  
S37456  
Ig mu chain - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S37456  
R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.  
submitted to the EMBL Data Library, September 1993  
A;Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from  
A;Reference number: S37453  
A;Accession: S37456  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-116 <NCI>  
A;Cross-references: EMBL:X75024; NID:g404313; PIDN:CAA52932.1; PID:g758095  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;6-90/Domain: immunoglobulin homology <IMM>

Query Match 82.9%; Score 517; DB 2; Length 116;  
Best Local Similarity 85.3%; Pred. No. 3.9e-39;  
Matches 99; Conservative 4; Mismatches 5; Indels 8; Gaps 1;

Qy 10 GLVKPSQTLSTCTVSGGSISSGGYWTWIRQHPKGLGWIGFIYSGSTYYPNPSLSRV 69  
Db 1 GLVKPSQTLSTCTVSGGSISSGGYWSWIRQHPKGLGWIGFIYSGSTYYPNPSLSRV 60

Qy 70 TISVDTSKNQFSLKSSVTAADTAVYYCAREGDFDY-----KGQGLTVTVSS 117  
Db 61 TISVDTSKNQFSLKSSVTAADTAVYYCARGGYSGYYYNYMDWKGKTTVTVSS 116

RESULT 10  
S31511  
Ig heavy chain - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S31511  
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autoantibodies from  
A;Reference number: S31509  
A;Accession: S31511  
A;Status: preliminary



A; Cross-references: EMBL:Z33398; NID:9871347; PIDN:CAA83849.1; PID:9887460  
 A; Note: the sequence of residues 108-122 and the corresponding nucleic acid sequence are  
 C; Superfamily: immunoglobulin V region; immunoglobulin homology  
 F; 15-99/Domain: immunoglobulin homology <IMM>

Query Match	80.7%;	Score	503.5;	DB	2;	Length	122;
Best Local Similarity	79.5%;	Pred. No.	6.5e-38;				
Matches	97;	Conservative	11;	Mismatches	9;	Indels	5; Gaps 2;

  

QY	1	OVLQSGGGLVKPVSQTLSLTCVTSGGSISGGYYWTWIRHCPKGLEWIGFIYVSSGY	60				
	:		:				
Dd	1	RVLQSGGGLVKPVSQTLSLTCVTSGGSISDGHFWNWRQHCPKGLEWIGNIYFSSGY	60				
	:		:				
QY	61	YNPSLKSRVTISVDTSKNQFSKLKSIVTAADTAVYYCAR---	EGD-GFDYWGQGTILVT	115			
	:		:				
Dd	61	YNPSLKRSRISVDTSKNQFSRLKSVTAADTAVYFCARGFFPRGT	VGLDTWGQGTILVRL	120			
	:		:				
QY	116	SS	117				
	:						
Dd	121	SS	122				
	:						

RESULT 15

S26803  
IG heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13  
C:Accession: S26803  
R:Weng, N.; Snyder, J. G.; Yu-Lee, L.; Marcus, D. M.  
Eur. J. Immunol. 22, 1075-1082, 1992  
A:Title: Polymorphism of human immunoglobulin V (H)4 germ-line genes.  
A:Reference number: S26800; MUID:92201299; PMID:1348029  
A:Accession: S26803  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-99 <WEN>  
A:Cross-references: EMBL:Z14238; NID:g37710; PIDN:CAA78607.1; PID:g1335374  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-99/Domain: immunoglobulin homology <IMM>

	Query Match	80.1%	Score 500;	DB 2;	Length 99;
	Best Local	Similarity 96.0%;	Pred. No. 1.le-37;		
	Matches	95;	Conservative 2;	Mismatches 2;	Indels 0; Gaps 0;
QY	1	QVQLQESGPGLVKPSQTL	SLTCTCVSGGSI	SSGGYYTWTWIRQHPCKGLEWIGFI	YSGSTY 60
Db	1	QVQLQESGPGLVKPSQTL	SLTCTCVSGGSI	SSGGYYTWTWIRQHPCKGLEWIGFI	YSGSTY 60
QY	61	YNPSLKSRTVTS	IVDTSKNQPSL	KLSSTVAADTAVYYCAR	99
Db	61	YNPSLKSRTVTS	IVDTSKNQPSL	KLSSTVAADTAVYYCAR	99

Search completed: November 9, 2005, 13:08:02  
Job time : 12.609 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:46:52 ; Search time 60.406 Seconds  
(without alignments)  
991.843 Million cell updates/sec

Title: US-10-660-357A-13  
Perfect score: 624  
Sequence: 1 QVQLQSGPGLVKPSQTL...AREGDFYWGQTLTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	552	88.5	476	2 Q6GMX1	Q6gm1 homo sapien
2	518.5	83.1	478	2 Q7Z379	Q7z379 homo sapien
3	507.5	81.3	465	2 Q6GMX6	Q6gm6 homo sapien
4	506	81.1	119	2 Q9UL73	Q9ul73 homo sapien
5	503.5	80.7	150	2 Q95973	Q95973 homo sapien
6	499.5	80.0	436	2 Q96KX8	Q96kx8 homo sapien
7	492.5	79.7	477	2 Q6GMX7	Q6gm7 homo sapien
8	492.5	78.9	620	2 Q96EY0	Q96ey0 homo sapien
9	492	78.8	492	2 Q7Z374	Q7z374 homo sapien
10	488.5	78.3	576	2 Q6P418	Q6p418 homo sapien
11	481.5	77.2	130	2 Q81ZD7	Q81zd7 homo sapien
12	474.5	76.0	139	2 Q86SK2	Q86sx2 homo sapien
13	465	74.5	129	1 HV2F HUMAN	P01824 homo sapien
14	445	71.3	478	2 Q6NYH3	Q6nyh3 homo sapien
15	444	71.2	595	2 Q8WUX4	Q8wux4 homo sapien
16	444	71.2	597	2 Q6GMX5	Q6gm5 homo sapien
17	444	71.2	597	2 Q9BU10	Q9bu10 homo sapien
18	444	71.2	625	2 Q96AA6	Q96aa6 homo sapien
19	438	70.2	597	2 Q9BQB8	Q9bbq8 homo sapien
20	437.5	70.1	146	1 HV2I HUMAN	P06331 homo sapien
21	432	69.2	137	1 HV46 MOUSE	P01822 homo sapien
22	428.5	68.7	136	2 Q6L8Q5	Q6lbq5 mus musculus
23	425	68.1	479	2 Q99M22	Q99m22 mus musculus
24	423.5	67.9	122	2 Q9UL75	Q9ul75 mus sapien
25	419.5	67.2	473	2 Q8TC63	Q8tc63 homo sapien
26	415	66.5	117	1 HV2G HUMAN	P01825 homo sapien
27	410	65.2	262	2 Q65ZT1	Q65z1 mus musculus
28	407	65.2	116	2 Q7Z3V6	Q7z3v6 homo sapien
29	405	64.9	113	1 HV47 MOUSE	P01823 mus musculus
30	404	64.7	476	2 Q6WZX7	Q6wzx7 homo sapien
31	379.5	60.8	116	1 HV60 MOUSE	P18531 mus musculus

32	378	60.6	117	1 HV62 MOUSE	P18533 mus musculus
33	374.5	60.0	116	1 HV61 MOUSE	P18532 mus musculus
34	367	58.8	121	2 Q9UL96	Q9ul96 homo sapien
35	359.5	57.6	482	2 Q91X92	Q91x92 mus musculus
36	359	57.5	144	1 HV43 MOUSE	P01819 mus musculus
37	357.5	57.3	118	2 Q811U5	Q811u5 mus musculus
38	353.5	56.7	121	2 Q99NG4	Q99ng4 mus musculus
39	353.5	56.7	135	1 HV02 XENLA	P20957 xenopus lae
40	340	54.5	118	2 Q9UL74	Q9ul74 homo sapien
41	330	52.9	470	2 Q6RJ44	Q6rj44 homo sapien
42	329.5	52.8	118	2 Q9UL72	Q9ul72 homo sapien
43	329	52.7	240	2 Q6S2C9	Q6s2c9 homo sapien
44	328.5	52.6	147	2 Q9Y509	Q9y509 homo sapien
45	328	52.6	125	1 HV2D HUMAN	P01817 homo sapien

ALIGNMENTS

RESULT 1

Q6GMX1 PRELIMINARY; PRT; 476 AA.  
AC Q6GMX1;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Hypothetical protein.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalón D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RP Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RC TISSUE=Spleen;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
EMBL; BC073773; AAH3773.1; -;  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; C1-set; 3.  
DR Pfam; PF00047; IG; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00230; IG\_MHC; UNKNOWN\_2.



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1] NCBI\_TaxID=9606;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clim.1998.4531;  
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035041; AAD56277.1; -.  
 DR PIR; PH0876; PH0876.  
 DR PIR; S12416; S12416.  
 DR HSSP; P01820; 1G7J.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON TER 1  
 FT NON TER 119  
 SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;  
 Query Match 81.1%; Score 506; DB 2; Length 119;  
 Best Local Similarity 82.6%; Pred. No. 9.1e-44;  
 Matches 100; Conservative 7; Mismatches 8; Indels 6; Gaps 2;  
 QY 1 QVLOESGPGGLVKPSQTLSTCTVSGGSISSGGYWTWIRQHPKGLGWIGFIYSGSTY 60  
 Db 1 QVLOESGPGGLVKPSQTLSTCTVSGGSISSGGYWTWIRQHPKGLGWIGFIYSGSTN 58  
 QY 61 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAVVYCAREGDG---FDYWGQGTTLTVTS 116  
 Db 59 YTPSLKSRVTISVDRSKNQPSLKLSTLTAADTAVVYCARLSNWCYFYFDYWGQGTTLTVTS 118  
 QY 117 S 117  
 Db 119 S 119  
 RESULT 5  
 O95973 PRELIMINARY; PRT; 150 AA.  
 AC O95973;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE V4 heavy chain variable region precursor (fragment).  
 GN Name=IGM;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1] SEQUENCE FROM N.A.  
 RP Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;  
 RA Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AF103795; AAC79084.1; -.  
 DR PIR; S31673; S31673.  
 DR PIR; S78056; S78056.  
 DR HSSP; P01820; 1G7J.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Signal.  
 FT SIGNAL  
 FT CHAIN  
 FT NON TER 150  
 FT NON TER 150  
 SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;  
 Query Match 80.7%; Score 503.5; DB 2; Length 150;  
 Best Local Similarity 83.1%; Pred. No. 2.1e-43;

Matches 98; Conservative 8; Mismatches 11; Indels 1; Gaps 1;  
 QY 1 QVLOESGPGGLVKPSQTLSTCTVSGGSISSGGYWTWIRQHPKGLGWIGFIYSGSTY 60  
 Db 20 QLOLQESGPGGLVKPSQTLSTCTVSGGSISSGGYWTWIRQHPKGLGWIGFIYSGSDY 79  
 QY 61 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAVVYCAREGDG---FDYWGQGTTLTVTS 117  
 Db 80 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAVVYCARLGMGAFDFWGHGTMVTVSS 137  
 RESULT 6  
 Q96KX8 PRELIMINARY; PRT; 496 AA.  
 AC Q96KX8;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE MGC27165 protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1] SEQUENCE FROM N.A.  
 RP TISSUE=Lung;  
 RC MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2] SEQUENCE FROM N.A.  
 RP TISSUE=Lung;  
 RC Strausberg R.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC016369; AAH16369.1; -.  
 DR HSSP; P01876; 1OW0.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
 SQ SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;  
 Query Match 80.0%; Score 499.5; DB 2; Length 496;  
 Best Local Similarity 79.0%; Pred. No. 2e-42;  
 Matches 98; Conservative 4; Mismatches 15; Indels 7; Gaps 1;  
 QY 1 QVLOESGPGGLVKPSQTLSTCTVSGGSISSGGYWTWIRQHPKGLGWIGFIYSGSTY 60  
 Db 20 QLOLQESGPGGLVKPSQTLSTCTVSGGSISSGGYWTWIRQHPKGLGWIGFIYSGTY 79  
 QY 61 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAVVYCAREGD-----DGFYWGQGTTLV 113





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Qy 116 SS 117
Db 145 SS 146

RESULT 9
Q72374 PRELIMINARY; PRT; 492 AA.
AC Q72374;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZ5686C02218 (Fragment).
GN Name=DKFZ5686C02218;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloeker H., Bocher M., Newes H.W., Weil B., Amid C., Osanger A.,
RA Robo G., Han M., Wleemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538077; CAD98001.1; -.
DR HSP; P01820; 1G7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;

Query Match 78.8%; Score 492; DB 2; Length 492;
Best Local Similarity 77.7%; Pred. No. 1.1e-41;
Matches 94; Conservative 11; Mismatches 12; Indels 4; Gaps 1;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYVYTWIRQHPKGLIEWIGFIYSGSTY 60
Db 32 QLQLQESGPGLVKPSQTLSTCTVSGSVNRNYWGWIRQHPKGLIEWIGSIYNYNTY 91
Qy 61 YNPSLKSRTVISVDTSKNQFSLKSLSSVTAADTAVYYCAREGDG----FDYWGQGLTVTS 116
Db 92 YSPSLKSLRTIFVDTSKNHFSRLTSLTCAVSGSISSSN-WMSWVRQPPKGLIEWIGSIYSGSTN 151
Qy 117 S 117
Db 152 S 152

RESULT 10
Q6P418 PRELIMINARY; PRT; 576 AA.
AC Q6P418;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGH domain protein.
GN Name=IGHD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Jang Y.-J., Chung J., Park J.-Y.;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063384; AAH63384.1; -.
DR HSP; P01820; 1A7N.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 576 AA; 63363 MW; FB897C949D720F1E CRC64;

Query Match 78.3%; Score 488.5; DB 2; Length 576;
Best Local Similarity 81.8%; Pred. No. 3.1e-41;
Matches 99; Conservative 4; Mismatches 13; Indels 5; Gaps 2;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYVYTWIRQHPKGLIEWIGFIYSGSTY 60
Db 27 QVQLQESGPGLVKPSQTLSTCTVSGSISSSN-WMSWVRQPPKGLIEWIGSIYSGSTN 85
Qy 61 YNPSLKSRTVISVDTSKNQFSLKSLSSVTAADTAVYYCAREGD---GFDYWGQGLTVTS 116
Db 86 YNPSLKSRTVISVDTSKNQFSLKSLSSVTAADTAVYYCAREGDYWGQGLTVTS 145
Qy 117 S 117
Db 146 S 146

RESULT 11
Q81ZD7 PRELIMINARY; PRT; 130 AA.
AC Q81ZD7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-thyroglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jang Y.-J., Chung J., Park J.-Y.;

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RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV145445; AAN64329.1; -.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 130
FT SEQUENCE 130 AA; 13901 MW; 0361311FC6EC1551E CRC64;

Query Match 77.2%; Score 481.5; DB 2; Length 130;
Best Local Similarity 75.4%; Pred. No. 3.2e-41;
Matches 98; Conservative 6; Mismatches 13; Indels 13; Gaps 3;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWYTWIRQHPGKLEWIGFTIYSGST- 59
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWYTWIRQHPGKLEWIGFTIYSGSTV 60

QY 60 ----YNPISLKSRTVISVDTSKNQFSLKLSSTAAADTAVYYCAR----EGDG----FDYW 107
Db 61 SGSPYAPSLRSLRVIIISVDTSKNQFSLKLSSTAAADTAVYYCAR----EGDG----FDYW 120

QY 108 GQGLTVTVSS 117
Db 121 GQGLTVTVSS 130

RESULT 12
Q86SX2 PRELIMINARY; PRT; 139 AA.
AC Q86SX2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Full-length cDNA clone CS0DL004YM19 of B cells (Ramos cell line) of
DE Homo sapiens (human) (Fragment).
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=B cells;
RC SEQUENCE FROM N.A.
RA Li W.B., Gruber C., Jesse J., Polayes D.;
RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX248300; CAD62627.1; -.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;

Query Match 76.0%; Score 474.5; DB 2; Length 139;
Best Local Similarity 89.5%; Pred. No. 1.8e-40;
Matches 94; Conservative 4; Mismatches 2; Indels 5; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWYTWIRQHPGKLEWIGFTIYSGSTY 60
Db 33 QVQLQESGPGLVKPSQTLSTCTVSGGSISS--YVWSWIRQHPGKLEWIGFTIYSGSTN 90

QY 61 YNPISLKSRTVISVDTSKNQFSLKLSSTAAADTAVYYCARE---GD 102
Db 91 YNPISLKSRTVISVDTSKNQFSLKLSSTAAADTAVYYCARDTVRGD 135

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RESULT 13
HV2F_HUMAN STANDARD; PRT; 129 AA.
ID HV2F_HUMAN
AC P01824;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-II region WAH.
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82222235; PubMed=6806818;
RA Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;
RT "Complete amino acid sequence of the delta heavy chain of human
RT immunoglobulin D.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854 (1982).
CC -!- MISCELLANEOUS: This chain was isolated from an IgD myeloma
CC protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02099; D2HUWA.
DR HSSP; P01820; IG7J.
DR GlycoSuiteDB; P01824; -.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 113
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Query Match 74.5%; Score 465; DB 1; Length 129;
Best Local Similarity 69.0%; Pred. No. 1.5e-39;
Matches 89; Conservative 10; Mismatches 18; Indels 12; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWYTWIRQHPGKLEWIGFTIYSGSTY 60
Db 1 RLQLQESGPGLVKPSQTLSTCTVSGGPIRRRTGYWGWIRQPPGKLEWIGGYVYSGSY 60

QY 61 YNPISLKSRTVISVDTSKNQFSLKLSSTAAADTAVYYCAR-----EGDGFDYWG 108
Db 61 YNPISLGRVTISVDTSRNQFSLNLRMSAADTAMYYCARGNPPYYDICTGSDGDDVDWG 120

QY 109 QGTLTVTVSS 117
Db 121 QGTLTVTVSS 129

RESULT 14
Q6NYH3 PRELIMINARY; PRT; 478 AA.
ID Q6NYH3
AC Q6NYH3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RA Strausberg R.;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC066594; AAH66594.1; -  
 DR HSSP; P01820; 1A7N.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 2.  
 DR SMART; SM00409; IG; 4.  
 DR SMART; SM00407; IGcl; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 478 AA; 51856 MW; 5F8B98F60F077256 CRC64;

Query Match 71.3%; Score 445; DB 2; Length 478;  
 Best Local Similarity 71.1%; Pred. No. 7e-37;  
 Matches 86; Conservative 17; Mismatches 12; Indels 6; Gaps 2;  
 QY 1 QVQLQSGPGLVPSQTLSTCTVSGGSISSGGYVYTWIRQHPGKGLWIGFIYSGSTY 60  
 Db 20 QVQLQSGPGLVPSQTLSTCTVSGGSISSGGYVYTWIRQHPGKGLWIGFIYSGSTY 77  
 QY 61 YNPGLSRVTISVDTSKNQFSLKSSVTAADTAAYVCAREGDG---FDYWGQGLTVTVS 116  
 Db 78 YNPGLSRVTISVDTSKNQFSLKSSVTAADTAAYVCAREGDG---FDYWGQGLTVTVS 137  
 QY 117 S 117  
 Db 138 S 138

## RESULT 15

Q8WUX4 PRELIMINARY; PRT; 595 AA.  
 AC Q8WUX4;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RA Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC019235; AAH19235.2; -  
 DR PIR; G34964; G34964.  
 DR HSSP; P01861; 1ADQ.  
 DR Pfam; PF07654; Cl-set; 4.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 4.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 595 AA; 65290 MW; 0D4B50776545714E CRC64;  
 Query Match 71.2%; Score 444; DB 2; Length 595;  
 Best Local Similarity 73.2%; Pred. No. 1.1e-36;  
 Matches 93; Conservative 6; Mismatches 16; Indels 12; Gaps 3;  
 QY 1 QVQLQSGPGLVPSQTLSTCTVSGGSISSGGYVYTWIRQHPGKGLWIGFIYSGSTY 60  
 Db 27 QVQLQSGPGLVPSQTLSTCTVSGGSISSGGYVYTWIRQHPGKGLWIGFIYSGSTY 84  
 QY 61 YNPGLSRVTISVDTSKNQFSLKSSVTAADTAAYVCAR-----EGD-GFDYWGQ 110  
 Db 85 YNPGLSRVTISVDTSKNQFSLKSSVTAADTAAYVCAR-----EGD-GFDYWGQ 144  
 QY 111 TLTVSS 117  
 Db 145 TLTVSS 151

Search completed: November 9, 2005, 13:05:48  
 Job time : 61.406 secs

CHINA XIN KONG CHIA

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:43:32 ; Search time 74.6015 Seconds  
(without alignments)  
627.306 Million cell updates/sec

Title: US-10-660-357A-17

Perfect score: 649

Sequence: 1 QVQLQESGGLVLRPSETLSL.....WLLPDAFDIWGQGMVTMTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	649	100.0	121	7	Adc99772 Anti-huma
2	649	100.0	121	7	Adc99788 Anti-huma
3	649	100.0	121	7	Adc99788 Anti-huma
4	649	100.0	121	7	Adc99788 Anti-huma
5	649	100.0	121	7	Adc99788 Anti-huma
6	649	100.0	121	7	Adc99788 Anti-huma
7	643	99.1	121	7	Adc99780 Human ant
8	643	99.1	121	7	Adc99780 Anti-huma
9	643	99.1	121	7	Adc99822 Human ant
10	597	92.0	121	7	Adc99808 Anti-huma
11	597	92.0	121	7	Adc99808 Anti-huma
12	597	92.0	121	7	Adc99850 Human ant
13	565.5	87.1	243	8	Adc998076 S9 cell d
14	547	84.3	121	5	Abg92884 Human imm
15	545.5	84.1	121	5	Abb07171 ebvHigM M
16	545.5	84.1	121	8	Adi26658 Human ant
17	545.5	84.1	122	7	Adp03887 Murine-ex
18	545.5	84.1	122	7	Adp03884 Murine-ex
19	544.5	83.9	122	7	Adp03885 Murine-ex
20	544.5	83.9	122	7	Adp03889 Murine-ex
21	540	83.2	119	2	Aaw27554 Human Ab
22	540	83.2	119	6	Abj18676 Antibody
23	539.5	83.1	118	8	Adp22272 Human ant
24	539	83.1	123	6	Ada89258 Human ant
25	538.5	83.0	122	7	Adp03931 Murine-ex

## ALIGNMENTS

## RESULT 1

ADC99772  
ID ADC99772 standard; protein; 121 AA.

XX AC ADC99772;

XX AC (first entry)

DT 01-JAN-2004 (first entry)

DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 1.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
KW cytotatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
KW lung cancer; human.

XX Homo sapiens.

XX WO2003057838-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

XX Gudas J;

XX WPI; 2003-587113/55.

XX N-PSDB; ADC99774.

XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
or condition associated with expression of MUC18 in a patient, e.g.

XX tumors, cancers, and other malignancies.

XX Claim 1; SEQ ID NO 1; 78pp; English.

XX The invention relates to a novel isolated monoclonal antibody comprising  
a heavy or light chain amino acid or a heavy or light chain variable  
domain where the antibody binds to MUC18. The monoclonal antibody of the  
invention demonstrates cytostatic activity and may be useful for treating  
a disease or condition associated with the expression of MUC18 on the  
cell surface such as tumours, specifically melanoma, oesophageal,  
pancreatic or colorectal tumours, carcinomas, particularly cervical  
carcinomas and cervical intraepithelial neoplasia and cancers including  
colorectal, breast or lung cancer, as well as other malignancies. The  
current sequence is that of the anti-human MUC18 monoclonal antibody

Adp03864 Murine-ex  
Adp03862 Murine-ex  
Adp03984 Murine-ex  
Adp03973 Murine-ex  
Aay15126 Anti-muri  
Adp03933 Murine-ex  
Adp03886 Murine-ex  
Abp43199 Human ova  
Adp19313 Heavy cha  
Aaw90287 Human ant  
Abg92888 Human imm  
Adp03868 Murine-ex  
Adp03876 Murine-ex  
Abg97827 Human MPL  
Adg93304 Thrombopo  
Abg97829 Mouse 12E  
Abg35331 Thrombopo  
Aay06718 Antibody  
Ado39737 Human C-m

CC heavy chain protein of the invention.  
 XX  
 SQ Sequence 121 AA;

Query Match 100.0%; Score 649; DB 7; Length 121;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-46;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSGPGLVKPSETLSLTCTVSGSISSSYYWMIROPPGKGLWIGYIYYTWTSNYN 60  
 |||||  
 Db 1 QVQLQSGPGLVKPSETLSLTCTVSGSISSSYYWMIROPPGKGLWIGYIYYTWTSNYN 60  
 |||||

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
 |||||  
 Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
 |||||

QY 121 S 121  
 ||  
 Db 121 S 121

RESULT 2  
 ADC99788

ID ADC99788 standard; protein; 121 AA.

XX  
 AC ADC99788;

XX  
 DT 01-JAN-2004 (first entry)

XX Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 17.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;

XX cytotatic; melanoma; oesophageal; pancreatic; colorectal tumour;

XX cervical carcinoma; intraepithelial neoplasia; colorectal; breast;

XX lung cancer; human.

XX Homo sapiens.

XX WO2003057838-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

XX Gudas J;

XX WPI; 2003-587113/55.

XX N-PSDB; ADC99790.

XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease

XX or condition associated with expression of MUC18 in a patient, e.g.

XX tumors, cancers, and other malignancies.

XX Claim 1; SEQ ID NO 17; 78pp; English.

XX The invention relates to a novel isolated monoclonal antibody comprising

XX a heavy or light chain amino acid or a heavy or light chain variable

XX domain where the antibody binds to MUC18. The monoclonal antibody of the

XX invention demonstrates cytostatic activity and may be useful for treating

XX a disease or condition associated with the expression of MUC18 on the

XX cell surface such as tumours, specifically melanoma, oesophageal,

XX pancreatic or colorectal tumours, carcinomas, particularly cervical

XX carcinomas and cervical intraepithelial neoplasia and cancers including

XX colorectal, breast or lung cancer, as well as other malignancies. The

XX current sequence is that of the anti-human MUC18 monoclonal antibody

XX heavy chain protein of the invention.

XX  
 SQ Sequence 121 AA;

Query Match 100.0%; Score 649; DB 7; Length 121;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-46;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSGPGLVKPSETLSLTCTVSGSISSSYYWMIROPPGKGLWIGYIYYTWTSNYN 60  
 |||||  
 Db 1 QVQLQSGPGLVKPSETLSLTCTVSGSISSSYYWMIROPPGKGLWIGYIYYTWTSNYN 60  
 |||||

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
 |||||  
 Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
 |||||

QY 121 S 121

Db 121 S 121

RESULT 3

ADD05376

ID ADD05376 standard; protein; 121 AA.

XX  
 AC ADD05376;

XX  
 DT 01-JAN-2004 (first entry)

XX Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 1.

XX monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;

XX antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.

XX Homo sapiens.

XX WO2003057006-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041582.

XX 28-DEC-2001; 2001US-0346460P.

XX (ABGE-) ABGENIX INC.

XX Gudas J, Bar-Eli M;

XX WPI; 2003-577496/54.

XX N-PSDB; ADD05378.

XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and

XX treating tumors, inhibiting tumor growth, inhibiting cell invasion

XX associated with melanoma, or increasing survival of an animal having a

XX metastatic tumor.

XX Claim 1; SEQ ID NO 1; 87pp; English.

XX The invention relates to a novel monoclonal antibody used for inhibiting

XX tumor growth in an animal. The tumor inhibition process comprises

XX selecting an animal in need of treatment for a tumour, providing a

XX monoclonal antibody comprising a heavy chain amino acid, where the

XX antibody consists of any one of 10 fully defined sequences of 117-123

XX amino acids given in the specification, and where the monoclonal antibody

XX binds MUC18, and contacting the tumour with the antibody resulting in

XX inhibited proliferation of the cells. The monoclonal antibody has

XX cytostatic and can be used in the production of a vaccine. The monoclonal

XX antibodies against the MUC18 antigen are useful for diagnosing and

XX treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or

XX tumour metastasis), inhibiting cell invasion associated with melanoma, or

XX increasing survival of an animal having a metastatic tumour. This

XX sequence represents an anti-MUC18 antibody heavy chain, variable region,

XX protein of the invention.

XX  
 SQ Sequence 121 AA;

Query Match 100.0%; Score 649; DB 7; Length 121;

Best Local Similarity 100.0%; Pred. No. 6.4e-46;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPESETLSLTCTVSGGSISSYYMSWIRQPPGKGLEWIGIYYTWTSNYN 60  
Db 1 QVQLQESGPGLVKPESETLSLTCTVSGGSISSYYMSWIRQPPGKGLEWIGIYYTWTSNYN 60

Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGQGTMTVTS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGQGTMTVTS 120

Qy 121 S 121  
Db 121 S 121

RESULT 4  
ADD05392  
ID ADD05392 standard; protein; 121 AA.  
XX AC ADD05392;  
XX DT 01-JAN-2004 (first entry)  
XX DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 17.  
XX KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
XX KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.  
XX OS Homo sapiens.  
XX PN WO2003057006-A2.  
XX PD 17-JUL-2003.  
XX PF 26-DEC-2002; 2002WO-US041582.  
XX PR 28-DEC-2001; 2001US-0346460P.  
XX PA (ABGE-) ABGENIX INC.  
XX PI Gudas J, Bar-Eli M;  
XX WPI: 2003-577496/54.  
XX N-PSDB; ADD05394.  
XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
PT associated with melanoma, or increasing survival of an animal having a  
PT metastatic tumor.  
XX Claim 1; SEQ ID NO 17; 87pp; English.

XX The invention relates to a novel monoclonal antibody used for inhibiting  
CC tumour growth in an animal. The tumour inhibition process comprises  
CC selecting an animal in need of treatment for a tumour, providing a  
CC monoclonal antibody comprising a heavy chain amino acid, where the  
CC antibody consists of any one of 10 fully defined sequences of 117-123  
CC amino acids given in the specification, and where the monoclonal antibody  
CC binds MUC18, and contacting the tumour with the antibody resulting in  
CC inhibited proliferation of the cells. The monoclonal antibody has  
CC cytostatic and can be used in the production of a vaccine. The monoclonal  
CC antibodies against the MUC18 antigen are useful for diagnosing and  
CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or  
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or  
CC increasing survival of an animal having a metastatic tumour. This  
CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
CC protein of the invention.

XX Sequence 121 AA;  
Query Match 100.0%; Score 649; DB 7; Length 121;  
Best Local Similarity 100.0%; Pred. No. 6.4e-46;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPESETLSLTCTVSGGSISSYYMSWIRQPPGKGLEWIGIYYTWTSNYN 60  
Db 1 QVQLQESGPGLVKPESETLSLTCTVSGGSISSYYMSWIRQPPGKGLEWIGIYYTWTSNYN 60

Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGQGTMTVTS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGQGTMTVTS 120

Qy 121 S 121  
Db 121 S 121

RESULT 5  
ADF09814  
ID ADF09814 standard; protein; 121 AA.  
XX AC ADF09814;  
XX DT 12-FEB-2004 (first entry)  
XX DE Human anti-MUC18 monoclonal antibody heavy chain #1.  
XX KW cell proliferation inhibition; MUC18 tumour antigen;  
XX KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
XX KW carcinoma; cancer; malignancy; heavy chain; human.  
XX OS Homo sapiens.  
XX PN WO2003057837-A2.  
XX PD 17-JUL-2003.  
XX PF 26-DEC-2002; 2002WO-US041580.  
XX PR 28-DEC-2001; 2001US-0346414P.  
XX PA (ABGE-) ABGENIX INC.  
XX PI Gudas J;  
XX WPI: 2003-598367/56.  
XX N-PSDB; ADF09816.  
XX Inhibiting cell proliferation associated with expression of MUC18 tumour  
PT antigen, involves incubating and inhibiting cell by administering anti-  
PT MUC18 monoclonal antibody.  
XX Claim 1; SEQ ID NO 1; 83pp; English.

XX The invention comprises a method for inhibiting cell proliferation  
CC associated with expression of MUC18 tumour antigen. The method involves  
CC administering anti-MUC18 monoclonal antibody. The method of the invention  
CC is useful for inhibiting cell (e.g. melanoma or tumour cell)  
CC proliferation associated with the expression of MUC18 tumour antigen, the  
CC method is preferably useful for inhibiting tumour metastasis. The method  
CC is useful for inhibiting cell proliferation in patients with tumours,  
CC carcinomas, cancer and other malignancies. The present amino acid  
CC sequence represents a heavy chain from an MUC18 tumour antigen-specific  
CC monoclonal antibody.

XX Sequence 121 AA;  
Query Match 100.0%; Score 649; DB 7; Length 121;  
Best Local Similarity 100.0%; Pred. No. 6.4e-46;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPESETLSLTCTVSGGSISSYYMSWIRQPPGKGLEWIGIYYTWTSNYN 60  
Db 1 QVQLQESGPGLVKPESETLSLTCTVSGGSISSYYMSWIRQPPGKGLEWIGIYYTWTSNYN 60

```
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPDAFDIWGGTMTVTS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPDAFDIWGGTMTVTS 120
QY 121 S 121
Db 121 S 121

RESULT 6
ADF09830
ID ADF09830 standard; protein; 121 AA.
XX
AC ADF09830;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human anti-MUC18 monoclonal antibody heavy chain #5.
XX
KW cell proliferation inhibition; MUC18 tumour antigen;
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
KW carcinoma; cancer; malignancy; heavy chain; human.
XX
OS Homo sapiens.
XX
PN WO2003057837-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041580.
XX
PR 28-DEC-2001; 2001US-0346414P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
WPI; 2003-598367/56.
DR N-PSDB; ADF09832.
XX
XX
PT Inhibiting cell proliferation associated with expression of MUC18 tumor
PT antigen, involves incubating and inhibiting cell by administering anti-
PT MUC18 monoclonal antibody.
XX
PS Claim 1; SEQ ID NO 17; 83pp; English.
XX
XX
CC The invention comprises a method for inhibiting cell proliferation
CC associated with expression of MUC18 tumour antigen. The method involves
CC administering anti-MUC18 monoclonal antibody. The method of the invention
CC is useful for inhibiting cell (e.g. melanoma or tumour cell)
CC proliferation associated with the expression of MUC18 tumour antigen, the
CC method is preferably useful for inhibiting tumour metastasis. The method
CC is useful for inhibiting cell proliferation in patients with tumours,
CC carcinomas, cancer and other malignancies. The present amino acid
CC sequence represents a heavy chain from an MUC18 tumour antigen-specific
CC monoclonal antibody.
XX
SQ Sequence 121 AA;
Query Match 100.0%; Score 649; DB 7; Length 121;
Best Local Similarity 100.0%; Pred. No. 6.4e-46;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLEWIGYIYTTSTNYN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLEWIGYIYTTSTNYN 60
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPDAFDIWGGTMTVTS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPDAFDIWGGTMTVTS 120
QY 121 S 121
Db 121 S 121

RESULT 7
ADC99780
ID ADC99780 standard; protein; 121 AA.
XX
AC ADC99780;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 9.
XX
KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
KW lung cancer; human.
XX
OS Homo sapiens.
XX
PN WO2003057838-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041581.
XX
PR 28-DEC-2001; 2001US-0346299P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
WPI; 2003-587113/55.
DR N-PSDB; ADC99782.
XX
XX
PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease
PT or condition associated with expression of MUC18 in a patient, e.g.
PT tumors, cancers, and other malignancies.
XX
PS Claim 1; SEQ ID NO 9; 78pp; English.
XX
XX
CC The invention relates to a novel isolated monoclonal antibody comprising
CC a heavy or light chain amino acid or a heavy or light chain variable
CC domain where the antibody binds to MUC18. The monoclonal antibody of the
CC invention demonstrates cytostatic activity and may be useful for treating
CC a disease or condition associated with the expression of MUC18 on the
CC cell surface such as tumours, specifically melanoma, oesophageal,
CC pancreatic or colorectal tumours, carcinomas, particularly cervical
CC carcinomas and cervical intraepithelial neoplasia and cancers including
CC colorectal, breast or lung cancer, as well as other malignancies. The
CC current sequence is that of the anti-human MUC18 monoclonal antibody
CC heavy chain protein of the invention.
XX
SQ Sequence 121 AA;
Query Match 99.1%; Score 643; DB 7; Length 121;
Best Local Similarity 98.3%; Pred. No. 2e-45;
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLEWIGYIYTTSTNYN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLEWIGYIYTTSTNYN 60
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPDAFDIWGGTMTVTS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPDAFDIWGGTMTVTS 120
QY 121 S 121
Db 121 S 121

RESULT 8
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ADD05384
ID  ADD05384 standard; protein; 121 AA.
XX
AC  ADD05384;
XX
DT  01-JAN-2004 (first entry)
XX
DE  Anti-MUC18 antibody heavy chain variable region protein, SEQ ID NO 9.
XX
KW  monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW  antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
XX
OS  Homo sapiens.
XX
PN  WO2003057006-A2.
XX
PD  17-JUL-2003.
XX
PF  26-DEC-2002; 2002WO-US041582.
XX
PR  28-DEC-2001; 2001US-0346460P.
XX
PA  (ABGE-) ABGENIX INC.
XX
PI  Gudas J, Bar-Eli M;
XX
WPI; 2003-577496/54.
DR  N-PSDB; ADD05386.
XX
PT  Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT  treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT  associated with melanoma, or increasing survival of an animal having a
PT  metastatic tumor.
XX
PS  Claim 1; SEQ ID NO 9; 87pp; English.
XX
CC  The invention relates to a novel monoclonal antibody used for inhibiting
CC  tumour growth in an animal. The tumour inhibition process comprises
CC  selecting an animal in need of treatment for a tumour, providing a
CC  monoclonal antibody comprising a heavy chain amino acid, where the
CC  antibody consists of any one of 10 fully defined sequences of 117-123
CC  amino acids given in the specification, and where the monoclonal antibody
CC  binds MUC18, and contacting the tumour with the antibody resulting in
CC  inhibited proliferation of the cells. The monoclonal antibody has
CC  cytostatic and can be used in the production of a vaccine. The monoclonal
CC  antibodies against the MUC18 antigen are useful for diagnosing and
CC  treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC  tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC  increasing survival of an animal having a metastatic tumour. This
CC  sequence represents an anti-MUC18 antibody heavy chain, variable region,
CC  protein of the invention.
XX
SQ  Sequence 121 AA;

Query Match      99.1%; Score 643; DB 7; Length 121;
Best Local Similarity 98.3%; Pred. No. 2e-45;
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY  1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVWSWIRPPGKLEWIGIYYTWTN 60
Db  1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVWSWIRPPGKLEWIGIYYTWTN 60

QY  61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
Db  61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120

QY  121 S 121
Db  121 S 121

RESULT 10
ADC99808
ID  ADC99808 standard; protein; 121 AA.
XX
AC  ADC99808;
XX
DT  01-JAN-2004 (first entry)
XX
DE  Anti-MUC18 monoclonal antibody heavy chain #3.
XX
KW  cell proliferation inhibition; MUC18 tumour antigen;
KW  anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
KW  carcinoma; cancer; malignancy; heavy chain; human.
XX
OS  Homo sapiens.
XX
PN  WO2003057837-A2.
XX
PD  17-JUL-2003.
XX
PF  26-DEC-2002; 2002WO-US041580.
XX
PR  28-DEC-2001; 2001US-0346414P.
XX
PA  (ABGE-) ABGENIX INC.
XX
PI  Gudas J;
XX
WPI; 2003-598367/56.
DR  N-PSDB; ADF09824.
XX
PT  Inhibiting cell proliferation associated with expression of MUC18 tumour
PT  antigen, involves incubating and inhibiting cell by administering anti-
PT  MUC18 monoclonal antibody.
XX
PS  Claim 1; SEQ ID NO 9; 83pp; English.
XX
CC  The invention comprises a method for inhibiting cell proliferation
CC  associated with expression of MUC18 tumour antigen. The method involves
CC  administering anti-MUC18 monoclonal antibody. The method of the invention
CC  is useful for inhibiting cell (e.g. melanoma or tumour cell)
CC  proliferation associated with the expression of MUC18 tumour antigen, the
CC  method is preferably useful for inhibiting tumour metastasis. The method
CC  is useful for inhibiting cell proliferation in patients with tumours,
CC  carcinomas, cancer and other malignancies. The present amino acid
CC  sequence represents a heavy chain from an MUC18 tumour antigen-specific
CC  monoclonal antibody.
XX
SQ  Sequence 121 AA;

Query Match      99.1%; Score 643; DB 7; Length 121;
Best Local Similarity 98.3%; Pred. No. 2e-45;
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY  1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVWSWIRPPGKLEWIGIYYTWTN 60
Db  1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVWSWIRPPGKLEWIGIYYTWTN 60

QY  61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
Db  61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120

QY  121 S 121
Db  121 S 121

RESULT 10
ADC99808
ID  ADC99808 standard; protein; 121 AA.
XX
AC  ADC99808;
XX
DT  01-JAN-2004 (first entry)
XX
DE  Anti-MUC18 monoclonal antibody heavy chain #3.
XX
KW  cell proliferation inhibition; MUC18 tumour antigen;
KW  anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
KW  carcinoma; cancer; malignancy; heavy chain; human.
XX
OS  Homo sapiens.
XX
PN  WO2003057837-A2.
XX
PD  17-JUL-2003.
XX
PF  26-DEC-2002; 2002WO-US041580.
XX
PR  28-DEC-2001; 2001US-0346414P.
XX
PA  (ABGE-) ABGENIX INC.
XX
PI  Gudas J;
XX
WPI; 2003-598367/56.
DR  N-PSDB; ADF09824.
XX
PT  Inhibiting cell proliferation associated with expression of MUC18 tumour
PT  antigen, involves incubating and inhibiting cell by administering anti-
PT  MUC18 monoclonal antibody.
XX
PS  Claim 1; SEQ ID NO 9; 83pp; English.
XX
CC  The invention comprises a method for inhibiting cell proliferation
CC  associated with expression of MUC18 tumour antigen. The method involves
CC  administering anti-MUC18 monoclonal antibody. The method of the invention
CC  is useful for inhibiting cell (e.g. melanoma or tumour cell)
CC  proliferation associated with the expression of MUC18 tumour antigen, the
CC  method is preferably useful for inhibiting tumour metastasis. The method
CC  is useful for inhibiting cell proliferation in patients with tumours,
CC  carcinomas, cancer and other malignancies. The present amino acid
CC  sequence represents a heavy chain from an MUC18 tumour antigen-specific
CC  monoclonal antibody.
XX
SQ  Sequence 121 AA;

Query Match      99.1%; Score 643; DB 7; Length 121;
Best Local Similarity 98.3%; Pred. No. 2e-45;
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY  1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVWSWIRPPGKLEWIGIYYTWTN 60
Db  1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVWSWIRPPGKLEWIGIYYTWTN 60

QY  61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
Db  61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120

QY  121 S 121
Db  121 S 121

RESULT 9
ADF09822

```

```

DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 37.
XX
KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
KW cytotatic; melanoma; oesophageal; pancreatic; colorectal tumour;
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
KW lung cancer; human.
XX
OS Homo sapiens.
XX
PN WO2003057838-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041581.
XX
PR 28-DEC-2001; 2001US-0346299P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
WPI; 2003-587113/55.
DR N-PSDB; ADC99810.
XX
XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease
PT or condition associated with expression of MUC18 in a patient, e.g.
PT tumors, cancers, and other malignancies.
XX
XX Claim 1; SEQ ID NO 37; 78pp; English.
XX
CC The invention relates to a novel isolated monoclonal antibody comprising
CC a heavy or light chain amino acid or a heavy or light chain variable
CC domain where the antibody binds to MUC18. The monoclonal antibody of the
CC invention demonstrates cytostatic activity and may be useful for treating
CC a disease or condition associated with the expression of MUC18 on the
CC cell surface such as tumours, specifically melanoma, oesophageal,
CC pancreatic or colorectal tumours, carcinomas, particularly cervical
CC carcinomas and cervical intraepithelial neoplasia and cancers including
CC colorectal, breast or lung cancer, as well as other malignancies. The
CC current sequence is that of the anti-human MUC18 monoclonal antibody
CC heavy chain protein of the invention.
XX
SQ Sequence 121 AA;

Query Match          92.0%; Score 597; DB 7; Length 121;
Best Local Similarity 90.9%; Pred. No. 1.2e-41;
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISYYVWSWIRQPPGKLEWIGYIYYTWSNYN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISYYVWSWIRQPPGKLEWIGYIYYTWSNYN 60
QY 61 PSLKSRVTISVDTSKNQFSLRLSVTAADTAVYYCARDQGWLLPDAFDIWGGQTMVTVS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSVTAADTAVYYCARDQGWLLPDAFDIWGGQTMVTVS 120
QY 121 S 121
Db 121 S 121

RESULT 11
ADD05412
ID ADD05412 standard; protein; 121 AA.
XX
AC ADD05412;
XX
DT 01-JAN-2004 (first entry)
XX
XX Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 37.
XX monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
KW

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XX Homo sapiens.
OS
XX WO2003057006-A2.
PN
XX 17-JUL-2003.
XX
XX 26-DEC-2002; 2002WO-US041582.
PF
XX 28-DEC-2001; 2001US-0346460P.
PR
XX (ABGE-) ABGENIX INC.
XX
XX Gudas J, Bar-Eli M;
PI
XX WPI; 2003-577496/54.
DR N-PSDB; ADD05414.
XX
XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX
XX Claim 1; SEQ ID NO 37; 87pp; English.
XX
CC The invention relates to a novel monoclonal antibody used for inhibiting
CC tumour growth in an animal. The tumour inhibition process comprises
CC selecting an animal in need of treatment for a tumour, providing a
CC monoclonal antibody comprising a heavy chain amino acid, where the
CC antibody consists of any one of 10 fully defined sequences of 117-123
CC amino acids given in the specification, and where the monoclonal antibody
CC binds MUC18, and contacting the tumour with the antibody resulting in
CC inhibited proliferation of the cells. The monoclonal antibody has
CC cytostatic and can be used in the production of a vaccine. The monoclonal
CC antibodies against the MUC18 antigen are useful for diagnosing and
CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC increasing survival of an animal having a metastatic tumour. This
CC sequence represents an anti-MUC18 antibody heavy chain, variable region,
CC protein of the invention.
XX
SQ Sequence 121 AA;

Query Match          92.0%; Score 597; DB 7; Length 121;
Best Local Similarity 90.9%; Pred. No. 1.2e-41;
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISYYVWSWIRQPPGKLEWIGYIYYTWSNYN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISYYVWSWIRQPPGKLEWIGYIYYTWSNYN 60
QY 61 PSLKSRVTISVDTSKNQFSLRLSVTAADTAVYYCARDQGWLLPDAFDIWGGQTMVTVS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSVTAADTAVYYCARDQGWLLPDAFDIWGGQTMVTVS 120
QY 121 S 121
Db 121 S 121

RESULT 12
ADF09850
ID ADF09850 standard; protein; 121 AA.
XX
AC ADF09850;
XX
DT 12-FEB-2004 (first entry)
XX
XX Human anti-MUC18 monoclonal antibody heavy chain #10.
XX cell proliferation inhibition; MUC18 tumour antigen;
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
KW carcinoma; cancer; malignancy; heavy chain; human.
KW

```

XX OS Homo sapiens.  
 XX PN WO2003057837-A2.  
 XX PD 17-JUL-2003.  
 XX PF 26-DEC-2002; 2002WO-US041580.  
 XX PR 28-DEC-2001; 2001US-0346414P.  
 XX PA (ABGE-) ABGENIX INC.  
 XX PI Gudas J;  
 XX DR WPI; 2003-598367/56.  
 XX DR N-PSDB; ADF09852.  
 XX PT Inhibiting cell proliferation associated with expression of MUC18 tumor  
 PT antigen, involves incubating and inhibiting cell by administering anti-  
 PT MUC18 monoclonal antibody.  
 XX PS Claim 1; SEQ ID NO 37; 83pp; English.  
 XX CC The invention comprises a method for inhibiting cell proliferation  
 CC associated with expression of MUC18 tumour antigen. The method involves  
 CC administering anti-MUC18 monoclonal antibody. The method of the invention  
 CC is useful for inhibiting cell (e.g. melanoma or tumour cell)  
 CC proliferation associated with the expression of MUC18 tumour antigen, the  
 CC method is preferably useful for inhibiting tumour metastasis. The method  
 CC is useful for inhibiting cell proliferation in patients with tumours,  
 CC carcinomas, cancer and other malignancies. The present amino acid  
 CC sequence represents a heavy chain from an MUC18 tumour antigen-specific  
 CC monoclonal antibody.  
 XX SQ Sequence 121 AA;  
 Query Match 92.0%; Score 597; DB 7; Length 121;  
 Best Local Similarity 90.9%; Pred. No. 1.2e-41;  
 Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISYYSWIRQPPGKLEWIGYIYYTWTN 60  
 DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISYYSWIRQPPGKLEWIGYIYYTWTN 60  
 QY 61 PSLKSRVTISVDTSKNQPSLRLSSVTAADTAVYYCARDQGWLLPDADFIDWGQTMVTS 120  
 DB 61 PSLKSRVTISVDTSKNQPSLRLSSVTAADTAVYYCARDQGWLLPDADFIDWGQTMVTS 120  
 QY 121 S 121  
 DB 121 S 121  
 RESULT 13  
 ID ADO58076 standard; protein; 243 AA.  
 XX AC ADO58076;  
 XX DT 12-AUG-2004 (first entry)  
 XX DE S9 cell derived human scFvL-VH protein.  
 XX KW B cell; surface immunoglobulin; Ig; binding site; antigen; human CD28;  
 KW closed system; detection laser-beam; catcher tube;  
 KW electrochemical device; fluorescence activated cell sorter; FACS;  
 KW antibody variable region; human.  
 XX OS Homo sapiens.  
 XX PN WO2004044584-A1.

PD 27-MAY-2004.  
 XX XX  
 PF 12-NOV-2003; 2003WO-EP012664.  
 XX PR 13-NOV-2002; 2002EP-00025335.  
 XX PA (MICR-) MICROMET AG.  
 XX PI Baeuerle P, Hoffmann P, Weinberger S, Kischel R;  
 XX DR WPI; 2004-449579/42.  
 XX DR N-PSDB; ADO58077.  
 XX PT Identifying a B cell carrying a surface immunoglobulin molecule having a  
 PT binding site for an antigen of interest, useful for constructing  
 PT therapeutic antibodies, comprises contacting a sample with the antigen  
 PT and a receptor.  
 XX PS Claim 22; SEQ ID NO 76; 156pp; English.  
 XX CC The invention relates to a novel method for identifying a B cell carrying  
 CC a surface immunoglobulin (Ig) molecule having a binding site for an  
 CC antigen of interest. The method comprises contacting a sample putatively  
 CC containing the B cell with the antigen of interest and with a receptor  
 CC specifically binding to the Ig molecule, and assessing the presence of  
 CC the detectable signal. The invention further comprises: an antibody  
 CC generated by the method above which is specific for human CD28 or  
 CC comprising an amino acid(s) sequence(s) given in the specification,  
 CC and/or are encoded by a nucleic acid sequence(s) also given in the  
 CC specification; and a device for assessing the presence of a detectable  
 CC signal defined above, where the device comprises a closed system for the  
 CC detection laser-beam and a catcher tube, and where the B cell of interest  
 CC can be collected as a single cell by means of an electrochemical device,  
 CC which is triggered by an electric signal generated by the fluorescence  
 CC activated cell sorter (FACS) device, where the electrochemical device  
 CC moves the nozzle of the steady catcher tube liquid stream for a  
 CC programmed time over a collecting tube, microtiter plate or other  
 CC container after a B cell is sorted. The method is useful for identifying  
 CC a B cell carrying a surface Ig molecule having a binding site for an  
 CC antigen of interest. The method is also useful for cloning of antibody  
 CC variable regions from the identified B cells, which may subsequently be  
 CC employed in the construction of proteins such as antibodies or its  
 CC fragments or derivatives useful in therapeutic approaches. The method is  
 CC useful as an alternative to phage display for the gain of antibodies or  
 CC its fragments. This sequence represents an S2 cell derived human  
 CC polypeptide of the invention.  
 XX SQ Sequence 243 AA;  
 Query Match 87.1%; Score 565.5; DB 8; Length 243;  
 Best Local Similarity 90.1%; Pred. No. 9.5e-39;  
 Matches 109; Conservative 6; Mismatches 5; Indels 1; Gaps 1;  
 QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISYYSWIRQPPGKLEWIGYIYYTWTN 60  
 DB 124 QVQLQESGPGLVKPSSETLSLTCTVSGGISYYSWIRQPPGKLEWIGYIYYTWTN 183  
 QY 61 PSLKSRVTISVDTSKNQPSLRLSSVTAADTAVYYCARDQGWLLPDADFIDWGQTMVTS 120  
 DB 184 PSLKSRVTISVDTSKNQPSLRLSSVTAADTAVYYCARDQGWLLPDADFIDWGQTMVTS 242  
 QY 121 S 121  
 DB 243 S 243  
 RESULT 14  
 ID ADO58076 standard; protein; 243 AA.  
 XX AC ADO58076;  
 XX DT 19-NOV-2002 (first entry)

```

XX DE Human immunoglobulin variable light domain #1.
XX
KW Immunoglobulin; variable heavy chain; variable light chain; human;
KW G-protein chemokine receptor; CCR5; HDGMR10; cancer; inflammation;
KW immunologic deficiency syndrome; blood protein disorder; nephritis;
KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;
KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;
KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;
KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;
KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;
KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;
KW lymphocytopenia.
XX
OS Homo sapiens.
XX
XX WO200264612-A2.
XX
XX 22-AUG-2002.
XX
XX 08-FEB-2002; 2002WO-US003634.
XX
XX 09-FEB-2001; 2001US-00779880.
XX
XX 09-FEB-2001; 2001WO-US004153.
XX
XX 12-JUN-2001; 2001US-0297257P.
XX
XX 08-AUG-2001; 2001US-0310458P.
XX
XX 12-OCT-2001; 2001US-0328447P.
XX
XX 21-DEC-2001; 2001US-0341725P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Roschke V, Rosen CA, Ruben SM;
XX
XX WPI; 2002-643455/69.
XX
XX N-PSDB; ABS68607.
XX
XX New human G-protein Chemokine Receptor gene (HDGMR10) useful for
XX treating, preventing, ameliorating or monitoring diseases or disorders
XX associated with aberrant expression of HDGMR10 e.g. cancer.
XX
XX Example 55; Fig 4; 562pp; English.
XX
XX The invention describes an isolated polynucleotide encoding a first
XX antibody at least 95-100% identical to a second antibody consisting of an
XX amino acid sequence comprising at least one, two or three CDR regions of
XX a variable heavy (VH) or variable light (VL) domain of the antibody
XX expressed by a hybridoma cell line consisting of XF3.5P1, XF11.1P8,
XX XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9B6, XF27/28.7D5, XF27/28.18B5,
XX XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody
XX is useful treating, preventing, ameliorating, prognosing or monitoring
XX cancers or other diseases or disorders e.g. immunologic deficiency
XX syndromes such as blood protein disorders and ataxia telangiectasia,
XX inflammation associated disorders such as endotoxin lethality, nephritis
XX and inflammatory bowel disease, conditions associated with an increase in
XX certain haematopoietic cells such as histiocytosis, defective or aberrant
XX chemotaxis of immune cells or T-cell antigen presenting cell interaction,
XX an infectious disease, an autoimmune disease such as Addison's disease,
XX dermatitis and rheumatoid arthritis, allergies, a neurodegenerative
XX disorder, a viral infection e.g. HIV infection, cytomegalovirus or
XX poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma,
XX cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a
XX disease or disorder associated with aberrant expression of novel human G-
XX protein chemokine receptor (CCR5) HDGMR10. This is the amino acid
XX sequence of human immunoglobulin sequence associated with the antibodies
XX against HDGMR10
XX
XX Sequence 121 AA;
XX
XX Query Match 84.3%; Score 547; DB 5; Length 121;
XX Best Local Similarity 86.0%; Pred. No. 1.6e-37;
XX Matches 104; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
XX
XX 1 QVQLQESGFLVKPSETLSLCTVSGGSISSYFWSWIRQPGKGLDWIGRIYTSNTYN 60

```

```

Db 1 QVQLQESGFLVKPSETLSLCTVSGGSISSYFWSWIRQPGKGLDWIGRIYTSNTYN 60
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
QY 121 S 121
Db 121 S 121
RESULT 15
ABB07171
ID ABB07171 standard; protein; 121 AA.
XX
XX ABB07171;
XX
XX 13-MAR-2002 (first entry)
XX
XX ebvHigM MS19D10 heavy chain variable region sequence.
XX
XX Neuromodulatory; central nervous system; CNS; sHIGM22; LYM 22; AKJR4;
XX ebvHigM MS19D10; ebv HIGM CB2BG8; CB2IE12; CB2IE7; MS19E5; virucide;
XX antiparkinsonian; neuroprotective; nontropic; vulnerary.
XX
XX Homo sapiens.
XX
XX WO200185797-A1.
XX
XX 15-NOV-2001.
XX
XX 30-MAY-2000; 2000WO-US014902.
XX
XX 10-MAY-2000; 2000US-00568351.
XX
XX (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX
XX Rodriguez M, Miller DJ, Pease LR;
XX
XX WPI; 2002-066596/09.
XX
XX N-PSDB; ABA94218.
XX
XX Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting
XX neurite outgrowth, regeneration, remyelination and neuroprotection in
XX central nervous system, useful to treat post-infectious
XX encephalomyelitis.
XX
XX Claim 23; Fig 19; 219pp; English.
XX
XX The invention provides a neuromodulatory agent (I) capable of promoting
XX neurite outgrowth, regeneration, remyelination and neuroprotection in
XX central nervous system (CNS). (I) is capable of inducing remyelination,
XX promoting cellular proliferation of glial cells, and promoting Ca2+
XX signaling with oligodendrocytes. An humanised antibody to (I) can be
XX selected from antibody sHIGM22 (LYM 22), ebvHigM MS19D10, ebv HIGM
XX CB2BG8, AKJR4, CB2IE12, CB2IE7 or MS19E5. (I) is useful for stimulating
XX remyelination of CNS axons, stimulating proliferation of glial cells in
XX CNS axons, or treating demyelinating disease of CNS in a mammal in need
XX of such therapy. (I) is capable of binding to structures and cells within
XX CNS. (I) is preferably useful for treating a demyelinating disease of CNS
XX of a mouse infected with Strain DA of Theiler's murine encephalomyelitis
XX (TMEV) or for treating a human being having multiple sclerosis, or a
XX human or domestic animal with a viral demyelinating disease, or a post-
XX neural disease of CNS. (I) is also useful for an in vitro method of
XX stimulating the proliferation of glial cells from mixed cell culture. (I)
XX is also useful for stimulating remyelination of CNS axons. The antibodies
XX are useful for preventing infection by a bacterium, virus or like
XX pathogen that causes demyelination or other neurodegenerative condition
XX in a subject. Methods where (I) is administered to a patient are useful
XX for treating multiple sclerosis, Parkinson's disease, Alzheimer's
XX disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating
XX disease, CNS diseases, and other conditions in the CNS where nerves are

```

CC damaged as by trauma. The present sequence represents the ebvHigM  
CC MS119D10 heavy chain variable region amino acid sequence

yy  
=====

yy

Sequence 121 AA;

Query Match	84.1%	Score 545.5	DB 5	Length 121
Best Local Similarity	87.6%	Pred. No. 2.1e-37		
Matches 106	Conservative	6	Mismatches 8	Indels 1
				Gaps 1

QY 1 QVQLOESGPGCLVKPSETLSLCTCTVSGGSISSYWSWIRQPPGKLEWIGIYIYTTWTSNYN 60

Db 1 QVQLQESGPGCLVKPSETLSLTCTVSGGSISSYYVSWIWPQPGKGLEWIGVYYSGSTNYN 60

QY 61 PSLKSRVTTISVDTSKNOFSLRLSSVTAADTAVYYCARDQGWLLPDADFIDWGQGTMTVTS 120

```

Db      61  PSLKSRVTISVDTSKNQFSLKSSVTAADTAVVYCARSQQQLV-VYFDYWGQGLTVTS 119

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Qy 121 S 121.

Db 120 S 120

Search completed: November 9, 2005, 12:55:26  
Job time : 75.6015 secs

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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:29:55 ; Search time 18.802 Seconds  
(without alignments)  
480.403 Million cell updates/sec

Title: US-10-660-357A-17

Perfect score: 649

Sequence: 1 QVQLQSGGLVPESETLSL.....WLLPDAFDIWGQGTWTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database :

- Issued Patents AA:\*
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  - 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
  - 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
  - 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/iaa/6C\_COMB.pep.\*
  - 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	540	83.2	119	3	US-09-025-769B-39
2	540	83.2	119	3	US-09-025-769B-65
3	540	83.2	119	4	US-09-490-070A-39
4	540	83.2	119	4	US-09-490-070A-65
5	540	83.2	119	4	US-09-490-153-39
6	540	83.2	119	4	US-09-490-153-65
7	540	83.2	119	4	US-09-490-324-39
8	540	83.2	119	4	US-09-490-324-65
9	531.5	81.9	118	3	US-09-025-769B-25
10	531.5	81.9	118	4	US-09-490-070A-25
11	531.5	81.9	118	4	US-09-490-153-25
12	531.5	81.9	118	4	US-09-490-324-25
13	531.5	81.9	120	4	US-09-424-840B-20
14	529.5	81.6	244	3	US-08-918-148-79
15	529.5	81.6	244	4	US-09-138-091A-77
16	515.5	79.4	473	3	US-09-049-672A-4
17	502	77.3	142	2	US-08-480-774A-2
18	500	77.0	117	4	US-09-720-493-2
19	499.5	77.0	139	4	US-09-471-276-837
20	498.5	76.8	122	1	US-08-360-125-11
21	498.5	76.8	122	2	US-08-450-578-11
22	498.5	76.8	122	2	US-09-017-628-11
23	498.5	76.8	122	2	US-09-014-880-11
24	498.5	76.8	122	4	US-08-450-363-11
25	498.5	76.8	122	4	US-09-467-903-11
26	494.5	76.2	487	4	US-09-800-729-145
27	488	75.2	116	3	US-08-545-809A-140

28	485	74.7	119	1	US-08-360-125-5	Sequence 5, Appli
29	485	74.7	119	2	US-08-450-578-5	Sequence 5, Appli
30	485	74.7	119	2	US-09-017-628-5	Sequence 5, Appli
31	485	74.7	119	2	US-09-014-880-5	Sequence 5, Appli
32	485	74.7	119	4	US-08-450-363-5	Sequence 5, Appli
33	485	74.7	119	4	US-09-467-903-5	Sequence 5, Appli
34	484	74.6	119	2	US-08-652-816A-10	Sequence 10, Appli
35	479.5	73.9	172	4	US-09-472-087-7	Sequence 7, Appli
36	479.5	73.9	172	4	US-09-472-087-86	Sequence 86, Appli
37	479	73.8	123	3	US-08-793-450-4	Sequence 4, Appli
38	477	73.5	118	3	US-08-545-809A-142	Sequence 142, App
39	476	73.3	472	3	US-08-793-450-8	Sequence 8, Appli
40	472.5	72.8	139	4	US-09-203-768A-2	Sequence 2, Appli
41	471	72.6	155	4	US-09-471-276-888	Sequence 888, App
42	470.5	72.5	118	4	US-09-343-698-6	Sequence 6, Appli
43	470.5	72.5	118	4	US-08-325-955-6	Sequence 6, Appli
44	469.5	72.3	832	3	US-08-630-820-7	Sequence 7, Appli
45	469.5	72.3	832	4	US-09-273-453-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1  
US-09-025-769B-39  
; Sequence 39, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-025-769B-39  
  
Query Match 83.2%; Score 540; DB 3; Length 119;  
Best Local Similarity 86.8%; Pred. No. 7.3e-45;  
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;





Patent No. 6696248  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
STREET: 1666 K Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,070A  
FILING DATE: 24-Jan-2000  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Colin G. Sandercock, Esq.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37629-0005  
TELEPHONE: (202) 912-2000  
TELEFAX: (202) 912-2020  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE DESCRIPTION: SEQ ID NO: 65:  
US-09-490-070A-65  
Query Match 83.2%; Score 540; DB 4; Length 119;  
Best Local Similarity 86.8%; Pred. No. 7.3e-45;  
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;  
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Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIQPPGKLEWIGYIYYTWTSNYN 60  
Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDDQGWLLPDAFDIWGGTWTVTVS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDDQGWLLPDAFDIWGGTWTVTVS 120  
Qy 121 S 121  
Db 119 S 119  
RESULT 5  
US-09-490-153-39  
Sequence 39, Application US/09490153  
Patent No. 6706484  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas

TITLE OF INVENTION: Protein/(poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,153  
FILING DATE: 24-Jan-2000  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-490-153-39  
Query Match 83.2%; Score 540; DB 4; Length 119;  
Best Local Similarity 86.8%; Pred. No. 7.3e-45;  
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;  
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Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDDQGWLLPDAFDIWGGTWTVTVS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDDQGWLLPDAFDIWGGTWTVTVS 120  
Qy 121 S 121  
Db 119 S 119  
RESULT 6  
US-09-490-153-65  
Sequence 65, Application US/09490153  
Patent No. 6706484  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York

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;
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
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; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
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; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
;
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-153-65

Query Match 83.2%; Score 540; DB 4; Length 119;
Best Local Similarity 86.8%; Pred. No. 7.3e-45;
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLWIGYIYVTSN 60
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Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPDAFDIWGGTMTVTS 120
QY 121 S 121
Db 119 S 119

RESULT 7
US-09-490-324-39
; Sequence 39, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
;
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
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; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
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; FILING DATE: 24-Jan-2000
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
;
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-324-39

Query Match 83.2%; Score 540; DB 4; Length 119;
Best Local Similarity 86.8%; Pred. No. 7.3e-45;
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLWIGYIYVTSN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMIROPPGKGLWIGYIYVTSN 60
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPDAFDIWGGTMTVTS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPDAFDIWGGTMTVTS 120
QY 121 S 121
Db 119 S 119

RESULT 8
US-09-490-324-65
; Sequence 65, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
;
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
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; FILING DATE: 18-FEB-1998  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 65:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 65:  
US-09-490-324-65  
  
Query Match 83.2%; Score 540; DB 4; Length 119;  
Best Local Similarity 86.8%; Pred. No. 7.3e-45;  
Matches 105; Conservative 5; Mismatches 9; Indels 2; Gaps 1;  
  
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Db 1 QVQLQESGPGLVKPKSETLSLTCTVSGGSISSYYWMTIRQPPGKGLEWIGIYYTWTSTN 60  
  
Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 118  
  
Qy 121 S 121  
Db 119 S 119  
  
RESULT 9  
US-09-025-769B-25  
; Sequence 25, Application US/09025769B  
; Patent No. 630064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckhuhn, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000

; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 118 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-025-769B-25  
  
Query Match 81.9%; Score 531.5; DB 3; Length 118;  
Best Local Similarity 85.1%; Pred. No. 4.9e-44;  
Matches 103; Conservative 7; Mismatches 8; Indels 3; Gaps 1;  
  
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Db 1 QVQLQESGPGLVKPKSETLSLTCTVSGGSISSYYWMTIRQPPGKGLEWIGIYYTWTSTN 60  
  
Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 117  
  
Qy 121 S 121  
Db 118 S 118  
  
RESULT 10  
US-09-490-070A-25  
; Sequence 25, Application US/09490070A  
; Patent No. 6696248  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckhuhn, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
; White & McAuliffe  
; STREET: 1666 K Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/490,070A  
; FILING DATE: 24-Jan-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Colin G. Sandercock, Esq.  
; REGISTRATION NUMBER: 31,298  
; REFERENCE/DOCKET NUMBER: 37629-0005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 912-2000  
; TELEFAX: (202) 912-2020  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 118 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

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; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-070A-25

Query Match      81.9%; Score 531.5; DB 4; Length 118;
Best Local Similarity 85.1%; Pred. No. 4.8e-44;
Matches 103; Conservative 7; Mismatches 8; Indels 3; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWISWIRPPGKGLEWIGIYYTWTSTNN 60
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   |||||

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARGDQGWLLPDAFDIWGGTMTVTS 120
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Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARGDQGWLLPDAFDIWGGTMTVTS 120
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QY 121 S 121
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Db 118 S 118

RESULT 11
US-09-490-153-25
; Sequence 25, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-153-25

Query Match      81.9%; Score 531.5; DB 4; Length 118;
Best Local Similarity 85.1%; Pred. No. 4.8e-44;
Matches 103; Conservative 7; Mismatches 8; Indels 3; Gaps 1;

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QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARGDQGWLLPDAFDIWGGTMTVTS 120
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QY 121 S 121
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Db 118 S 118

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; Sequence 25, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
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Query Match      81.9%; Score 531.5; DB 4; Length 118;
Best Local Similarity 85.1%; Pred. No. 4.8e-44;
Matches 103; Conservative 7; Mismatches 8; Indels 3; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWISWIRPPGKGLEWIGIYYTWTSTNN 60
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QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARGDQGWLLPDAFDIWGGTMTVTS 120
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Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARGDQGWLLPDAFDIWGGTMTVTS 120
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OM protein - protein search, using sw model  
Run on: November 9, 2005, 11:40:37 ; Search time 67.2222 Seconds  
(without alignments)  
753.137 Million cell updates/sec

Title: US-10-660-357A-17  
Perfect score: 649  
Sequence: 1 QVQLQSGPGLVPSSETLSL.....WLLPDAFDIWGQGTWTVSS 121

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 1867879 seqs, 418409474 residues  
Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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22:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	649	100.0	121	14	US-10-330-613-17
3	649	100.0	121	14	US-10-330-530-1
4	649	100.0	121	16	US-10-330-530-17
5	649	100.0	121	16	US-10-660-357-1
6	649	100.0	121	16	US-10-660-357-17
7	643	99.1	121	14	US-10-330-613-9
8	643	99.1	121	14	US-10-330-530-9
9	643	99.1	121	16	US-10-660-357-9
10	597	92.0	121	14	US-10-330-613-37
11	597	92.0	121	14	US-10-330-530-37

12	597	92.0	121	16	US-10-660-357-37	Sequence 37, Appl
13	553.5	85.3	118	15	US-10-292-088-142	Sequence 142, App
14	549.5	84.7	118	15	US-10-292-088-109	Sequence 109, App
15	547	84.3	121	14	US-10-067-800-60	Sequence 60, Appl
16	547	84.3	121	18	US-10-994-679-60	Sequence 60, Appl
17	545.5	84.1	121	14	US-10-010-729-11	Sequence 11, Appl
18	545.5	84.1	122	15	US-10-309-762-24	Sequence 24, Appl
19	545.5	84.1	122	15	US-10-309-762-27	Sequence 27, Appl
20	545	84.0	119	17	US-10-937-596-23	Sequence 23, Appl
21	544.5	83.9	122	15	US-10-309-762-25	Sequence 25, Appl
22	544.5	83.9	122	15	US-10-309-762-29	Sequence 29, Appl
23	540	83.2	119	14	US-10-125-687-5	Sequence 5, Appl
24	540	83.2	119	18	US-10-996-191-5	Sequence 5, Appl
25	539.5	83.1	118	17	US-10-727-155-178	Sequence 178, App
26	539	83.1	123	15	US-10-371-942-102	Sequence 102, App
27	538.5	83.0	122	15	US-10-309-762-71	Sequence 71, Appl
28	538.5	83.0	141	15	US-10-309-762-90	Sequence 90, Appl
29	536.5	82.7	120	15	US-10-309-762-4	Sequence 4, Appl
30	536.5	82.7	120	15	US-10-309-762-102	Sequence 102, App
31	536.5	82.7	121	15	US-10-309-762-154	Sequence 154, App
32	536	82.6	119	15	US-10-309-762-143	Sequence 143, App
33	536	82.6	125	15	US-10-309-762-11	Sequence 11, Appl
34	534.5	82.4	142	17	US-10-893-576-37	Sequence 37, Appl
35	534.5	82.4	141	15	US-10-309-762-73	Sequence 73, Appl
36	534.5	82.4	141	15	US-10-309-762-94	Sequence 94, Appl
37	533.5	82.2	116	18	US-10-822-306A-5	Sequence 5, Appl
38	533.5	82.2	124	15	US-10-309-762-26	Sequence 26, Appl
39	533.5	82.2	193	15	US-10-264-049-4331	Sequence 4331, Ap
40	532.5	82.0	118	17	US-10-706-689-10	Sequence 10, Appl
41	532.5	82.0	118	18	US-10-988-360-10	Sequence 10, Appl
42	532.5	82.0	128	15	US-10-173-551-24	Sequence 24, Appl
43	531.5	81.9	120	16	US-10-844-424-20	Sequence 20, Appl
44	531.5	81.9	121	17	US-10-805-177-56	Sequence 56, Appl
45	531.5	81.9	126	14	US-10-067-800-68	Sequence 68, Appl

ALIGNMENTS

RESULT 1  
US-10-330-613-1  
; Sequence 1, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-1

Query Match 100.0%; Score 649; DB 14; Length 121;  
Best Local Similarity 100.0%; Pred. No. 1.8e-50;  
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Db	1	QVQLQSGPGLVPSSETLSLCTCTVSGGSSSYSSYWSWIRQPPGKLEWIGYVYWTNSYN	60
QY	61	PSLKSRTVISDTSKNQFSRLSSVTAADTAVYVCARDQGWLLPDAFDIWGQGTWTVS	120
Db	61	PSLKSRTVISDTSKNQFSRLSSVTAADTAVYVCARDQGWLLPDAFDIWGQGTWTVS	120
QY	121	\$	121

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Db      121 S 121

RESULT 2
US-10-330-613-17
; Sequence 17, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-17

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Best Local Similarity 100.0%; Pred. No. 1.8e-50;
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QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
QY 121 S 121
Db 121 S 121

RESULT 3
US-10-330-530-1
; Sequence 1, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-1

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Best Local Similarity 100.0%; Pred. No. 1.8e-50;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIROPKGLGWIGYIYYTWTSNYN 60
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
QY 121 S 121
Db 121 S 121

RESULT 4
US-10-330-530-17
; Sequence 17, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-17

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Best Local Similarity 100.0%; Pred. No. 1.8e-50;
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QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
QY 121 S 121
Db 121 S 121

RESULT 5
US-10-660-357-1
; Sequence 1, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-1

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Best Local Similarity 100.0%; Pred. No. 1.8e-50;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIROPKGLGWIGYIYYTWTSNYN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIROPKGLGWIGYIYYTWTSNYN 60
QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120
QY 121 S 121
Db 121 S 121
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US-10-660-357-17  
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; Publication No. US20040115205A1  
; GENERAL INFORMATION:  
; APPLICANT: Bar-Eli, Menashe  
; APPLICANT: Green, Larry L.  
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18  
; TITLE OF INVENTION: ANTIGEN  
; FILE REFERENCE: ABGENIX 030C1  
; CURRENT APPLICATION NUMBER: US/10/660,357  
; CURRENT FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 10/330,580  
; PRIOR FILING DATE: 2002-12-26  
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; ORGANISM: Homo Sapiens  
US-10-660-357-17

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QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
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QY 121 S 121  
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Db 121 S 121

## RESULT 7

US-10-330-613-9  
; Sequence 9, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX 022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-9

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Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWMIROPPGKGLWIGYIYTTN 60  
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QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
|  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
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QY 121 S 121  
|  
Db 121 S 121

## RESULT 8

US-10-330-530-9  
; Sequence 9, Application US/10330530  
; Publication No. US20030152514A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES  
; FILE REFERENCE: ABGENIX 031A  
; CURRENT APPLICATION NUMBER: US/10/330,530  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: US 60/346414  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-530-9

Query Match 99.1%; Score 643; DB 14; Length 121;  
Best Local Similarity 98.3%; Pred. No. 6.1e-50;  
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWMIROPPGKGLWIGYIYTTN 60  
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Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWMIROPPGKGLWIGYIYTTN 60  
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QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
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Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120  
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QY 121 S 121  
|  
Db 121 S 121

## RESULT 9

US-10-660-357-9  
; Sequence 9, Application US/10660357  
; Publication No. US20040115205A1  
; GENERAL INFORMATION:  
; APPLICANT: Bar-Eli, Menashe  
; APPLICANT: Green, Larry L.  
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18  
; TITLE OF INVENTION: ANTIGEN  
; FILE REFERENCE: ABGENIX 030C1  
; CURRENT APPLICATION NUMBER: US/10/660,357  
; CURRENT FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 10/330,580  
; PRIOR FILING DATE: 2002-12-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-660-357-9

Query Match 99.1%; Score 643; DB 16; Length 121;  
Best Local Similarity 98.3%; Pred. No. 6.1e-50;  
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy	1	QVQLQESGGGLVQPKSETISLTCTVSGGSISSYYKSWIRQPPKGLGLEWIGYIYYTWTNTN 60
Db	1	QVQLQESGGGLVQPKSETISLTCTVSGGSISSYYKSWIRQPPKGLGLEWIGYIYYTWTNTN 60
Qy	61	PSLGRVTISVDTSKNQFSLRLSSVTAADTAVYCARDQGWLLPDAFDIWGGQTMTVTS 120
Db	61	PSLGRVTISVDTSKNQFSLRLSSVTAADTAVYCARDQGWLLPDAFDIWGGQTMTVTS 120
Qy	121	\$ 121
Db	121	\$ 121

```

RESULT 10
US-10-330-613-37
; Sequence 37, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: AGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-37

```

```
Query Match          92.0%; Score 597; DB 14; Length 121;
Best Local Similarity 90.9%; Pred. NO. 8e-46;
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
```

Qy	1	QVQLQESGGPGVLRKPSSETLSLTCTCTVSGGSISSYYKSWITROPCKGLEWIGYLYYVWTSTSYN	60
Db	1	QVQLQESGGPGVLRKPSSETLSLTCTCTVSGGSISSYYKSWITROPCKGLEWIGYLYYVWTSTSYN	60
Qy	61	PSLKSRTVITISVDTSKNQFSLRLSVTAADTAVVYCARDQGGWMLLPDAPDIWGQGTMTVTS	120
Db	61	PSLKSRTVTSVDTSKNQFSLKLSVTAADTAVVYCARDPGQWLVPDAPDIWGQGTMTSVTS	120
Qy	121	S 121	
Db	121	S 121	

```

RESULT 11
US-10-330-530-37
; Sequence 37, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: AGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-37

```

```
Query Match          92.0%; Score 597; DB 14; Length 121;
Best Local Similarity 90.9%; Pred. NO. 8e-46;
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
```

Qy	1	QVOLOESGGLVVPKSETLSLCTCTVSGSISSVYWSWIRDPGKCLEMIGVYVYTWTSNYN	60
			:
Db	1	QVOLOESGGLVVPKSETLSLCTCTVSGSISVYWSWIRDPGKCLEMIGVYVYTWTSNYN	60
			:
Qy	61	PSLKSRVTISVDTSKNQFSLRLSVTAADTAVVYCARDQGWLLPDAFDIWGQGTWTVVS	120
			:
Db	61	PSLKSRVTISVDTSKNQFSLRLSVTAADTAVVYCARDQGWLLPDAFDIWGQGTWTVVS	120
Qy	121	\$ 121	
		—	
Db	121	\$ 121	

```

RESULT 12
US-10-660-357-37
; Sequence 37, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-10-660-357-37

```

Query Match 92.0%; Score 597; DB 16; Length 121;  
Best Local Similarity 90.9%; Pred. No. 8e-46;  
Matches 110: Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy	1	QVQLQESGPGLVKPKSETLSLTCTVCSGSISSVYQWSWIRQPPGKGLEWIGIYYVTWTNNYN	60
Db	1	QVQLQESGPGLVKPKSETLSLTCTVCSGSISSVYQWSWIRQPPGKGLEWIGIYYVTGNTYYN	60
Qy	61	PSLKSRTVISVDTSKNQPSLRLSVTAADTAVYYCARDQCGWILLPDAFDIWGOGTMTVTS	120
Db	61	PSLKSRTVISVDTSKNQPSLKLNSVTAADTAVYYCARDPCGWLPDADFIDWGOGTMTVS	120
Qy	121	S 121	
Db	121	S 121	

```

RESULT 13
US-10-292-088-142
; Sequence 142, Application US/10292088
; Publication No. US2003021100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 142
; LENGTH: 118

```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-142

Query Match      85.3%; Score 553.5; DB 15; Length 118;
Best Local Similarity 87.6%; Pred. No. 6.2e-42;
Matches 106; Conservative 7; Mismatches 5; Indels 3; Gaps 1;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGIYYTWTSNYN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGIYYTWTSNYN 60
Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQOGWLLPDAFDIWGQGTMTVTS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDYGDY---NWFDPWGQGTMTVTS 117
Qy 121 S 121
Db 118 S 118
```

```
RESULT 14
US-10-292-088-109
; Sequence 109, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PP/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 109
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-109
```

```
Query Match      84.7%; Score 549.5; DB 15; Length 118;
Best Local Similarity 87.6%; Pred. No. 1.4e-41;
Matches 106; Conservative 5; Mismatches 7; Indels 3; Gaps 1;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGIYYTWTSNYN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGIYYTWTSNYN 60
Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQOGWLLPDAFDIWGQGTMTVTS 120
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDYGG---NSYFDYWGQGTMTVTS 117
Qy 121 S 121
Db 118 S 118
```

```
RESULT 15
US-10-067-800-60
; Sequence 60, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRs) HDGNR10
; FILE REFERENCE: 1488.1150001
; CURRENT APPLICATION NUMBER: US/10/067,800
```

```
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/341,725
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-60
```

```
Query Match      84.3%; Score 547; DB 14; Length 121;
Best Local Similarity 86.0%; Pred. No. 2.4e-41;
Matches 104; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGIYYTWTSNYN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKLEWIGIYYTWTSNYN 60
Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQOGWLLPDAFDIWGQGTMTVTS 120
Db 61 PSLKSRVTISVDTSKNRFSKLKSSVTAADTAVYYCARDRGSSWYPDADFIDWGQGTMTVTS 120
Qy 121 S 121
Db 121 S 121
```

Search completed: November 9, 2005, 12:43:00  
Job time : 68.2222 secs

THE FINEST OF ALL

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 12:25:58 ; Search time 13.0401 Seconds  
(without alignments)  
892.802 Million cell updates/sec

Title: US-10-660-357A-17

Perfect score: 649

Sequence: 1 QVQLQSGGPGLVKPSSETLSL.....WLLPDAFDIWGQGMVTMTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	543	83.7	140	2	Ig variable region
2	536	82.6	155	2	Ig heavy chain - h
3	533	82.1	130	2	Ig heavy chain - h
4	533	82.1	155	2	Ig heavy chain - h
5	526.5	81.1	139	2	Ig heavy chain - h
6	518.5	79.9	130	2	Ig heavy chain - h
7	512.5	79.0	137	2	Ig heavy chain - h
8	509.5	78.5	118	2	Ig heavy chain - h
9	505	77.8	147	2	Ig heavy chain - h
10	498.5	76.8	140	2	Ig heavy chain - h
11	495	76.3	135	2	Ig heavy chain - h
12	490	75.5	105	2	Ig heavy chain - h
13	489	75.3	97	2	Ig heavy chain - h
14	489	75.3	146	2	Ig heavy chain - h
15	488	75.2	116	2	Ig heavy chain - h
16	486	74.9	97	2	Ig heavy chain - h
17	486	74.9	121	2	Ig heavy chain - h
18	485	74.7	140	2	Ig heavy chain - h
19	481	74.1	123	2	Ig heavy chain - h
20	481	74.1	139	2	Ig heavy chain - h
21	477	73.5	118	2	Ig heavy chain - h
22	474.5	73.1	129	2	Ig heavy chain - h
23	473.5	73.0	126	2	Ig heavy chain - h
24	473.5	73.0	145	2	Ig heavy chain - h
25	468.5	72.2	118	2	Ig heavy chain - h
26	467	72.0	99	2	Ig heavy chain - h
27	467	72.0	99	2	Ig heavy chain - h
28	467	72.0	220	2	Ig gamma-1 heavy c
29	466	71.8	97	2	Ig heavy chain - h

30	465	71.6	99	2	S12412	Ig heavy chain V r
31	462	71.2	143	2	B49028	Ig heavy chain V-I
32	460	70.9	97	2	S26804	Ig heavy chain V r
33	460	70.9	116	2	S18557	Ig heavy chain V r
34	459.5	70.8	122	2	D41287	Ig heavy chain V-I
35	458	70.6	99	2	S26801	Ig heavy chain V r
36	458	70.6	134	2	S54906	Ig heavy chain V r
37	458	70.6	146	2	S09710	Ig heavy chain V r
38	455.5	70.2	110	2	S44110	Ig heavy chain V-D
39	454.5	70.0	146	1	GIHUH2	Ig heavy chain pre
40	454	70.0	99	2	S12418	Ig heavy chain V r
41	453.5	69.9	122	2	S69912	Ig V-D-J region (N
42	452	69.6	140	2	A24770	hypothetical hybri
43	451	69.5	109	2	PH1673	Ig heavy chain V r
44	451	69.5	135	2	S31604	Ig heavy chain V r
45	449	69.2	115	2	S57464	Ig heavy chain V-J

ALIGNMENTS

RESULT 1

I37782

Ig variable region (VDJ) (clone T23-9) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999

C;Accession: I37782; S25476

R;Demaision, C.; Chastagner, P.; Theze, J.; Zouali, M.

Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994

A;Title: Somatic diversification in the heavy chain variable region genes expressed by

A;Reference number: A36876; MUID:94119917; PMID:8290556

A;Accession: I37782

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-140 <RES>

A;Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;46-128/Domain: immunoglobulin homology <IMW>

Query Match 83.7%; Score 543; DB 2; Length 140;

Best Local Similarity 86.0%; Pred. No. 3.5e-41;

Matches 104; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 1 QVQLQSGGPGLVKPSSETLSLCTVSGSISYVSWIRPPGKGLWIGIYYTWTN 60

Db 20 QVQLQSGGPGLVKPSSETLSLCTVSGSISYVSWIRPPGKGLWIGIYYTWTN 79

QY 61 PSLSKRVITISVDTSKNQFSLRLSSVTAADTAVYYCARTDQGWLLPDAFDIWGQGMVTVS 120

Db 80 PSLSKRVITISVDTSKNQFSLRLSSVTAADTAVYYCARTDQGWLLPDAFDIWGQGMVTVS 139

QY 121 S 121

Db 140 S 140

RESULT 2

S31512

Ig heavy chain - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999

C;Accession: S31512

R;Chastagner, P.; Demaision, C.; Theze, J.; Zouali, M.

submitted to the EMBL data Library, December 1992

A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA au

A;Reference number: S31509

A;Accession: S31512

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-155 <CHA>

A;Cross-references: EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PID:g33083

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;47-129/Domain: immunoglobulin homology <IMM>

Query Match 82.6%; Score 536; DB 2; Length 155;  
Best Local Similarity 82.9%; Pred. No. 1.6e-40;  
Matches 102; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIROPKGLGWIGYIYVTSN 60  
DB 33 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIROPKGLGWIGYIYVTSN 92

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQG--QWLLPDAFDIWGQGTMT 118  
DB 93 PPKLSRVITISVDTSKNQFSLKVSSTAADTAVYYCARGGSISSYYWYGGNDWVGQGTMT 152

QY 119 VSS 121  
DB 153 VSS 155

#### RESULT 3

S31690  
Ig heavy chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S31690  
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.  
submitted to the EMBL Data Library, June 1992  
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A:Reference number: S31585  
A:Accession: S31690  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-130 <CUI>  
A:Cross-references: EMBL:Z14199; NID:g30984; PIDN:CAA78568.1; PID:g30985  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;20-102/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 533; DB 2; Length 130;  
Best Local Similarity 84.0%; Pred. No. 2.5e-40;  
Matches 105; Conservative 5; Mismatches 11; Indels 4; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIROPKGLGWIGYIYVTSN 60  
DB 6 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIROPKGLGWIGYIYVTSN 65

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWL---LPDAFDIWGQGT 116  
DB 66 PSLKSRVTISVDTSKNQFSLKLSSTAADTAVYYCARGSSVLLWFGELLYFDYWGQGT 125

QY 117 VTVSS 121  
DB 126 VTVSS 130

#### RESULT 4

S31511  
Ig heavy chain - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S31511  
R;Chasagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto  
A:Reference number: S31509  
A:Accession: S31511  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-155 <CHA>  
A:Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID:g33095  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;47-129/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 533; DB 2; Length 155;  
Best Local Similarity 83.7%; Pred. No. 3e-40;  
Matches 103; Conservative 5; Mismatches 13; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIROPKGLGWIGYIYVTSN 60  
DB 33 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIROPKGLGWIGYIYVTSN 92

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQG--QWLLPDAFDIWGQGTMT 118  
DB 93 PPKLSRVITISVDTSKNQFSLKVSSTAADTAVYYCARGGSISSYYWYGGNDWVGQGTMT 152

QY 119 VSS 121  
DB 153 VSS 155

#### RESULT 5

S31586  
Ig heavy chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S31586  
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.  
submitted to the EMBL Data Library, June 1992  
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A:Reference number: S31585  
A:Accession: S31586  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-139 <CUI>  
A:Cross-references: EMBL:Z14196; NID:g30978; PIDN:CAA78565.1; PID:g30979  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 81.1%; Score 526.5; DB 2; Length 139;  
Best Local Similarity 86.0%; Pred. No. 1e-39;  
Matches 104; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIROPKGLGWIGYIYVTSN 60  
DB 20 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIROPKGLGWIGYIYVTSN 79

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLDPDAFDIWGQGTMT 120  
DB 80 PSLKSRVTISVDTSKNQFSLKLSSTAADTAVYYCARG-GLGIRRGAFDIWGQGTMT 138

QY 121 S 121  
DB 139 S 139

#### RESULT 6

S30534  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Aug-1996  
C:Accession: S30534  
R;Mariette, X.  
submitted to the EMBL Data Library, October 1992  
A:Reference number: S30520  
A:Accession: S30534  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-130 <MAR>  
A:Cross-references: EMBL:Z18320  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 79.9%; Score 518.5; DB 2; Length 130;

```
Best Local Similarity 81.5%; Pred. No. 4.8e-39;
Matches 106; Conservative 6; Mismatches 9; Indels 9; Gaps 3;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGYIYYTWTSN 58
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGRIYYTSGSTN 60

Qy 59 YNPSLKSRTVISVDTSKNQFSLRLSSVTAADTAVYYCARDQGW-LPDAFDI 111
Db 61 YNPSLKSRTVISVDTSKNQFSLRLSSVTAADTAVYYCARDKGGFWSGYYTNSRAAFDI 120

Qy 112 GQGTMTVTSS 121
Db 121 GQGTMTVTSS 130

RESULT 7
S31676
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31676
R;Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31676
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-137 <CUI>
A;Cross-references: EMBL:Z14182; NID:G31031; PIDN:CAA78551.1; PID:G31032
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 512.5; DB 2; Length 137;
Best Local Similarity 83.5%; Pred. No. 1.7e-38;
Matches 101; Conservative 6; Mismatches 11; Indels 3; Gaps 1;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGYIYYTWTSN 60
Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGRIYYTSGSTN 79

Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDI 120
Db 80 PSLKSRVTMSVDTSKNQFSLRLSSVTAADTAVYYCARDAP--LMYGMVDVWGQGTMTVT 136

Qy 121 S 121
Db 137 S 137

RESULT 8
S20780
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S20780
R;Mortari, F.; Wang, J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A;Description: Analysis of human cord blood Ig heavy chain IgA and IgG repertoire.
A;Reference number: S20764
A;Accession: S20780
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-118 <MOR>
A;Cross-references: EMBL:Z11958; NID:G33893; PIDN:CAA78015.1; PID:G33894
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 78.5%; Score 509.5; DB 2; Length 118;
Best Local Similarity 81.0%; Pred. No. 2.7e-38;
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Matches 98; Conservative 11; Mismatches 9; Indels 3; Gaps 1;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGYIYYTWTSN 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIAFIYYTGSTHYN 60

Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDI 120
Db 61 PSLKSRVTMSVDTSKNQFSLRLSSVTAADTAVYSCARDGR---DGGFDI 117

Qy 121 S 121
Db 118 S 118

RESULT 9
S13519
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S13519
R;Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.
Nucleic Acids Res. 19, 673, 1991
A;Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked
A;Reference number: S13519; MUID:91187691; PMID:2011536
A;Accession: S13519
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-147 <MOR>
A;Cross-references: EMBL:X56158; NID:G37724; PIDN:CAA39626.1; PID:G37725
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;41-125/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 505; DB 2; Length 147;
Best Local Similarity 82.1%; Pred. No. 8.6e-38;
Matches 101; Conservative 7; Mismatches 11; Indels 4; Gaps 3;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGYIYYTWTSN 58
Db 27 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKLEWIGSIYYSGSTY 86

Qy 59 YNPSLKSRTVISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDI 118
Db 87 YNPSLKSRTVISVDTSKNQFSLRLSSVTAADTAVYYCARPL-LW-FCGLFDYWGQGTMTVT 144

Qy 119 VSS 121
Db 145 VSS 147

RESULT 10
S78052
Ig heavy chain precursor V-D-J region (clone mAB 63VH) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78052; S23717
R;Harindranath, N.
submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78052
A;Molecule type: mRNA
A;Residues: 1-140 <HAR>
A;Cross-references: EMBL:X54441; NID:G37815; PIDN:CAA38308.1; PID:9330118
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Nokin
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and
patient.
A;Reference number: S23716; MUID:92031262; PMID:1718404
A;Accession: S23717
A;Molecule type: mRNA
A;Residues: 15-111 <HAW>
A;Cross-references: EMBL:X54441
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Search completed: November 9, 2005, 13:08:03  
Job time : 14.0401 secs

## RESULT 14

S09711  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
C:Accession: S09711  
R:Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.  
Biochem. J. 268, 135-140, 1990  
A:Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains c  
A:Reference number: S09710; MUID:90262535; PMID:2111699  
A:Accession: S09711  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-146 <HUG>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-118/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 489; DB 2; Length 146;  
Best Local Similarity 74.0%; Pred. No. 2.2e-36;  
Matches 97; Conservative 11; Mismatches 9; Indels 14; Gaps 3;  
  
Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISS--YVSWIRPPGKGLEWIGYIYYTWSN 58  
Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISS--YVSWIRPPGKGLEWIGYIYYTWSN 79  
  
Qy 59 YNPISLKSRTVISVDTSKNQFSLRLSSVTAADTAVYYCAR-----DQGWLLPDAFDI 110  
Db 80 YNPISLKSRTVISVDTSKNQFSLRLSSVTAADTAVYYCARLVLSRTSISQVSYNM---DV 135  
  
Qy 111 WGQGTMTVTSS 121  
Db 136 WGKGTMTVTSS 146

## RESULT 15

B26340  
Ig heavy chain precursor V-II region (71-4) - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Jun-1988 #sequence\_revision 30-Jun-1991 #text\_change 23-Jul-1999  
C:Accession: B26340  
R:Kodaira, M.; Kinashi, T.; Umemura, I.; Matsuda, F.; Noma, T.; Ono, Y.; Honjo, T.  
J. Mol. Biol. 190, 529-541, 1986  
A:Title: Organization and evolution of variable region genes of the human immunoglobulin  
A:Reference number: A26340; MUID:87061007; PMID:3037326  
A:Accession: B26340  
A:Molecule type: DNA  
A:Residues: 1-116 <KOD>  
A:Cross-references: GB:X05711; NID:g33602; PIDN:CAA29183.1; PID:g296660  
A:Note: the authors translated the codon GAG for residue 25 as Gln  
C:Genetics:  
A:Introns: 16/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-116/Product: Ig heavy chain V region 71-4 #status predicted <MAT>  
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 75.2%; Score 488; DB 2; Length 116;  
Best Local Similarity 93.8%; Pred. No. 2.1e-36;  
Matches 91; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVSWIRPPGKGLEWIGYIYYTWSNYN 60  
Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVSWIRPPGKGLEWIGYIYYTWSNYN 79  
  
Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCAR 97  
Db 80 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCAR 116

.....

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:46:52 ; Search time 62.4712 Seconds  
(without alignments)  
991.843 Million cell updates/sec

Title: US-10-660-357A-17

Perfect score: 649

Sequence: 1 QVQLQESGPGVGLVPSSETLSL.....WLLPDAFDINGQGTMTVTS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	516	79.5	476	2	O6GMX1	O6gm1 homo sapien
2	515	79.4	119	2	Q9UL73	Q9ul73 homo sapien
3	508.5	78.4	465	2	O6GMX6	O6gm6 homo sapien
4	501.5	77.3	620	2	Q9ERY0	Q9ey0 homo sapien
5	498.5	76.8	477	2	O6GMX7	O6gm7 homo sapien
6	495	76.3	139	2	O6GSX2	O6gsx2 homo sapien
7	493.5	76.0	478	2	Q72379	Q72379 homo sapien
8	482.5	74.3	150	2	O95973	O95973 homo sapien
9	472.5	72.8	576	2	O6P418	O6p418 homo sapien
10	472	72.7	492	2	Q72374	Q72374 homo sapien
11	460.5	71.0	496	2	O96KX8	O96kx8 homo sapien
12	454.5	70.0	146	1	HV21 HUMAN	HV21 HUMAN
13	451	69.5	595	2	O8WUX4	O8wux4 homo sapien
14	451	69.5	597	2	O6GMX5	O6gm5 homo sapien
15	451	69.5	597	2	Q9BU10	Q9bu10 homo sapien
16	451	69.5	625	2	O96AA6	O96aa6 homo sapien
17	450	69.3	478	2	O6NYH3	O6nyh3 homo sapien
18	449	69.2	597	2	O9BQB8	O9bqb8 homo sapien
19	445	68.6	117	1	HV20G HUMAN	HV20G HUMAN
20	444	68.4	129	1	HV2F HUMAN	HV2F HUMAN
21	435.5	67.1	130	2	Q81ZD7	Q81zd7 homo sapien
22	416.5	64.2	116	2	Q723Y6	Q723y6 homo sapien
23	411.5	63.4	122	2	Q9UL75	Q9ul75 homo sapien
24	407	62.7	479	2	O99M22	O99m22 mus musculus
25	398	61.3	476	2	O6MZX7	O6mzx7 homo sapien
26	394.5	60.8	136	2	O6LB05	O6lb05 mus musculus
27	394	60.7	137	1	HV46_MOUSE	HV46_MOUSE
28	390.5	60.2	473	2	Q8TC63	Q8tc63 homo sapien
29	375	57.8	113	1	HV47_MOUSE	HV47_MOUSE
30	372	57.3	262	2	O65Z11	O65z11 mus musculus
31	369.5	56.9	482	2	Q91X92	Q91x92 mus musculus

32	366.5	56.5	116	1	HV60_MOUSE	P18531 mus musculus
33	355	54.7	117	1	HV62_MOUSE	P18533 mus musculus
34	354.5	54.6	116	1	HV61_MOUSE	P18532 mus musculus
35	348	53.6	118	2	Q9UL74	Q9ul74 homo sapien
36	348	53.6	144	1	HV43_MOUSE	P01819 mus musculus
37	347.5	53.5	118	2	Q811U5	Q811u5 mus musculus
38	345.5	53.2	121	2	Q99NG4	Q99ng4 mus musculus
39	343.5	52.9	135	1	HV02_XENLA	P20957 xenopus lae
40	333	51.3	121	2	Q9UL96	Q9ul96 homo sapien
41	332	51.2	470	2	Q6PJA4	Q6pja4 homo sapien
42	330.5	50.9	613	2	Q8WUK1	Q8wuk1 homo sapien
43	328.5	50.6	118	2	Q9UL91	Q9ul91 homo sapien
44	324.5	50.0	606	2	Q6GMV2	Q6gmv2 homo sapien
45	320	49.3	240	2	Q65ZC9	Q65zc9 homo sapien

## ALIGNMENTS

RESULT 1  
O6GMX1 PRELIMINARY; PRT; 476 AA.  
ID O6GMX1  
AC O6GMX1;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Strausberg R.;  
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC073773; AAH73773.1; -.  
DR InterPro; IPR003593; Ig-like.  
DR InterPro; IPR007110; Ig-cl.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00654; C1-set; 3.  
DR Pfam; PF00047; ig; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.

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KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDESD CRC64;

Query Match 79.5%; Score 516; DB 2; Length 476;
Best Local Similarity 79.7%; Pred. No. 3.6e-43;
Matches 102; Conservative 10; Mismatches 8; Indels 8; Gaps 3;

QY 1 QVQLQESGPGLVKPSSTLSLTCTVSGGSISS--YYNSWIROPKGLGWIGYIYVTSN 58
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 QVQLQESGPGLVKPSQSLTCTVSGGSISSGDIYNSWIROPKGLGWIGYIYSGSTY 79
Rn |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 59 YNPSLSKRVITISVDTSKNQFSLRLSSVTAADTAVYVCARDQGW-----LLPDAFDIWGQ 113
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
80 YNPSLSKRVITISLDTSKNQFSLKWNVTAADTAVYFCAR-AGVWGFSRWAIDGFNIWGQ 138
Rn |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 114 GTWVTVSS 121
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
139 GTWVTVSS 146
Rn |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 2
Q9UL73 PRELIMINARY; PRT; 119 AA.
AC Q9UL73;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RC MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Bernay S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035041; AAD56277.1; -.
DR PIR; PH0876; PH0876.
DR PIR; S12416; S12416.
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1_1
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13219 MW; 1BD886B6420EA0BE CRC64;

Query Match 79.4%; Score 515; DB 2; Length 119;
Best Local Similarity 82.6%; Pred. No. 1e-43;
Matches 100; Conservative 8; Mismatches 11; Indels 2; Gaps 2;

QY 1 QVQLQESGPGLVKPSSTLSLTCTVSGGSISSYYNSWIROPKGLGWIGYIYVTSN 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 QVQLQESGPGLVKPSSTLSLTCTVSGGSISSYYNSWIROPKGLGWIGYIYSGSTNYT 60
Rn |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPDAFDIWGQMTVTVS 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYFCAR-LSNW-GPYFYDWGQGLTVTVS 118
Rn |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 $ 121
Db |
119 $ 119

RESULT 3
Q6GMX6 PRELIMINARY; PRT; 465 AA.
ID Q6GMX6
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AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RC Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00407; IGV; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 78.4%; Score 508.5; DB 2; Length 465;
Best Local Similarity 81.8%; Pred. No. 2e-42;
Matches 99; Conservative 8; Mismatches 9; Indels 5; Gaps 1;

QY 1 QVQLQESGPGLVKPSSTLSLTCTVSGGSISSYYNSWIROPKGLGWIGYIYVTSN 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 QVQLQESGPGLVKPSSTLSLTCTVSGGSISSYYNSWIROPKGLGWIGYIYSGSTNYN 79
Rn |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPDAFDIWGQMTVTVS 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
80 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARGRFTY-----FDYWGQGLTVTVS 134
Rn |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 $ 121
Db |
135 $ 135

RESULT 4
Q96EY0
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Q96EY0 PRELIMINARY; PRT; 620 AA.  
 AC Q96EY0; 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE IGHM protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raba S.S., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC011857; AAH11857.2; --  
 DR PIR: S15590; S15590.  
 DR HSP: P01820; IGJ.  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig cl.  
 DR InterPro: IPR003006; Ig MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF07654; Cl-set; 4.  
 DR Pfam: PF00047; Ig; 2.  
 DR SMART: SM00409; IG1; 4.  
 DR SMART: SM00406; IG1; 1.  
 DR SMART: SM00406; IG1; 3.  
 DR PROSITE: PS00835; IG LIKE; 5.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN 3.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN 3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 620 AA; 58125 MW; 950A1A4A6E8FF27B CRC64;  
 Query Match 77.3%; Score 501.5; DB 2; Length 620;  
 Best Local Similarity 82.0%; Pred. No. 1.4e-41;  
 Matches 100; Conservative 6; Mismatches 13; Indels 3; Gaps 2;  
 Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVSWIRQPPGKLEWIGYIYVTSNYN 60  
 Db 27 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVSWIRQPPGKLEWIGYIYVTSNYN 86  
 Qy 61 PSLKSRVTVISVDTSKNQFSLRLSSVTAADTAIVYCARDQGWLLPD-APDWGGTMTV 119  
 Db 87 PSLKSRVTVISVDTSKNQFSLRLSSVTAADTAIVYCASQ--PWELPTVGLFYWGGLTV 144  
 Qy 120 SS 121  
 Db 145 SS 146

RESULT 5

Q6GMX7 PRELIMINARY; PRT; 477 AA.  
 AC Q6GMX7; 05-JUL-2004 (TRENBLrel. 27, Created)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC073765; AAH73765.1; --  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig cl.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF07654; Cl-set; 2.  
 DR Pfam: PF00047; Ig; 3.  
 DR SMART: SM00409; IG1; 4.  
 DR SMART: SM00406; IG1; 1.  
 DR SMART: SM00406; IG1; 3.  
 DR PROSITE: PS00835; IG LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN 2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CFF85 CRC64;  
 Query Match 76.8%; Score 498.5; DB 2; Length 477;  
 Best Local Similarity 81.0%; Pred. No. 2e-41;  
 Matches 98; Conservative 8; Mismatches 12; Indels 3; Gaps 2;  
 Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVSWIRQPPGKLEWIGYIYVTSNYN 60  
 Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYVSWIRQPPGKLEWIGYIYVTSNYN 79  
 Qy 61 PSLKSRVTVISVDTSKNQFSLRLSSVTAADTAIVYCARDQGWLLPD-APDWGGTMTV 120  
 Db 80 PSLKSRVTVISVDTSKNQFSLRLSSVTAADTAIVYCAHG--SSW--DFAFDYWGQGLTV 136  
 Qy 121 S 121  
 Db 137 S 137

RESULT 6	Q86SX2	PRELIMINARY;	PRT;	139 AA.
ID	Q86SX2			
AC	Q86SX2;			
DT	01-JUN-2003	(TrEMBLrel. 24, Created)		
DT	01-JUN-2003	(TrEMBLrel. 24, Last sequence update)		
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)		
DE	Full-length cDNA clone CS0DL004YM19 of B cells (Ramos cell line) of			
DE	Homo sapiens (human) (fragment).			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
[1]				
RN	SEQUENCE FROM N.A.			
RP	TISSUE=B cells;			
RC				
RA	Li W.B., Gruber C., Jessee J., Polayes D.;			
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.			
[2]				
RA	Genoscope;			
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BX248300; CAD62627.1; -.			
DR	HSSP; P01820; 1G7J.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003596; IG_v.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
FT	NON TER			
SQ	SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;			
Query Match 76.3%; Score 495; DB 2; Length 139;				
Best Local Similarity 94.9%; Pred. No. 1.2e-41;				
Matches 93; Conservative 4; Mismatches 1; Indels 0; Gaps 0;				
Qy	1 QVQLQESGPGLVKPSSETLSLTCTVSGGISISSYMSWIRQPPGKLEWIGIYYTWTISNYN 60			
Db	33 QVQLQESGPGLVKPSSETLSLTCTVSGGISISSYMSWIRQPPGKLEWIGIYYTWTISNYN 92			
Qy	61 PSLKSRVTISVDTSKNQFSLSLSSVTAAADTAVYYCARD 98			
Db	93 PSLKSRVTISVDTSKNQFSLSLSSVTAAADTAVYYCARD 130			
RESULT 7	Q72379	PRELIMINARY;	PRT;	478 AA.
ID	Q72379			
AC	Q72379;			
DT	01-OCT-2003	(TrEMBLrel. 25, Created)		
DT	01-OCT-2003	(TrEMBLrel. 25, Last sequence update)		
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)		
DE	Hypothetical protein DKFP686K04218 (fragment).			
GN	Name=DKFP686K04218;			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
[1]				
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Human rectum tumor;			
RC				
RA	Bloeker H., Bocher M., Mewes H.W., Weil B., Amid C., Osanger A.,			
RA	Fobo G., Han M., Wiemann S.;			
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BX538066; CAD97996.1; -.			
DR	HSSP; P01820; 1G7J.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003597; IG cl.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; IG_v.			
DR	Pfam; Pf07654; Cl-set; 2.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG LIKE; 4.			

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AC Q6P4I8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE DE
DE IGHD protein.
GN Name=IGHD;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalski U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DE EMBL; BC063384; AAB63384.1; -
DR HSP; P01820; I47N.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00407; IG; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;

Query Match 72.8%; Score 472.5; DB 2; Length 576;
Best Local Similarity 76.2%; Pred. No. 1e-38;
Matches 96; Conservative 9; Mismatches 10; Indels 11; Gaps 3;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSI--SSYYWSWIRQPPGKGLWIGIYYTWSNY 59
Db 27 QVQLQESGPGLVKPSGTLSTLCAVSGGSISSNNWWSWRQPPGKGLWIGIYHSGSTNY 86

Qy 60 NPSLKSRTTISVDTSKNQFSLRLSSVTAADTAVYVCARDQGWLLPDPF-----DIWQGT 115
Db 87 NPSLKSRTTISVDTSKNQFSLRLSSVTAADTAVYVCAS-----LGIYYIGMDVWQGT 140

Qy 116 MVTVSS 121
Db 141 TVTVSS 146

RESULT 10
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Q7Z374
ID Q7Z374 PRELIMINARY; PRT; 492 AA.
AC Q7Z374;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686C02218 (Fragment).
GN Names=DKFZp686C02218;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Pobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DE EMBL; BX538077; CAD98001.1; -
DR HSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;

Query Match 72.7%; Score 472; DB 2; Length 492;
Best Local Similarity 75.4%; Pred. No. 9.5e-39;
Matches 95; Conservative 9; Mismatches 12; Indels 10; Gaps 4;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSI--SYYSWIRQPPGKGLWIGIYYTWSN 58
Db 32 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSNNWWSWRQPPGKGLWIGIYNYNTY 91

Qy 59 YNPSLKSRTTISVDTSKNQFSLRLSSVTAADTAVYVCARD-QGQ--WLLPDPFQWQGT 115
Db 92 YNPSLKSRLTIFVDTSKNHFSLRLTSVTAADTAVYCVRHVEGPGYGV-----FDPWQGT 146

Qy 116 MVTVSS 121
Db 147 LVTVSS 152

RESULT 11
Q96KX8
ID Q96KX8 PRELIMINARY; PRT; 496 AA.
AC Q96KX8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MG27165 protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
```





DR Pfam; PF07654; Cl-set; 4.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGc1; 4.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS00835; IG-LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
 DR Hypothetical protein.  
 KW SEQUENCE 595 AA; 0D4B50776545714E CRC64;  
 SQ  
 Query Match 69.5%; Score 451; DB 2; Length 595;  
 Best Local Similarity 69.8%; Pred. No. 1.5e-36;  
 Matches 90; Conservative 10; Mismatches 17; Indels 12; Gaps 2;  
 QY 1 QVQLQESGPGLVKPSETLSLTCTVSGSISYYWYWIQQPGKLEWIGYIYTWTSNYN 60  
 Db 27 QVQLQWAGAGLLKPKSETLSLTCTGVYGSFGSYWYWIQQPGKLEWIGEINHSNSTYN 86  
 QY 61 PSLKSRVTISVDTSKQFSLRLSSVTAADTAVYYCAR-----DQGWLLPDAFDIWG 112  
 Db 87 PSLKSRVTISVDTSKQFSLRLSSVTAADTAVYYCARVITRASPFGTDGRY----GMDVWG 142  
 QY 113 QGTMTVTSS 121  
 Db 143 QGTMTVTSS 151

RESULT 14  
 Q6GMX5  
 ID Q6GMX5 PRELIMINARY; PRT; 597 AA.  
 AC Q6GMX5;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalon D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Richards S., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Schmutz J., Smilus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073767; AAH73767.1; -  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF07654; Cl-set; 4.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGc1; 4.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS00835; IG-LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
 DR Hypothetical protein.  
 KW SEQUENCE 597 AA; 2A1E75F6AED85230 CRC64;  
 SQ  
 Query Match 69.5%; Score 451; DB 2; Length 597;  
 Best Local Similarity 69.8%; Pred. No. 1.5e-36;  
 Matches 90; Conservative 10; Mismatches 17; Indels 12; Gaps 2;  
 QY 1 QVQLQESGPGLVKPSETLSLTCTVSGSISYYWYWIQQPGKLEWIGYIYTWTSNYN 60  
 Db 20 QVQLQWAGAGLLKPKSETLSLTCTGVYGSFGSYWYWIQQPGKLEWIGEINHSNSTYN 79  
 QY 61 PSLKSRVTISVDTSKQFSLRLSSVTAADTAVYYCAR-----DQGWLLPDAFDIWG 112  
 Db 80 PSLKSRVTISVDTSKQFSLRLSSVTAADTAVYYCARVITRASPFGTDGRY----GMDVWG 135  
 QY 113 QGTMTVTSS 121  
 Db 136 QGTMTVTSS 144

RESULT 15  
 Q9BU10  
 ID Q9BU10 PRELIMINARY; PRT; 597 AA.  
 AC Q9BU10;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE IGHM protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalon D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Richards S., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Schmutz J., Smilus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RA Strausberg R.;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC002963; AAH02963.1; -  
 DR HSSP; P01861; IADQ.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.



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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:43:32 ; Search time 75.8346 Seconds  
(without alignments)  
627.306 Million cell updates/sec

Title: US-10-660-357A-21

Perfect score: 653

Sequence: 1 QVQLVQSGAEVKKPGASVKV.....GVHYIGMDVWGQTTVTWSS 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseq1980s:\*

2: Geneseq1990s:\*

3: Geneseq2000s:\*

4: Geneseq2001s:\*

5: Geneseq2002s:\*

6: Geneseq2003as:\*

7: Geneseq2003bs:\*

8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	653	100.0	123	7 ADC99792	Adc99792 Anti-huma
2	653	100.0	123	7 ADD05396	Add05396 Anti-MUC1
3	653	100.0	123	7 ADF09834	Adf09834 Human ant
4	593	90.8	125	6 ABR55813	Abr55813 Heavy cha
5	587.5	90.0	251	5 ABP45910	Abp45910 Human Bly
6	587.5	90.0	251	7 ADG96737	Adg96737 Single ch
7	576	88.2	127	7 ADK18819	Adk18819 Anti-huma
8	576	88.2	127	7 ADK18901	Adk18901 Anti-huma
9	576	88.2	127	7 ADK18607	Adk18607 Anti-huma
10	576	88.2	127	8 ADL25432	Adl25432 Human mAb
11	565	86.5	121	4 AAU02549	Aau02549 Anti-adip
12	561	85.9	125	7 ADK18783	Adk18783 Anti-huma
13	561	85.9	125	7 ADK18618	Adk18618 Anti-huma
14	561	85.9	125	8 ADL25452	Adl25452 Human mAb
15	558.5	85.5	126	7 ADK18920	Adk18920 Anti-huma
16	557	85.3	251	5 ABP45551	Abp45551 Human Bly
17	557	85.3	251	7 ADG96378	Adg96378 Single ch
18	556	85.1	123	6 ABR55819	Abr55819 Heavy cha
19	554.5	84.9	247	5 ABP45862	Abp45862 Human Bly
20	554.5	84.9	247	7 ADG96689	Adg96689 Single ch
21	552	84.5	257	5 ABP45599	Abp45599 Human Bly
22	552	84.5	257	7 ADG96426	Adg96426 Single ch
23	551.5	84.5	249	8 ADI58070	Adi58070 Reg IV-sp
24	551	84.4	248	5 ABP45461	Abp45461 Human Bly
25	551	84.4	248	7 ADG96288	Adg96288 Single ch

ALIGNMENTS

RESULT 1

ID ADC99792 standard; protein; 123 AA.

XX AC ADC99792;

XX AC

DT 01-JAN-2004 (first entry)

DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 21.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;

KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;

KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;

KW lung cancer; human.

XX Homo sapiens.

XX WO2003057838-A2.

XX 17-JUL-2003.

PF 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

PI Gudas J;

DR WPI; 2003-587113/55.

XX N-PSDB; ADC99794.

PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease

PT or condition associated with expression of MUC18 in a patient, e.g.

PT tumors, cancers, and other malignancies.

PS Claim 1; SEQ ID NO 21; 78pp; English.

CC The invention relates to a novel isolated monoclonal antibody comprising

CC a heavy or light chain amino acid or a heavy or light chain variable

CC domain where the antibody binds to MUC18. The monoclonal antibody of the

CC invention demonstrates cytostatic activity and may be useful for treating

CC a disease or condition associated with the expression of MUC18 on the

CC cell surface such as tumours, specifically melanoma, oesophageal,

CC pancreatic or colorectal tumours, carcinomas, particularly cervical

CC carcinomas and cervical intraepithelial neoplasia and cancers including

CC colorectal, breast or lung cancer, as well as other malignancies. The

CC current sequence is that of the anti-human MUC18 monoclonal antibody

CC heavy chain protein of the invention.

XX SQ Sequence 123 AA;  
Query Match 100.0%; Score 653; DB 7; Length 123;  
Best Local Similarity 100.0%; Pred. No. 7.3e-53;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QVQLVQSGAEVKKPKGASVKVCKASGYTFSSYGFSWVRQAPQGGLWLGWISAYNGNTNY 60  
Db 1 QVQLVQSGAEVKKPKGASVKVCKASGYTFSSYGFSWVRQAPQGGLWLGWISAYNGNTNY 60  
QY 61 AQKLQGRVTMTTDTSTAYMELSLRSDDTAVYYCARETKVRGVHYYGMDVWGQGTTVT 120  
Db 61 AQKLQGRVTMTTDTSTAYMELSLRSDDTAVYYCARETKVRGVHYYGMDVWGQGTTVT 120  
QY 121 VSS 123  
Db 121 VSS 123  
RESULT 2  
ADD05396  
ID ADD05396 standard; protein; 123 AA.  
XX  
AC ADD05396;  
DT 01-JAN-2004 (first entry)  
DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 21.  
XX monoclinal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.  
XX Homo sapiens.  
OS  
XX WO2003057006-A2.  
PN  
XX 17-JUL-2003.  
PD  
XX 26-DEC-2002; 2002WO-US041582.  
PF  
XX 28-DEC-2001; 2001US-0346460P.  
PR  
XX (ABGE-) ABGENIX INC.  
PA  
XX Gudas J, Bar-Eli M;  
PI  
XX WPI: 2003-577496/54.  
DR  
XX N-PSDB; ADD05398.  
DR  
XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
PT associated with melanoma, or increasing survival of an animal having a  
PT metastatic tumor.  
XX  
PS Claim 1; SEQ ID NO 21; 87pp; English.  
XX  
XX The invention relates to a novel monoclonal antibody used for inhibiting  
CC tumour growth in an animal. The tumour inhibition process comprises  
CC selecting an animal in need of treatment for a tumour, providing a  
CC monoclonal antibody comprising a heavy chain amino acid, where the  
CC antibody consists of any one of 10 fully defined sequences of 117-123  
CC amino acids given in the specification, and where the monoclonal antibody  
CC binds MUC18, and contacting the tumour with the antibody resulting in  
CC inhibited proliferation of the cells. The monoclonal antibody has  
CC cytostatic and can be used in the production of a vaccine. The monoclonal  
CC antibodies against the MUC18 antigen are useful for diagnosing and  
CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or  
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or  
CC increasing survival of an animal having a metastatic tumour. This  
CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
CC protein of the invention.

XX SQ Sequence 123 AA;  
Query Match 100.0%; Score 653; DB 7; Length 123;  
Best Local Similarity 100.0%; Pred. No. 7.3e-53;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QVQLVQSGAEVKKPKGASVKVCKASGYTFSSYGFSWVRQAPQGGLWLGWISAYNGNTNY 60  
Db 1 QVQLVQSGAEVKKPKGASVKVCKASGYTFSSYGFSWVRQAPQGGLWLGWISAYNGNTNY 60  
QY 61 AQKLQGRVTMTTDTSTAYMELSLRSDDTAVYYCARETKVRGVHYYGMDVWGQGTTVT 120  
Db 61 AQKLQGRVTMTTDTSTAYMELSLRSDDTAVYYCARETKVRGVHYYGMDVWGQGTTVT 120  
QY 121 VSS 123  
Db 121 VSS 123  
RESULT 3  
ADF09834  
ID ADF09834 standard; protein; 123 AA.  
XX  
AC ADF09834;  
DT 12-FEB-2004 (first entry)  
DE Human anti-MUC18 monoclonal antibody heavy chain #6.  
XX cell proliferation inhibition; MUC18 tumour antigen;  
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
KW carcinoma; cancer; malignancy; heavy chain; human.  
XX Homo sapiens.  
OS  
XX WO2003057837-A2.  
PN  
XX 17-JUL-2003.  
PD  
XX 26-DEC-2002; 2002WO-US041580.  
PF  
XX 28-DEC-2001; 2001US-0346414P.  
PR  
XX (ABGE-) ABGENIX INC.  
PA  
XX Gudas J;  
PI  
XX WPI: 2003-598367/56.  
DR  
XX N-PSDB; ADF09836.  
DR  
XX Inhibiting cell proliferation associated with expression of MUC18 tumor  
PT antigen, involves incubating and inhibiting cell by administering anti-  
PT MUC18 monoclonal antibody.  
XX  
PS Claim 1; SEQ ID NO 21; 83pp; English.  
XX  
XX The invention comprises a method for inhibiting cell proliferation  
CC associated with expression of MUC18 tumour antigen. The method involves  
CC administering anti-MUC18 monoclonal antibody. The method of the invention  
CC is useful for inhibiting cell (e.g. melanoma or tumour cell)  
CC proliferation associated with the expression of MUC18 tumour antigen, the  
CC method is preferably useful for inhibiting tumour metastasis. The method  
CC is useful for inhibiting cell proliferation in patients with tumours,  
CC carcinomas, cancer and other malignancies. The present amino acid  
CC sequence represents a heavy chain from an MUC18 tumour antigen-specific  
CC monoclonal antibody.  
XX  
SQ Sequence 123 AA;  
Query Match 100.0%; Score 653; DB 7; Length 123;  
Best Local Similarity 100.0%; Pred. No. 7.3e-53;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFYSGFSGSWVRQAPGGQGLEWLGWISAYNGNTNY 60  
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFYSGFSGSWVRQAPGGQGLEWLGWISAYNGNTNY 60  
Qy 61 AQKQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKVRRGVHHYGMVDMVGQGT 120  
Db 61 AQKQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKVRRGVHHYGMVDMVGQGT 120  
Qy 121 VSS 123  
Db 121 VSS 123

RESULT 4  
ABR55813  
ID ABR55813 standard; protein; 125 AA.  
XX  
AC ABR55813;  
XX  
DT 02-SEP-2003 (first entry)  
XX  
DE Heavy chain variable region of anti-Ang-2 antibody FJ-G11 HC.  
XX  
KW Ang-2; angiotensin-2; anorectic; cytostatic; antiarteriosclerotic;  
KW gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;  
KW angiogenesis; antibody.  
XX  
OS Homo sapiens.  
XX  
PH Key Location/Qualifiers  
FT Region 26..36  
FT /note= "complementarity determining region (CDR) 1"  
FT Region 50..66  
FT /note= "complementarity determining region (CDR) 2"  
FT Region 96..115  
FT /note= "complementarity determining region (CDR) 3"  
XX  
XX WO2003030833-A2.  
XX  
XX 17-APR-2003.  
XX  
XX 11-OCT-2002; 2002WO-US032613.  
XX  
XX 11-OCT-2001; 2001US-0328604P.  
XX  
XX 10-OCT-2002; 2002US-00269805.  
XX  
XX (AMGE-) AMGEN INC.  
XX  
XX Oliner JD;  
XX  
XX WPI; 2003-504963/47.  
XX  
XX New specific binding agents (i.e. anti-Angiopoietin-2 antibodies), useful  
XX for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,  
XX hemangioma, arteriosclerosis, atherosclerosis or endometriosis.  
XX  
XX Claim 1; Page 92; 161pp; English.  
XX  
XX The invention relates to a specific binding agent, which comprises at  
XX least one peptide selected from any of 62 peptides (ABR55769-830) or its  
XX fragment. The binding agents are antibodies that recognize and bind to  
XX angiopoietin-2 (Ang-2). The specific binding agent, particularly the  
XX antibody, is useful for inhibiting undesired angiogenesis, treating  
XX cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-  
XX 2 activity, modulating vascular permeability or plasma leakage, or  
XX treating a disease (e.g. ocular neovascular disease, obesity,  
XX haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,  
XX inflammatory disorders, atherosclerosis, endometriosis, neoplastic  
XX disease, bone-related disease, or psoriasis) in a mammal. The present  
XX sequence represents a heavy chain variable region of an anti-Ang-2  
XX antibody

SQ Sequence 125 AA;

Query Match 90.8%; Score 593; DB 6; Length 125;  
Best Local Similarity 90.4%; Pred. No. 2.7e-47;  
Matches 113; Conservative 4; Mismatches 6; Indels 2; Gaps 1;  
Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFYSGFSGSWVRQAPGGQGLEWLGWISAYNGNTNY 60  
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFYSGFSGSWVRQAPGGQGLEWLGWISAYNGNTNY 60  
Qy 61 AQKQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKV--RGVHHYGMVDMVGQGT 118  
Db 61 AQKQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKV--RGVHHYGMVDMVGQGT 120  
Qy 119 VTVSS 123  
Db 121 VTVSS 125

RESULT 5

ABP45910  
ID ABP45910 standard; protein; 251 AA.  
XX  
AC ABP45910;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human BlyS binding scFv SEQ ID 1921.  
XX  
KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
OS Homo sapiens.  
XX  
XX WO200202641-A1.  
XX  
XX 10-JAN-2002.  
XX  
XX 15-JUN-2001; 2001WO-US019110.  
XX  
XX 16-JUN-2000; 2000US-0212210P.  
XX  
XX 17-OCT-2000; 2000US-0240816P.  
XX  
XX 16-MAR-2001; 2001US-0276248P.  
XX  
XX 21-MAR-2001; 2001US-0277379P.  
XX  
XX 25-MAY-2001; 2001US-0293499P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.  
XX  
XX  
XX Antibodies against B lymphocyte stimulating polypeptides, useful for the  
XX diagnosis and treatment of cancers and immune disorders.  
XX  
XX Claim 1; Page 2693-2694; 3148pp; English.  
XX  
XX This invention describes novel antibodies that immunospecifically bind to  
XX B lymphocyte stimulator (BlyS) polypeptides. BlyS is a member of the  
XX tumour necrosis factor (TNF) super family and induces B cell  
XX proliferation and differentiation. The antibodies of the invention have  
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
XX antirheumatic and antiAIDS activity and can be used in vaccines to  
XX inhibit the expression and activity of BlyS. The antibodies bind to BlyS  
XX and so may be used to detect and quantitate the presence of BlyS in  
XX biological samples and may be used in this way to diagnose disease  
XX associated with aberrant expression of BlyS. They may also be  
XX administered to treat diseases associated with aberrant BlyS expression

CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
SQ Sequence 251 AA;

Query Match 90.0%; Score 587.5; DB 5; Length 251;  
Best Local Similarity 88.3%; Pred. No. 1.9e-46;  
Matches 113; Conservative 4; Mismatches 6; Indels 5; Gaps 1;

QY 1 QVOLVQSGAEVKKPGASVKVCKASGYTFSSYGFSGVWRQAPGQGLEWLGWISAYNGNTNY 60  
DB 1 QVOLVQSGAEVKKPGASVKVCKASGYTFSSYGFSGVWRQAPGQGLEWLGWISAYNGNTNY 60

QY 61 AQKLGQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKV-----RGVHYGYGMDVMGQ 115  
DB 61 AQKLGQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKV-----RGVHYGYGMDVMGQ 120

QY 116 GTTIVTVSS 123  
DB 121 GTTIVTVSS 128

RESULT 6  
ADG96737  
ID ADG96737 standard; protein; 251 AA.

AC ADG96737;

XX 11-MAR-2004 (first entry)

XX Single chain antibody that immunospecifically binds BlyS SeqID 1921.  
XX antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;  
KW B cell proliferation; differentiation; scFv; myasthenia gravis;  
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;  
KW carcinoma; lymphoma; anti-rheumatic; antiarthritic; neuroprotective;  
KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.

XX Unidentified.

OS WO2003055979-A2.

XX 10-JUL-2003.

XX 14-NOV-2002; 2002WO-US036496.

XX 16-NOV-2001; 2001US-0331469P.

PR 19-DEC-2001; 2001US-0340817P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

XX WPI; 2003-505530/47.

XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator  
PT (BlyS), useful for detecting and treating diseases or disorders e.g.  
PT rheumatoid arthritis, asthma and leukemia.

XX Example 1; SEQ ID NO 1921; 394pp; English.

XX This invention relates to novel antibodies that immunospecifically bind  
CC to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to  
CC chromosome 13q34 and encodes a protein that is a member of the tumour  
CC necrosis factor superfamily and induces both in vivo and in vitro B cell  
CC proliferation and differentiation. Specifically, it refers to single  
CC chain antibody molecules (scFvs) derived, preferably, from the variable  
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or  
CC fragment thereof, of either human, murine, rat or monkey BlyS. The

CC present invention refers to the use of such antibodies in various methods  
CC for the detection, diagnosis and prognosis of diseases related to the  
CC aberrant expression or inappropriate function of BlyS or its receptor. As  
CC such, these compositions are useful for identifying immune disorders  
CC including myasthenia gravis and multiple sclerosis, inflammatory  
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such  
CC as AIDS and proliferative disorders including leukaemia, carcinoma and  
CC lymphoma. Accordingly, they can be described as exhibiting various  
CC activities such as antirheumatic, antiallergic, neuroprotective,  
CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This  
CC polypeptide sequence is a single chain antibody that binds BlyS of the  
CC invention. NOTE: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published pct\_sequences.  
XX  
SQ Sequence 251 AA;

Query Match 90.0%; Score 587.5; DB 7; Length 251;  
Best Local Similarity 88.3%; Pred. No. 1.9e-46;  
Matches 113; Conservative 4; Mismatches 6; Indels 5; Gaps 1;

QY 1 QVOLVQSGAEVKKPGASVKVCKASGYTFSSYGFSGVWRQAPGQGLEWLGWISAYNGNTNY 60  
DB 1 QVOLVQSGAEVKKPGASVKVCKASGYTFSSYGFSGVWRQAPGQGLEWLGWISAYNGNTNY 60

QY 61 AQKLGQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKV-----RGVHYGYGMDVMGQ 115  
DB 61 AQKLGQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKV-----RGVHYGYGMDVMGQ 120

QY 116 GTTIVTVSS 123  
DB 121 GTTIVTVSS 128

RESULT 7

ADK18819  
ID ADK18819 standard; protein; 127 AA.

XX ADK18819;

XX 06-MAY-2004 (first entry)

XX Anti-human PDGF-D antibody protein related sequence #45.

XX antiinflammatory; immunomodulator; cytostatic; gene therapy.

XX Homo sapiens.

XX WO2003057857-A2.

XX 17-JUL-2003.

XX 06-JAN-2003; 2003WO-US000398.

XX 07-JAN-2002; 2002US-00041860.

XX (ABGE-) ABGENIX INC.

XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
XX Bezabeh B;  
XX WPI; 2003-587119/55.

XX New human monoclonal antibody that binds to platelet-derived growth  
PT factor-D (PDGF-D), useful for treating chronic and recurrent human  
PT diseases, such as inflammation, autoimmunity and cancer.  
XX Disclosure; SEQ ID NO 243; 255pp; English.

XX The invention relates to a human monoclonal antibody that binds to  
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
CC treating chronic and recurrent human diseases, such as inflammation,  
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are

CC useful for modulating collagen formation, and for staging various  
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
CC generated using an active protein fragment of the gene product from the  
CC clone 30664188.0.99 arising in the conditioned medium obtained when  
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
CC sequence corresponds to a protein used in the invention.

XX Sequence 127 AA;

Query Match 88.2%; Score 576; DB 7; Length 127;  
Best Local Similarity 87.4%; Pred. No. 1.1e-45;  
Matches 111; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVCKASGYTFSSYGFSGVSWVRQAPGGQLEWLGWISAYNGNTNY 60

DB 1 QVQLVQSGAEVKKPGASVKVCKASGYTFSSYGFSGVSWVRQAPGGQLEWLGWISAYNGNTNY 60

QY 61 AQKLGQRVTMTTSTSTAYMELSLRSDDTAVYYCARETKVRG-----VHYGMDVWGQG 116

DB 61 AQKLGQRVTMTTSTSTAYMELSLRSDDTAVYYCARETKVRG-----VHYGMDVWGQG 120

QY 117 TTVTVSS 123

DB 121 TTVTVSS 127

RESULT 8

ADK18901

ID ADK18901 standard; protein; 127 AA.

AC ADK18901;

DT 06-MAY-2004 (first entry)

DE Anti-human PDGF-D antibody protein related sequence #127.

KW antiinflammatory; immunomodulator; cytostatic; gene therapy.

OS Homo sapiens.

PN W02003057857-A2.

XX 17-JUL-2003.

XX 06-JAN-2003; 2003WO-US000398.

XX 07-JAN-2002; 2002US-00041860.

XX (ABGE-) ABGENIX INC.

XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
XX Bezabeh B;

XX WPI; 2003-587119/55.

XX New human monoclonal antibody that binds to platelet-derived growth  
XX factor-D (PDGF-D), useful for treating chronic and recurrent human  
XX diseases, such as inflammation, autoimmunity and cancer.

PS Disclosure; SEQ ID NO 325; 255pp; English.

XX The invention relates to a human monoclonal antibody that binds to  
XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
XX treating chronic and recurrent human diseases, such as inflammation,  
XX autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
XX useful for modulating collagen formation, and for staging various  
XX cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
XX generated using an active protein fragment of the gene product from the  
XX clone 30664188.0.99 arising in the conditioned medium obtained when  
XX HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
XX sequence corresponds to a protein used in the invention.

XX Sequence 127 AA;

Query Match 88.2%; Score 576; DB 7; Length 127;  
Best Local Similarity 87.4%; Pred. No. 1.1e-45;  
Matches 111; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVCKASGYTFSSYGFSGVSWVRQAPGGQLEWLGWISAYNGNTNY 60

DB 1 QVQLVQSGAEVKKPGASVKVCKASGYTFSSYGFSGVSWVRQAPGGQLEWLGWISAYNGNTNY 60

QY 61 AQKLGQRVTMTTSTSTAYMELSLRSDDTAVYYCARETKVRG-----VHYGMDVWGQG 116

DB 61 AQKLGQRVTMTTSTSTAYMELSLRSDDTAVYYCARETKVRG-----VHYGMDVWGQG 120

QY 117 TTVTVSS 123

DB 121 TTVTVSS 127

RESULT 9

ADK18607

ID ADK18607 standard; protein; 127 AA.

XX ADK18607;

XX 06-MAY-2004 (first entry)

DE Anti-human PDGF-D antibody heavy chain protein sequence.

KW antiinflammatory; immunomodulator; cytostatic; gene therapy.

OS Homo sapiens.

PN W02003057857-A2.

XX 17-JUL-2003.

XX 06-JAN-2003; 2003WO-US000398.

XX 07-JAN-2002; 2002US-00041860.

XX (ABGE-) ABGENIX INC.

XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
XX Bezabeh B;

XX WPI; 2003-587119/55.

XX New human monoclonal antibody that binds to platelet-derived growth  
XX factor-D (PDGF-D), useful for treating chronic and recurrent human  
XX diseases, such as inflammation, autoimmunity and cancer.

PS Disclosure; SEQ ID NO 31; 255pp; English.

XX The invention relates to a human monoclonal antibody that binds to  
XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
XX treating chronic and recurrent human diseases, such as inflammation,  
XX autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
XX useful for modulating collagen formation, and for staging various  
XX cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
XX generated using an active protein fragment of the gene product from the  
XX clone 30664188.0.99 arising in the conditioned medium obtained when  
XX HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
XX sequence corresponds to a protein used in the invention.

XX Sequence 127 AA;

Query Match 88.2%; Score 576; DB 7; Length 127;  
Best Local Similarity 87.4%; Pred. No. 1.1e-45;  
Matches 111; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVCKASGYTFSSYGFSGVSWVRQAPGGQLEWLGWISAYNGNTNY 60

DB 1 QVQLVQSGAEVKKPGASVKVCKASGYTFSSYGFSGVSWVRQAPGGQLEWLGWISAYNGNTNY 60

Qy	61	AQKLQGRVTWTTDTSTSTAYMELSLRSDDTAVYYCARETKVRG----	HHYGMQDVMGQG 11
Db	61	AQKLQGRVTWTTDTSTSTAYMELSLRSDDTAVYYCARETKVRG----	HHYGMQDVMGQG 120
Qy	117	TTVTVSS 123	
Db	121	TTVTVSS 127	
RESULT 10			
ADL25432			
ID	ADL25432	standard; protein; 127 AA.	
XX	ADL25432;		
XX	17-JUN-2004	(first entry)	
XX	Human mAb 1.33	heavy chain variable region protein SEQ ID NO:42.	
XX	antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;		
XX	nephritis; mesangial cell proliferation inhibition;		
XX	mesangial proliferative glomerulonephritis; nephrotropic;		
XX	antiinflammatory; dermatological; immunosuppressive; antidiabetic;		
XX	gene therapy; human; monoclonal antibody; mAb.		
XX	Homo sapiens.		
XX	WO2004024098-A2.		
XX	25-MAR-2004.		
XX	16-SEP-2003; 2003WO-US029414.		
XX	16-SEP-2002; 2002US-0411137P.		
XX	(ABGE-) ABGENIX INC.		
XX	(CURA-) CURAGEN CORP.		
XX	Floegel J, Gazit-Bornstein G, Keyt B, Larochelle WJ, Lichenstein H;		
XX	WPI; 2004-269881/25.		
XX	N-PSDB; ADL25431.		
XX	Use of an antibody or its binding fragment that binds platelet derived		
XX	growth factor-DD (PDGF-DD) for preparing a medicament for treating		
XX	nephritis.		
XX	Disclosure; SEQ ID NO 42; 115pp; English.		
XX	The present invention describes an antibody or its binding fragment that		
XX	binds platelet derived growth factor-DD (PDGF-DD), where the antibody is		
XX	useful in preparing a medicament for treating nephritis. Also described:		
XX	(1) a method of detecting nephritis; (2) a method of treating nephritis;		
XX	(3) a method of inhibiting mesangial cell proliferation; and (4) a method		
XX	of treating mesangial proliferative glomerulonephritis. The antibody has		
XX	nephrotropic, antiinflammatory, dermatological, immunosuppressive and		
XX	antidiabetic activities, and can be used in gene therapy. The antibody or		
XX	its binding fragment, that binds PDGF-DD, can be used in preparing a		
XX	medicament for treating nephritis and related disorders, e.g., mesangial		
XX	proliferative glomerulonephritis. The present sequence represents a human		
XX	monoclonal antibody (mAb) variable region sequence, which is used in the		
XX	exemplification of the present invention.		
XX	Sequence 127 AA;		
XX	XX		





DT 17-JUN-2004 (first entry)  
 XX  
 DE Human mAb 1.48.1 heavy chain variable region protein SEQ ID NO:62.  
 XX  
 KW antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;  
 KW nephritis; mesangial cell proliferation inhibition;  
 KW mesangial proliferative glomerulonephritis; nephrotropic;  
 KW antiinflammatory; dermatological; immunosuppressive; antidiabetic;  
 KW gene therapy; human; monoclonal antibody; mAb.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004024098-A2.  
 XX  
 PD 25-MAR-2004.  
 XX  
 PF 16-SEP-2003; 2003WO-US029414.  
 XX  
 PR 16-SEP-2002; 2002US-0411137P.  
 XX  
 PA (ABGE-) AGENIX INC.  
 PA (CURA-) CURAGEN CORP.  
 XX  
 XX Floege J, Gazit-Bornstein G, Keyt B, Larochele WJ, Lichenstein H;  
 XX  
 XX WPI; 2004-269881/25.  
 DR N-PSDB; ADU25451.  
 DR  
 XX  
 XX Use of an antibody or its binding fragment that binds platelet derived  
 PT growth factor-DD (PDGF-DD) for preparing a medicament for treating  
 PT nephritis.  
 PT  
 XX  
 PS Disclosure; SEQ ID NO 62; 115pp; English.  
 XX  
 CC The present invention describes an antibody or its binding fragment that  
 CC binds platelet derived growth factor-DD (PDGF-DD), where the antibody is  
 CC useful in preparing a medicament for treating nephritis. Also described:  
 CC (1) a method of detecting nephritis; (2) a method of treating nephritis;  
 CC (3) a method of inhibiting mesangial cell proliferation; and (4) a method  
 CC of treating mesangial proliferative glomerulonephritis. The antibody has  
 CC nephrotropic, antiinflammatory, dermatological, immunosuppressive and  
 CC antidiabetic activities, and can be used in gene therapy. The antibody or  
 CC its binding fragment, that binds PDGF-DD, can be used in preparing a  
 CC medicament for treating nephritis and related disorders, e.g., mesangial  
 CC proliferative glomerulonephritis. The present sequence represents a human  
 CC monoclonal antibody (mAb) variable region sequence, which is used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 125 AA;  
 Query Match 85.9%; Score 561; DB 8; Length 125;  
 Best Local Similarity 87.2%; Pred. No. 2.6e-44;  
 Matches 109; Conservative 3; Mismatches 11; Indels 2; Gaps 1;  
 QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFPSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60  
 DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFPSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60  
 QY 61 AQKLGQRTVMTTDTSTSTAYMELSLRSDDTAVYYCARETK--VRGVHYHYGMDVWGQGT 118  
 DB 61 AQKLGQRTVMTTDTSTSTAYMELSLRSDDTAVYYCARETK--VRGVHYHYGMDVWGQGT 120  
 QY 119 VTVSS 123  
 DB 121 VTVSS 125

RESULT 15  
 ADK18930  
 ID ADK18930 standard; protein; 126 AA.  
 XX  
 AC ADK18930;  
 XX

DT 06-MAY-2004 (first entry)  
 XX  
 DE Anti-human PDGF-D antibody protein related sequence #156.  
 XX  
 KW antiinflammatory; immunomodulator; cytostatic; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003057857-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 06-JAN-2003; 2003WO-US000398.  
 XX  
 PR 07-JAN-2002; 2002US-00041860.  
 XX  
 PA (ABGE-) AGENIX INC.  
 XX  
 XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
 PI Bezabeh B;  
 XX  
 DR WPI; 2003-587119/55.  
 XX  
 XX New human monoclonal antibody that binds to platelet-derived growth  
 PT factor-D (PDGF-D), useful for treating chronic and recurrent human  
 PT diseases, such as inflammation, autoimmunity and cancer.  
 PT  
 XX  
 PS Disclosure; SEQ ID NO 354; 255pp; English.  
 XX  
 CC The invention relates to a human monoclonal antibody that binds to  
 CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
 CC treating chronic and recurrent human diseases, such as inflammation,  
 CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
 CC useful for modulating collagen formation, and for staging various  
 CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
 CC generated using an active protein fragment of the gene product from the  
 CC clone 30664188.0.99 arising in the conditioned medium obtained when  
 CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
 CC sequence corresponds to a protein used in the invention.  
 XX  
 SQ Sequence 126 AA;  
 Query Match 85.5%; Score 558.5; DB 7; Length 126;  
 Best Local Similarity 85.8%; Pred. No. 4.4e-44;  
 Matches 109; Conservative 4; Mismatches 9; Indels 5; Gaps 2;  
 QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFPSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60  
 DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFPSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60  
 QY 61 AQKLGQRTVMTTDTSTSTAYMELSLRSDDTAVYYCARETKV---RGVHYHYGMDVWGQ 116  
 DB 61 AQKLGQRTVMTTDTSTSTAYMELSLRSDDTAVYYCARETKV---RGVHYHYGMDVWGQ 119  
 QY 117 TTVTVSS 123  
 DB 120 TTVTVSS 126

Search completed: November 9, 2005, 12:55:28  
 Job time : 77.8346 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:29:55 ; Search time 19.1128 Seconds  
(without alignments)  
480.403 Million cell updates/sec

Title: US-10-660-357A-21

Perfect score: 653

Sequence: 1 QVQLVQSGAEVKKPGASVKV.....GVHYGMDVWGQGTITVSS 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCFUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	521.5	79.9	118	4	US-09-726-219A-165
2	517	79.2	121	1	US-08-264-093-3
3	501	76.7	117	3	US-08-545-809A-105
4	499.5	76.5	120	2	US-08-652-816A-19
5	491	75.2	129	2	US-08-561-521-45
6	491	75.2	129	3	US-08-525-339A-77
7	491	75.2	129	5	PCT-US95-01219-45
8	490.5	75.1	120	3	US-09-025-769B-36
9	490.5	75.1	120	3	US-09-025-769B-59
10	490.5	75.1	120	4	US-09-490-070A-36
11	490.5	75.1	120	4	US-09-490-070A-59
12	490.5	75.1	120	4	US-09-490-153-36
13	490.5	75.1	120	4	US-09-490-153-59
14	490.5	75.1	120	4	US-09-490-324-36
15	490.5	75.1	120	4	US-09-490-324-59
16	490	75.0	117	3	US-09-025-769B-22
17	490	75.0	117	4	US-09-490-070A-22
18	490	75.0	117	4	US-09-490-153-22
19	490	75.0	117	4	US-09-490-324-22
20	489.5	75.0	128	1	US-08-202-047-22
21	489.5	75.0	128	3	US-08-964-690-22
22	485	74.3	470	4	US-09-859-053-28
23	481	73.7	125	3	US-09-139-149-3
24	480	73.5	140	3	US-08-836-561-63
25	480	73.5	140	4	US-09-434-122-63
26	477	73.0	119	2	US-08-561-521-10
27	477	73.0	119	5	PCT-US95-01219-10

Sequence 41, Appl  
Sequence 21, Appl  
Sequence 19, Appl  
Sequence 19, Appl  
Sequence 18, Appl  
Sequence 14, Appl  
Sequence 12, Appl  
Sequence 12, Appl  
Sequence 4112, Ap  
Sequence 123, App  
Sequence 74, Appl  
Sequence 74, Appl  
Sequence 65, Appl  
Sequence 65, Appl  
Sequence 65, Appl  
Sequence 849, App  
Sequence 108, App  
Sequence 23, Appl

28 474 72.6 119 4 US-09-438-954-41  
29 473 72.4 139 3 US-08-933-983-21  
30 472.5 72.4 139 1 US-08-233-877C-19  
31 472.5 72.4 139 2 US-08-452-164A-19  
32 472.5 72.4 139 3 US-08-603-024-18  
33 472.5 72.4 139 4 US-08-450-809-14  
34 470 72.0 119 2 US-08-561-521-12  
35 470 72.0 119 5 PCT-US95-01219-12  
36 469 71.8 132 4 US-09-513-999C-4112  
37 468.5 71.7 139 4 US-09-289-921-123  
38 468 71.7 140 3 US-08-836-561-74  
39 468 71.7 140 3 US-09-434-122-74  
40 466 71.4 119 1 US-08-300-386A-65  
41 466 71.4 119 3 US-08-931-645-65  
42 466 71.4 119 5 PCT-US95-11235-65  
43 466 71.4 134 4 US-09-471-276-849  
44 464.5 71.1 139 4 US-09-269-921-108  
45 463 70.9 121 1 US-08-202-047-23

#### ALIGNMENTS

#### RESULT 1

US-09-726-219A-165

; Sequence 165, Application US/09726219A

; Patent No. 6806079

; GENERAL INFORMATION:

; APPLICANT: Cambridge Antibody Technology

; APPLICANT: Cambridge Antibody Technology Limited

; APPLICANT: Medical Research Council

; APPLICANT: McCafferty, John

; APPLICANT: Pope, Anthony

; APPLICANT: Johnson, Kevin

; APPLICANT: Hoogenboom, Hendricus

; APPLICANT: Griffiths, Andrew

; APPLICANT: Jackson, Ronald

; APPLICANT: Holliger, Kasper

; APPLICANT: Marks, James

; APPLICANT: Clarkson, Timothy

; APPLICANT: Chiswell, David

; APPLICANT: Winter, Gregory

; APPLICANT: Bonert, Timothy

; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs

; FILE REFERENCE: 213839-00013

; CURRENT APPLICATION NUMBER: US/09/726,219A

; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: GB 9015198.6

; PRIOR FILING DATE: 1990-07-10

; PRIOR APPLICATION NUMBER: GB 9022845.3

; PRIOR FILING DATE: 1990-10-19

; PRIOR APPLICATION NUMBER: GB 9022845.3

; PRIOR FILING DATE: 1990-10-19

; PRIOR APPLICATION NUMBER: GB 9024503.6

; PRIOR FILING DATE: 1990-11-12

; PRIOR APPLICATION NUMBER: GB 9104744.9

; PRIOR FILING DATE: 1991-03-06

; PRIOR APPLICATION NUMBER: GB 9110549.4

; PRIOR FILING DATE: 1991-05-15

; PRIOR APPLICATION NUMBER: PCT/GB91/01134

; PRIOR FILING DATE: 1991-07-10

; PRIOR APPLICATION NUMBER: US 07/971,857

; PRIOR FILING DATE: 1993-01-08

; PRIOR APPLICATION NUMBER: US 08/484,893

; PRIOR FILING DATE: 1995-06-07

; NUMBER OF SEQ ID NOS: 272

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 165

; LENGTH: 118

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-726-219A-165

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Query Match          79.9%; Score 521.5; DB 4; Length 118;
Best Local Similarity 84.0%; Pred. No. 2.1e-43; Indels 3; Gaps 2;
Matches 100; Conservative 6; Mismatches 10; Indels 3; Gaps 2;

QY 1 QVOLVSGAEVKKPGASVKVCKASGYTFYSYGFSGVVRQAPGGLEWLGWISAYNGNTNY 60
   |||||
Db 1 QVOLVSGAEVKKPGASVKVCKASGYTFYSYGFSGVVRQAPGGLEWLGWISAYNGNTKY 60
   |||||

QY 61 AQKLGQRTVMTTDTSTSTAYMELRSDDTAVYYCAR--ETKRVGHYHGMVWGQGT 117
   |||||
Db 61 AQKLGQRTVMTTDTSTSTAYMELRSDDTAVYYCVRLPKRTATLHY--IDVWGKGT 118
   |||||

RESULT 2
US-08-264-093-3
; Sequence 3, Application US/08264093
; Patent No. 5639863
; GENERAL INFORMATION:
; APPLICANT: Michael D. Dan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ridout & Maybee
; STREET: 2300 Richmond-Adelaide Centre
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 2J7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS 6.00
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,093
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA: No. 5639863 applicable
; ATTORNEY/AGENT INFORMATION:
; NAME: Lake, James R.
; REGISTRATION NUMBER: 31081
; REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
; TELEPHONE: (416) 868-1482
; TELEFAX: (416) 362-0823
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS: not applicable
; TOPOLOGY: linear
US-08-264-093-3

Query Match          79.2%; Score 517; DB 1; Length 121;
Best Local Similarity 82.1%; Pred. No. 5.8e-43;
Matches 101; Conservative 8; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVOLVSGAEVKKPGASVKVCKASGYTFYSYGFSGVVRQAPGGLEWLGWISAYNGNTNY 60
   |||||
Db 1 QVOLVSGAEVKKPGASVKVCKASGYTFYGLSWVRQAPGGLEWLGWISAHNGNTNS 60
   |||||

QY 61 AQKLGQRTVMTTDTSTSTAYMELRSDDTAVYYCARETKRVGHYHGMVWGQGT 120
   |||||
Db 61 AQKFGQRTVMTTDTSTSTAYMEVRSDDTAVYYCARVGMWDLNLF--DYWGQGLT 118
   |||||

QY 121 VSS 123
Db 119 VSS 121
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```
RESULT 3
US-08-545-809A-105
; Sequence 105, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-105

Query Match          76.7%; Score 501; DB 3; Length 117;
Best Local Similarity 96.9%; Pred. No. 2e-41;
Matches 95; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVOLVSGAEVKKPGASVKVCKASGYTFYSYGFSGVVRQAPGGLEWLGWISAYNGNTNY 60
   |||||
Db 20 QVOLVSGAEVKKPGASVKVCKASGYTFTSYGISWVRQAPGGLEWLGWISAYNGNTNY 79
   |||||

QY 61 AQKLGQRTVMTTDTSTSTAYMELRSDDTAVYYCAR 98
   |||||
Db 80 AQKLGQRTVMTTDTSTSTAYMELRSDDTAVYYCAR 117
   |||||

RESULT 4
US-08-652-816A-19
; Sequence 19, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Osbourn, JK
; APPLICANT: Allen, DJ
; APPLICANT: McCafferty, JG
; TITLE OF INVENTION: Specific binding members, materials and
; TITLE OF INVENTION: methods.
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
```

COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652.816A  
FILING DATE: 23-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.4  
FILING DATE: 02-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.8  
FILING DATE: 02-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206318.9  
FILING DATE: 24-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206372.6  
FILING DATE: 23-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9535004.9  
FILING DATE: 07-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9610824.6  
FILING DATE: 23-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/02240  
FILING DATE: 02-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/244,597  
FILING DATE: 01-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: David W. Clough  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/33308  
TELEPHONE: 312-474-6300  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-652-816A-19

Query Match 76.58; Score 499.5; DB 2; Length 120;  
Best Local Similarity 80.5%; Pred. No. 2.9e-41;  
Matches 99; Conservative 7; Mismatches 14; Indels 3; Gaps 2;  
QY 1 QVOLVQSGAEVKKPGASVKVSKASGYTFPSYGFVSRVQAPGGQLEWLGWISAYNGNTNY 60  
DB 1 QVTLQSGAEVKKPGSPKVKVSKASGYTFYAGFNWVRVQAPGGQLEWV-WISAYSGNTKY 59  
QY 61 AQKLGQRTVMTTDTSTSTAYMELSLRSDTAVYICARETKKVRGVHYGMDVVGQGTVT 120  
DB 60 AQKFGQRTVMTTDTSTSTAYMELSLRSDTAVYICA--GRRGFRFRPMDVVGQGTMT 117  
QY 121 VSS 123  
DB 118 VSS 120

RESULT 5  
US-08-561-521-45  
Sequence 45, Application US/08561521  
Patent No. 5840299  
GENERAL INFORMATION:  
APPLICANT: Bendig, Mary M.  
APPLICANT: Leger, Olivier J.  
APPLICANT: Saldanha, Jose  
APPLICANT: Jones, S. Tarran  
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte

TITLE OF INVENTION: Adhesion Molecule VLA-4  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/561,521  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/186,269A  
FILING DATE: 25-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William L.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15270-14  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 129 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-561-521-45

Query Match 75.2%; Score 491; DB 2; Length 129;  
Best Local Similarity 76.3%; Pred. No. 2.1e-40;  
Matches 100; Conservative 5; Mismatches 16; Indels 10; Gaps 3;  
QY 1 QVOLVQSGAEVKKPGASVKVSKASGYTFPSYGFVSRVQAPGGQLEWLGWISAY-NGNTN 59  
DB 1 QVOLVQSGAEVKKPGASVKVSKASGYTFPSYGFVSRVQAPGGQLEWGMWNPYNGDNTN 60  
QY 60 YAKLQGRVTMTTDTSTSTAYMELSLRSDTAVYICARETK-----VRGVHYGMDV 112  
DB 61 YAKFGQRTVMTTDTSTSTAYMELSLRSDTAVYICARAPGYSGGGCYRG--DYXFDY 118  
QY 113 WGQGTVTVTSS 123  
DB 119 WGQGTVTVTSS 129

RESULT 6  
US-08-525-539A-77  
Sequence 77, Application US/08525539A  
Patent No. 6309636  
GENERAL INFORMATION:  
APPLICANT: DO COUTO, FERNANDO J.R.  
APPLICANT: CERIANI, ROBERTO L.  
APPLICANT: PETERSON, JERRY A.  
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE  
TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FORSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018

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/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/525,539A
/ FILING DATE: 14-SEP-1995
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: DYLAN, TYLER
/ REGISTRATION NUMBER: 37,612
/ REFERENCE/DOCKET NUMBER: 27633-20001.21
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 813-5600
/ TELEFAX: (415) 494-0792
/ TELEX: 706141
/ INFORMATION FOR SEQ ID NO: 77:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 129 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
/ US-08-525-539A-77
/
/ Query Match 75.2%; Score 491; DB 3; Length 129;
/ Best Local Similarity 76.3%; Pred. No. 2.1e-40;
/ Matches 100; Conservative 5; Mismatches 16; Indels 10; Gaps 3;
/
/ QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFYSGFSGVVRQAPGGLEWLGWISAY-NGNTN 59
/ Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFYSGFSGVVRQAPGGLEWLGWISAY-NGNTN 60
/
/ QY 60 YAKLQGRVTMTTDTSTAYMELSLRSDDTAVYYCARETK-----VRGVHYYGMDV 112
/ Db 61 YAKFGQRTITADTSTAYMELSLRSDDTAVYYCARAPGYSGGGCYRG--DYXFDY 118
/
/ QY 113 WGQGTTLTVSS 123
/ Db 119 WGQGTTLTVSS 129
/
/ RESULT 7
/ PCT-US95-01219-45
/ Sequence 45, Application PC/TUS9501219
/ GENERAL INFORMATION:
/ APPLICANT: Bendig, Mary M.
/ APPLICANT: Leger, Olivier J.
/ APPLICANT: Saidanha, Jose
/ APPLICANT: Jones, S. Tarran
/ TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
/ TITLE OF INVENTION: Adhesion Molecule VLA-4
/ NUMBER OF SEQUENCES: 45
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend Khourie and Crew
/ STREET: One Market Plaza, Steuart Tower, Suite 2000
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94105
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/01219
/ FILING DATE: 25-JAN-1995
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/186,269
/ FILING DATE: 25-JAN-1994
/ ATTORNEY/AGENT INFORMATION:
```

```
/
/ NAME: Smith, William L.
/ REGISTRATION NUMBER: 30,223
/ REFERENCE/DOCKET NUMBER: 15270-14
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-543-9600
/ TELEFAX: 415-543-5043
/ INFORMATION FOR SEQ ID NO: 45:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 129 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ PCT-US95-01219-45
/
/ Query Match 75.2%; Score 491; DB 5; Length 129;
/ Best Local Similarity 76.3%; Pred. No. 2.1e-40;
/ Matches 100; Conservative 5; Mismatches 16; Indels 10; Gaps 3;
/
/ QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFYSGFSGVVRQAPGGLEWLGWISAY-NGNTN 59
/ Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFYSGFSGVVRQAPGGLEWLGWISAY-NGNTN 60
/
/ QY 60 YAKLQGRVTMTTDTSTAYMELSLRSDDTAVYYCARETK-----VRGVHYYGMDV 112
/ Db 61 YAKFGQRTITADTSTAYMELSLRSDDTAVYYCARAPGYSGGGCYRG--DYXFDY 118
/
/ QY 113 WGQGTTLTVSS 123
/ Db 119 WGQGTTLTVSS 129
/
/ RESULT 8
/ US-09-025-769B-36
/ Sequence 36, Application US/09025769B
/ Patent No. 6300064
/ GENERAL INFORMATION:
/ APPLICANT: Knappik, Achim
/ APPLICANT: Pack, Peter
/ APPLICANT: Ilag, Vic
/ APPLICANT: Ge, Liming
/ APPLICANT: Moroney, Simon
/ APPLICANT: Plueckthun, Andreas
/ TITLE OF INVENTION: Protein/(Poly)peptide libraries
/ NUMBER OF SEQUENCES: 373
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
/ STREET: 1251 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10021
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/025,769B
/ FILING DATE: 18-FEB-1998
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 95 11 3021.0
/ FILING DATE: 18-AUG-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: James F. Haley, Jr., Esq.
/ REGISTRATION NUMBER: 27,794
/ REFERENCE/DOCKET NUMBER: MORPHO/5
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)596-9000
/ TELEFAX: (212)596-9090
/ INFORMATION FOR SEQ ID NO: 36:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 120 amino acids
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;  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-025-769B-36

Query Match 75.1%; Score 490.5; DB 3; Length 120;  
Best Local Similarity 78.9%; Pred. No. 2.2e-40;  
Matches 97; Conservative 5; Mismatches 18; Indels 3; Gaps 1;

Qy 1 QVOLVSGAEVKKPGASVKVCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60  
Db 1 QVOLVSGAEVKKPGASVKVCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60

Qy 61 AQKLGQVRVTMTDTSTSTAYMELSLRSDDTAVYYCARETKVRGVHYHYGMDVWGQGTITV 120  
Db 61 AQKLGQVRVTMTDTSTSTAYMELSLRSDDTAVYYCARETKVRGVHYHYGMDVWGQGTITV 117

Qy 121 VSS 123  
Db 118 VSS 120

RESULT 9  
US-09-025-769B-59  
; Sequence 59, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
FILING DATE: 18-FEB-1998  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-59

Query Match 75.1%; Score 490.5; DB 3; Length 120;  
Best Local Similarity 78.9%; Pred. No. 2.2e-40;  
Matches 97; Conservative 5; Mismatches 18; Indels 3; Gaps 1;

Qy 1 QVOLVSGAEVKKPGASVKVCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60  
Db 1 QVOLVSGAEVKKPGASVKVCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60  
Qy 61 AQKLGQVRVTMTDTSTSTAYMELSLRSDDTAVYYCARETKVRGVHYHYGMDVWGQGTITV 120  
Db 61 AQKLGQVRVTMTDTSTSTAYMELSLRSDDTAVYYCARETKVRGVHYHYGMDVWGQGTITV 117  
Qy 121 VSS 123  
Db 118 VSS 120

RESULT 10  
US-09-490-070A-36  
; Sequence 36, Application US/09490070A  
; Patent No. 6696248  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
; STREET: 1666 K Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20006

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,070A  
FILING DATE: 24-Jan-2000  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Colin G. Sandercock, Esq.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37629-0005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 912-2000  
TELEFAX: (202) 912-2020  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS: <unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
US-09-490-070A-36

Query Match 75.1%; Score 490.5; DB 4; Length 120;  
Best Local Similarity 78.9%; Pred. No. 2.2e-40;  
Matches 97; Conservative 5; Mismatches 18; Indels 3; Gaps 1;

Qy 1 QVOLVSGAEVKKPGASVKVCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60  
Db 1 QVOLVSGAEVKKPGASVKVCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60

Qy 61 AQKLGQVRVTMTDTSTSTAYMELSLRSDDTAVYYCARETKVRGVHYHYGMDVWGQGTITV 120  
Db 61 AQKLGQVRVTMTDTSTSTAYMELSLRSDDTAVYYCARETKVRGVHYHYGMDVWGQGTITV 117

QY 121 VSS 123  
|||  
Db 118 VSS 120

## RESULT 11

US-09-490-070A-59  
; Sequence 59, Application US/09490070A  
; Patent No. 6696248

## GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Pack, Peter

Ilag, Vic

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman

White & McAuliffe

STREET: 1666 K Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)

CURRENT APPLICATION DATA:

FILING DATE: 24-Jan-2000

PRIOR APPLICATION NUMBER: US/09/490,070A

APPLICATION DATA:

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 912-2000

TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 59:

SEQUENCE DESCRIPTION: SEQ ID NO: 59:

LENGTH: 120 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 59:

US-09-490-070A-59

Query Match 75.1%; Score 490.5; DB 4; Length 120;

Best Local Similarity 78.9%; Pred. No. 2.2e-40;

Matches 97; Conservative 5; Mismatches 18; Indels 3; Gaps 1;

QY 1 QVOLVSGAEVKKPGASVKVSCKASGYTFPSYFGFVSRQAPGQGLEWLGWISAYNGNTNY 60

Db 1 QVOLVSGAEVKKPGASVKVSCKASGYTFPSYFGFVSRQAPGQGLEWLGWISAYNGNTNY 60

QY 61 AQKLGQRVTMTTSTSTAYMELSLRSDTAVYYCARETKVGRVHYGMDVWGQGTFTVT 120

Db 61 AQKLGQRVTMTTSTSTAYMELSLRSDTAVYYCARETKVGRVHYGMDVWGQGTFTVT 120

QY 121 VSS 123

Db 118 VSS 120

RESULT 12

US-09-490-153-36

US-09-490-153-36

US-09-490-153-36

US-09-490-153-36

US-09-490-153-36

US-09-490-153-36

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US-09-490-153-36

US-09-490-153-36

US-09-490-153-36

US-09-490-153-36

US-09-490-153-36

; Sequence 36, Application US/09490153

; Patent No. 6706484

; GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Pack, Peter

Ilag, Vic

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,153

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 36:

US-09-490-153-36

Query Match 75.1%; Score 490.5; DB 4; Length 120;

Best Local Similarity 78.9%; Pred. No. 2.2e-40;

Matches 97; Conservative 5; Mismatches 18; Indels 3; Gaps 1;

QY 1 QVOLVSGAEVKKPGASVKVSCKASGYTFPSYFGFVSRQAPGQGLEWLGWISAYNGNTNY 60

Db 1 QVOLVSGAEVKKPGASVKVSCKASGYTFPSYFGFVSRQAPGQGLEWLGWISAYNGNTNY 60

QY 61 AQKLGQRVTMTTSTSTAYMELSLRSDTAVYYCARETKVGRVHYGMDVWGQGTFTVT 120

Db 61 AQKLGQRVTMTTSTSTAYMELSLRSDTAVYYCARETKVGRVHYGMDVWGQGTFTVT 120

QY 121 VSS 123

Db 118 VSS 120

RESULT 13

US-09-490-153-59

; Sequence 59, Application US/09490153

; Patent No. 6706484

; GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Pack, Peter

Ilag, Vic



Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,153  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 59:  
US-09-490-153-59  
Query Match 75.1%; Score 490.5; DB 4; Length 120;  
Best Local Similarity 78.9%; Pred. No. 2.2e-40;  
Matches 97; Conservative 5; Mismatches 18; Indels 3; Gaps 1;  
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFYSGFSGWVRQAPGQGLEWLGWISAYNGNTNY 60  
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFYSGFSGWVRQAPGQGLEWLGWISAYNGNTNY 60  
QY 61 AQKLQGRVTMTDTSTSTAYMELRSLRSDDTAVVYVCARETKVRGVHYGYGMDVWGQGTTLT 120  
Db 61 AQKFGQGVTRWTRDTSISTAYMELSLRSDDTAVVYCAR---WGDDGFYANDYWGQGTTLT 117  
QY 121 VSS 123  
Db 118 VSS 120  
RESULT 14  
US-09-490-324-36  
Sequence 36, Application US/09490324  
Patent No. 6828422  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,324  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
US-09-490-324-36  
Query Match 75.1%; Score 490.5; DB 4; Length 120;  
Best Local Similarity 78.9%; Pred. No. 2.2e-40;  
Matches 97; Conservative 5; Mismatches 18; Indels 3; Gaps 1;  
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFYSGFSGWVRQAPGQGLEWLGWISAYNGNTNY 60  
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFYSGFSGWVRQAPGQGLEWLGWISAYNGNTNY 60  
QY 61 AQKLQGRVTMTDTSTSTAYMELRSLRSDDTAVVYVCARETKVRGVHYGYGMDVWGQGTTLT 120  
Db 61 AQKFGQGVTRWTRDTSISTAYMELSLRSDDTAVVYCAR---WGDDGFYANDYWGQGTTLT 117  
QY 121 VSS 123  
Db 118 VSS 120  
RESULT 15  
US-09-490-324-59  
Sequence 59, Application US/09490324  
Patent No. 6828422  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/490,324  
; FILING DATE: 24-Jan-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769  
; FILING DATE: 18-FEB-1998  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 59:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 59:  
US-09-490-324-59

Query Match 75.1%; Score 490.5; DB 4; Length 120;  
Best Local Similarity 78.9%; Pred. No. 2.2e-40;  
Matches 97; Conservative 5; Mismatches 18; Indels 3; Gaps 1;  
  
Qy 1 QVQLVSGAEVKKPGASVKVCKASGYTFESYGFVSRQAPGQGLEWLGWISAYNGNTNY 60  
Db 1 QVQLVSGAEVKKPGASVKVCKASGYTFESYGFVSRQAPGQGLEWLGWISAYNGNTNY 60  
  
Qy 61 AQKLGKRVMTTDTSTAYMELSLRSDDTAVYVCARETKVGVHHYGVNDVWGQGTYYT 120  
Db 61 AQKLGKRVMTTDTSTAYMELSLRSDDTAVYVCARETKVGVHHYGVNDVWGQGTYYT 120  
  
Qy 121 VSS 123  
Db 118 VSS 120

Search completed: November 9, 2005, 11:46:39  
Job time : 20.1128 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:40:37 ; Search time 68.3333 Seconds  
(without alignments)  
753.137 Million cell updates/sec

Title: US-10-660-357A-21  
Perfect score: 653  
Sequence: 1 QVQLVQSGAEVKPGASVKV.....GVHYGMDVWGQGTITVTVSS 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
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- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
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- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	653	100.0	123	14	US-10-330-613-21
2	653	100.0	123	14	US-10-330-530-21
3	653	100.0	123	16	US-10-660-357-21
4	593	90.8	125	14	US-10-269-805-45
5	587.5	90.0	251	10	US-09-880-748-1921
6	587.5	90.0	251	15	US-10-293-418-1921
7	584.5	89.5	121	20	US-11-031-485-120
8	576	88.2	127	14	US-10-041-860-31
9	576	88.2	127	14	US-10-041-860-243
10	576	88.2	127	14	US-10-041-860-325
11	576	88.2	127	16	US-10-665-383-42
Sequence 21, Appl					
Sequence 21, Appl					
Sequence 45, Appl					
Sequence 1921, Ap					
Sequence 1921, Ap					
Sequence 120, App					
Sequence 31, Appl					
Sequence 243, App					
Sequence 325, App					
Sequence 42, Appl					

12	571.5	87.5	469	20	US-11-031-485-42	Sequence 42, Appl
13	569.5	87.2	469	20	US-11-031-485-34	Sequence 34, Appl
14	561	85.9	125	14	US-10-041-860-42	Sequence 42, Appl
15	561	85.9	125	14	US-10-041-860-207	Sequence 207, App
16	561	85.9	125	16	US-10-665-383-62	Sequence 62, Appl
17	558.5	85.5	126	14	US-10-041-860-354	Sequence 354, App
18	557	85.3	251	10	US-09-880-748-1562	Sequence 1562, Ap
19	557	85.3	251	15	US-10-293-418-1562	Sequence 1562, Ap
20	556	85.1	123	14	US-10-269-805-51	Sequence 51, Appl
21	554.5	84.9	125	20	US-11-031-485-133	Sequence 133, App
22	554.5	84.9	247	10	US-09-880-748-1873	Sequence 1873, Ap
23	554.5	84.9	247	15	US-10-293-418-1873	Sequence 1873, Ap
24	552	84.5	257	10	US-09-880-748-1610	Sequence 1610, Ap
25	552	84.5	257	15	US-10-293-418-1610	Sequence 1610, Ap
26	551.5	84.5	249	20	US-11-017-030-30	Sequence 30, Appl
27	551	84.4	248	10	US-09-880-748-1472	Sequence 1472, Ap
28	551	84.4	248	15	US-10-293-418-1472	Sequence 1472, Ap
29	551	84.4	255	10	US-09-880-748-1190	Sequence 1190, Ap
30	551	84.4	255	15	US-10-293-418-1190	Sequence 1190, Ap
31	551	84.4	257	10	US-09-880-748-1354	Sequence 1354, Ap
32	551	84.4	257	15	US-10-293-418-1354	Sequence 1354, Ap
33	550.5	84.3	251	10	US-09-880-748-1315	Sequence 1315, Ap
34	550.5	84.3	251	15	US-10-293-418-1315	Sequence 1315, Ap
35	550	84.2	248	10	US-09-880-748-1446	Sequence 1446, Ap
36	550	84.2	248	15	US-10-293-418-1446	Sequence 1446, Ap
37	549.5	84.2	132	17	US-10-506-743-18	Sequence 18, Appl
38	549	84.1	248	10	US-09-880-748-1778	Sequence 1778, Ap
39	549	84.1	248	15	US-10-293-418-1778	Sequence 1778, Ap
40	547.5	83.8	249	10	US-09-880-748-1425	Sequence 1425, Ap
41	547.5	83.8	249	15	US-10-293-418-1425	Sequence 1425, Ap
42	547.5	83.8	252	10	US-09-880-748-1674	Sequence 1674, Ap
43	547.5	83.8	252	15	US-10-293-418-1674	Sequence 1674, Ap
44	547	83.8	251	10	US-09-880-748-1586	Sequence 1586, Ap
45	547	83.8	251	10	US-09-880-748-1872	Sequence 1872, Ap

ALIGNMENTS

RESULT 1  
US-10-330-613-21  
; Sequence 21, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-19  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-21

Query Match	100.0%;	Score 653;	DB 14;	Length 123;
Best Local Similarity	100.0%;	Pred. No. 1e-54;		
Matches 123;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	QVQLVQSGAEVKPGASVKVCKASGYTFFSYGFSWVRQAPGGQLEWLGWISAYNGNTNY	60	
Db	1	QVQLVQSGAEVKPGASVKVCKASGYTFFSYGFSWVRQAPGGQLEWLGWISAYNGNTNY	60	
Qy	61	AQKLGQGVNTTDTSTSTAYMELRSRSDDTATVYVCARETKVRGVHYGMDVWGQGTITVT	120	
Db	61	AQKLGQGVNTTDTSTSTAYMELRSRSDDTATVYVCARETKVRGVHYGMDVWGQGTITVT	120	
Qy	121	VSS 123		

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Db      121 VSS 123

RESULT 2
US-10-330-530-21
; Sequence 21, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ARGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-21

Query Match      100.0%; Score 653; DB 14; Length 123;
Best Local Similarity 100.0%; Pred. No. 1e-54;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QVQLVQSGAEVKKPGASVKVSCKASGYTFPSYGFSGSWVRQAPGGGLEWLGWISAYNGNTNY 60
Db      1 QVQLVQSGAEVKKPGASVKVSCKASGYTFPSYGFSGSWVRQAPGGGLEWLGWISAYNGNTNY 60
Qy      61 AQKLQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKVGRGVHYGMDVWGQGT 120
Db      61 AQKLQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKVGRGVHYGMDVWGQGT 120
Qy      121 VSS 123
Db      121 VSS 123

RESULT 3
US-10-660-357-21
; Sequence 21, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ARGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-21

Query Match      100.0%; Score 653; DB 16; Length 123;
Best Local Similarity 100.0%; Pred. No. 1e-54;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QVQLVQSGAEVKKPGASVKVSCKASGYTFPSYGFSGSWVRQAPGGGLEWLGWISAYNGNTNY 60
Db      1 QVQLVQSGAEVKKPGASVKVSCKASGYTFPSYGFSGSWVRQAPGGGLEWLGWISAYNGNTNY 60
Qy      61 AQKLQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKVGRGVHYGMDVWGQGT 120
Db      61 AQKLQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKVGRGVHYGMDVWGQGT 120
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Qy      121 VSS 123
Db      121 VSS 123

RESULT 4
US-10-269-805-45
; Sequence 45, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-45

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Best Local Similarity 90.4%; Pred. No. 5.8e-49;
Matches 113; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

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Db      1 QVQLVQSGAEVKKPGASVKVSCKASGYTFPSYGFSGSWVRQAPGGGLEWLGWISAYNGNTNY 60
Qy      61 AQKLQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKV--RGVHYGMDVWGQGT 118
Db      61 AQKLQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCARETKV--RGVHYGMDVWGQGT 120
Qy      119 VTVSS 123
Db      121 VTVSS 125

RESULT 5
US-09-880-748-1921
; Sequence 1921, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYs
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1921
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1921

Query Match      90.0%; Score 587.5; DB 10; Length 251;
Best Local Similarity 88.3%; Pred. No. 4e-48;
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Matches 113; Conservative 4; Mismatches 6; Indels 5; Gaps 1;

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Qy 1 QVQLVQSGAEVKKPGASVKSCASGYTFYSGFSGWVRQAPGQGLEWLGWISAYNGNTNY 60
Db 1 QVQLVQSGAEVKKPGASVKSCASGYTFYSGFSGWVRQAPGQGLEWLGWISAYNGNTNY 60
Qy 61 AQLQGRVTMTTDTSTAYMELSLRSDDTAVYYCARETKV-----RGVHYGMDVWGQ 115
Db 61 AQLQGRVTMTTDTSTAYMELSLRSDDTAVYYCARETKV-----RGVHYGMDVWGQ 120
Qy 116 GTTVTVSS 123
Db 121 GTTVTVSS 128
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## RESULT 6

US-10-293-418-1921  
; Sequence 1921, Application US/10293418  
; Publication No. US20030223996A1  
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523P2  
; CURRENT APPLICATION NUMBER: US/10/293,418

; PRIOR FILING DATE: 2002-11-27

; PRIOR FILING DATE: 2001-11-16

; PRIOR FILING DATE: 2001-11-16

; PRIOR FILING DATE: 2001-12-19

; PRIOR FILING DATE: 2001-06-15

; PRIOR FILING DATE: 2001-05-25

; PRIOR FILING DATE: 2001-03-21

; PRIOR FILING DATE: 2001-03-16

; PRIOR FILING DATE: 2000-10-17

; PRIOR FILING DATE: 2000-06-16

; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 1921

; LENGTH: 251

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-293-418-1921

Query Match 90.0%; Score 587.5; DB 15; Length 251;  
Best Local Similarity 88.3%; Pred. No. 4e-48;  
Matches 113; Conservative 4; Mismatches 6; Indels 5; Gaps 1;

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Db 1 QVQLVQSGAEVKKPGASVKSCASGYTFYSGFSGWVRQAPGQGLEWLGWISAYNGNTNY 60
Qy 61 AQLQGRVTMTTDTSTAYMELSLRSDDTAVYYCARETKV-----RGVHYGMDVWGQ 115
Db 61 AQLQGRVTMTTDTSTAYMELSLRSDDTAVYYCARETKV-----RGVHYGMDVWGQ 120
Qy 116 GTTVTVSS 123
Db 121 GTTVTVSS 128
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## RESULT 7

US-11-031-485-120  
; Sequence 120, Application US/11031485  
; Publication No. US20050232917A1  
; GENERAL INFORMATION:

; APPLICANT: PULLEN, NICHOLAS

; APPLICANT: MOLLOY, ELIZABETH

; APPLICANT: KELLERMANN, SIRID-AIMEE

; APPLICANT: GREEN, LARRY L.  
; TITLE OF INVENTION: ANTIBODIES TO MACCAM  
; FILE REFERENCE: ABX-PF6  
; CURRENT APPLICATION NUMBER: US/11/031,485  
; PRIOR FILING DATE: 2005-01-07  
; PRIOR FILING DATE: 2004-01-09  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 120  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-031-485-120

Query Match 89.5%; Score 584.5; DB 20; Length 121;  
Best Local Similarity 91.1%; Pred. No. 3.6e-48;  
Matches 112; Conservative 3; Mismatches 5; Indels 3; Gaps 1;

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Db 1 QVQLVQSGAEVKKPGASVKSCASGYTFYSGFSGWVRQAPGQGLEWLGWISAYNGNTNY 60
Qy 61 AQLQGRVTMTTDTSTAYMELSLRSDDTAVYYCARETKVGVHYGMDVWGQGTITVT 120
Db 61 AQLQGRVTMTTDTSTAYMELSLRSDDTAVYYCARETKVGVHYGMDVWGQGTITVT 117
Qy 121 VSS 123
Db 118 VSS 120
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## RESULT 8

US-10-041-860-31  
; Sequence 31, Application US/10041860  
; Publication No. US20030157109A1  
; GENERAL INFORMATION:

; APPLICANT: Corvalan, Jose R.F.

; APPLICANT: Jia, Xiao-Chi

; APPLICANT: Feng, Xiao

; APPLICANT: Yang, Xiao-Dong

; APPLICANT: Chen, Francine

; APPLICANT: Gazit, Gadi

; APPLICANT: Weber, Richard

; APPLICANT: Bezabeh, Binyam

; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES

; FILE REFERENCE: THEREOF

; CURRENT APPLICATION NUMBER: US/10/041,860

; CURRENT FILING DATE: 2002-01-07

; NUMBER OF SEQ ID NOS: 377

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 31

; LENGTH: 127

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-041-860-31

Query Match 88.2%; Score 576; DB 14; Length 127;  
Best Local Similarity 87.4%; Pred. No. 2.5e-47;  
Matches 111; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

```
Qy 1 QVQLVQSGAEVKKPGASVKSCASGYTFYSGFSGWVRQAPGQGLEWLGWISAYNGNTNY 60
Db 1 QVQLVQSGAEVKKPGASVKSCASGYTFYSGFSGWVRQAPGQGLEWLGWISAYNGNTNY 60
Qy 61 AQLQGRVTMTTDTSTAYMELSLRSDDTAVYYCARETKV-----VHYGMDVWGQ 116
Db 61 AQLQGRVTMTTDTSTAYMELSLRSDDTAVYYCARETKV-----VHYGMDVWGQ 120
Qy 117 TTVTVSS 123
Db 118 TTVTVSS 123
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```
Db      121 TTVTVSS 127

RESULT 9
US-10-041-860-243
; Sequence 243, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 243
; LENGTH: 127
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-243

Query Match      88.2%; Score 576; DB 14; Length 127;
Best Local Similarity 87.4%; Pred. No. 2.5e-47;
Matches 111; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

QY      1 QVQLVQSGAEVKKPGASVKVCKASGYTFPSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60
Db      1 QVQLVQSGAEVKKPGASVKVCKASGYTFPSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60

QY      61 AQKLGQRTVMTTDTSTSTAYMELSLRSDDTAVYYCARETKVRG-----VHYYGMDVWGQ 116
Db      61 AQKLGQRTVMTTDTSTSTAYMELSLRSDDTAVYYCARETKVRG-----VHYYGMDVWGQ 116

QY      117 TTVTVSS 123
Db      121 TTVTVSS 127

RESULT 10
US-10-041-860-325
; Sequence 325, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 325
; LENGTH: 127
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-325

Query Match      88.2%; Score 576; DB 14; Length 127;
Best Local Similarity 87.4%; Pred. No. 2.5e-47;
Matches 111; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

QY      1 QVQLVQSGAEVKKPGASVKVCKASGYTFPSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60
Db      1 QVQLVQSGAEVKKPGASVKVCKASGYTFPSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60

QY      61 AQKLGQRTVMTTDTSTSTAYMELSLRSDDTAVYYCARETKVRG-----VHYYGMDVWGQ 116
Db      61 AQKLGQRTVMTTDTSTSTAYMELSLRSDDTAVYYCARETKVRG-----VHYYGMDVWGQ 116

QY      117 TTVTVSS 123
Db      121 TTVTVSS 127

RESULT 11
US-10-665-383-42
; Sequence 42, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Gazit, Gadi
; APPLICANT: Keyt, Bruce
; APPLICANT: LaRochelelle, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; FILE REFERENCE: ABGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/411,137
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 127
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-665-383-42

Query Match      88.2%; Score 576; DB 16; Length 127;
Best Local Similarity 87.4%; Pred. No. 2.5e-47;
Matches 111; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

QY      1 QVQLVQSGAEVKKPGASVKVCKASGYTFPSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60
Db      1 QVQLVQSGAEVKKPGASVKVCKASGYTFPSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60

QY      61 AQKLGQRTVMTTDTSTSTAYMELSLRSDDTAVYYCARETKVRG-----VHYYGMDVWGQ 116
Db      61 AQKLGQRTVMTTDTSTSTAYMELSLRSDDTAVYYCARETKVRG-----VHYYGMDVWGQ 116

QY      117 TTVTVSS 123
Db      121 TTVTVSS 127

RESULT 12
US-11-031-485-42
; Sequence 42, Application US/11031485
; Publication No. US20050232917A1
; GENERAL INFORMATION:
; APPLICANT: PULLEN, NICHOLAS
; APPLICANT: MOLLOY, ELIZABETH
; APPLICANT: KELLERMANN, SIRID-AIMEE
; APPLICANT: GREEN, LARRY L.
; APPLICANT: HAAK-FRENDSCHO, MARY
; TITLE OF INVENTION: ANTIBODIES TO MAGCAM
; FILE REFERENCE: ABX-PF6
; CURRENT APPLICATION NUMBER: US/11/031,485
; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: 60/535,490
```



Db 61 AQLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYICARDEVEYYDGSYYYPDYWGQCTL 120

Qy 119 VTVSS 123

|||

Db 121 VTVSS 125

Search completed: November 9, 2005, 12:43:01  
Job time : 69.3333 secs





```
A;Reference number: S24442
A;Accession: S24442
A;Molecule type: mRNA
A;Residues: 1-40, 'G'LSGWDGSA LMTVQTOSILDK', 61-118, 'T', 120-124 <JON>
A;Cross-references: EMBL:X61647; NID:g37667; PIDN:CAA43828.1; PID:g1335368
A;Note: the difference for residues 41-60 results from misplacement of 10 bases in the s
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match      84.2%; Score 549.5; DB 2; Length 124;
Best Local Similarity 85.6%; Pred. No. 8.1e-44;
Matches 107; Conservative 5; Mismatches 10; Indels 3; Gaps 2;

QY 1 QVOLVSGAEVKKPGASVKVSKASGYTFTSYGFSWVRQAPGGGLEWLGWISAYNGNTNY 60
   |||||
Db 1 QVOLVSGAEVKKPGASVKVSKASGYTFTSYGFSWVRQAPGGGLEWLGWISAYNGNTKY 60
   |||||

QY 61 AOKLQGRVTMTTDTSTSTAYMELRSLSDDTAVYYCAR--ETKVRGVHYGYMDVMGQGIT 118
   |||||
Db 61 AOKLQGRVTMTTDTSTSTAYMELRSLSDDTAVYYCVRLLPKRTATLHY--IDVWGKGTL 119
   |||||

QY 119 VTSS 123
   |||||
Db 120 VTSS 124
   |||||

RESULT 3
S36271
IG heavy chain V region (clone alpha-THV-29) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36271
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36271
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-122 <GRI>
A;Cross-references: EMBL:Z18832; NID:g33115; PIDN:CAA79284.1; PID:g939895
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match      81.6%; Score 533; DB 2; Length 122;
Best Local Similarity 85.2%; Pred. No. 2.7e-42;
Matches 104; Conservative 3; Mismatches 13; Indels 2; Gaps 1;

QY 1 QVOLVSGAEVKKPGASVKVSKASGYTFTSYGFSWVRQAPGGGLEWLGWISAYNGNTNY 60
   |||||
Db 1 QVOLVSGAEVKKPGASVKVSKASGYTFTSYGFSWVRQAPGGGLEWLGWISAYNGNTNY 60
   |||||

QY 61 AOKLQGRVTMTTDTSTSTAYMELRSLSDDTAVYYCARETKVRGVHY--YGMVDMVGQGIT 118
   |||||
Db 61 AOKLQGRVTMTTDTSTSTAYMELRSLSDDTAVYYCAADTGRIDDFWGSYFNFDYWGQGTL 120
   |||||

QY 119 VT 120
   ||
Db 121 VT 122
   ||

RESULT 4
PL0105
anti-PR2 erythrocyte autoantibody heavy chain precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 26-Apr-1996
C;Accession: PL0105
R;Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A;Title: Relationship of variable region genes expressed by a human B cell lymphoma sec
A;Reference number: PL0106; MUID:89235583; PMID:2541221
```

```
A;Accession: PL0105
A;Molecule type: mRNA
A;Residues: 1-160 <SIL>
A;Note: the authors translated the codon GAC for residues 108 and 109 as Glu
C;Comment: The antibody is one of the cold agglutinins that preferentially bind red blo
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: autoantibody; hemagglutinin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;34-117/Domain: immunoglobulin homology <IMM>
F;49-54/Region: complementarity-determining 1
F;118-131/Domain: complementarity-determining 2
F;132-144/Domain: D region <DRG>
F;145-160/Domain: J4 segment <JSG>
F;145-160/Domain: C region <CRG>

Query Match      79.8%; Score 521; DB 2; Length 160;
Best Local Similarity 82.4%; Pred. No. 4.6e-41;
Matches 103; Conservative 3; Mismatches 17; Indels 2; Gaps 1;

QY 1 QVOLVSGAEVKKPGASVKVSKASGYTFTSYGFSWVRQAPGGGLEWLGWISAYNGNTNY 60
   |||||
Db 20 QVOLVSGAEVKKPGASVKVSKASGYTFTSYGFSWVRQAPGGGLEWLGWISAYNGDNTY 79
   |||||

QY 61 AOKLQGRVTMTTDTSTSTAYMELRSLSDDTAVYYCARETKV--RGVHYGYMDVMGQGIT 118
   |||||
Db 80 AOKLQGRVTMTTDTSTSTAYMELRSLSDDTAVYYCARAPGYCSGGCGTRGDDYWGQGTL 139
   |||||

QY 119 VTSS 123
   |||||
Db 140 VTSS 144
   |||||

RESULT 5
S26919
IG heavy chain V region (DP-14) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26919
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26919
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12316; NID:g32855; PIDN:CAA78186.1; PID:g32856
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match      76.7%; Score 501; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 1.9e-39;
Matches 95; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVOLVSGAEVKKPGASVKVSKASGYTFTSYGFSWVRQAPGGGLEWLGWISAYNGNTNY 60
   |||||
Db 1 QVOLVSGAEVKKPGASVKVSKASGYTFTSYGFSWVRQAPGGGLEWLGWISAYNGNTNY 60
   |||||

QY 61 AOKLQGRVTMTTDTSTSTAYMELRSLSDDTAVYYCAR 98
   |||||
Db 61 AOKLQGRVTMTTDTSTSTAYMELRSLSDDTAVYYCAR 98
   |||||

RESULT 6
PH1666
IG heavy chain V region (clone 6C9) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH1666
R;Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyl
```

A;Reference number: PH1642; MUID:93301610; PMID:8315388  
A;Accession: PH1666  
A;Molecule type: mRNA  
A;Residues: 1-118 <HL>  
A;Experimental source: B cell  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 74.5%; Score 486.5; DB 2; Length 118;  
Best Local Similarity 79.7%; Pred. No. 5e-38; Mismatches 15; Indels 3; Gaps 1;  
Matches 94; Conservative 6;

Qy 9 AEVKKPGASVKSCASGYTFSSYGFSGVSRQAPGQGLEWLGWISAYNGNTNYAQKQGRV 68

Db 1 AEVKKPGASVKSCASGYTFSSYGFSGVSRQAPGQGLEWLGWISAYNGNTNYAQKQGRV 60

Qy 69 TWITDTSTAYMELSLRSDDTAVYVCARETKVRGV---HYGMDVWGQTTVTVSS 123

Db 61 TITRDTASTAYMELSLRSDDTAVYVCARETKVRGV---HYGMDVWGQTTVTVSS 118

## RESULT 7

S34014  
Ig heavy chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
C;Accession: S34014; S30535  
R;Mariette, X.; Tsapis, A.; Brouet, J.C.  
Eur. J. Immunol. 23, 846-851, 1993  
A;Title: Nucleotide sequence analysis of the variable domains of four human monoclonal  
A;Reference number: S34001; MUID:93209281; PMID:7681398  
A;Accession: S34014  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-127 <MAR>  
A;Cross-references: EMBL:Z18321  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 483; DB 2; Length 127;  
Best Local Similarity 72.7%; Pred. No. 1.1e-37; Mismatches 15; Indels 6; Gaps 2;  
Matches 93; Conservative 14;

Qy 1 QVOLVSGAEVKKPGASVKSCASGYTFSSYGFSGVSRQAPGQGLEWLGWISAYNGNTNY 60

Db 1 QVOLVSGAEVKKPGASVKSCASGYTFSSYGFSGVSRQAPGQGLEWLGWISAYNGNTNY 60

Qy 61 AQKQGRVTMTTDTSTAYMELSLRSDDTAVYVCARETK-----VRGVHYGYGMDVWGQ 115

Db 61 AQKQGRVTMTTDTSTAYMELSLRSDDTAVYVCARETK-----VRGVHYGYGMDVWGQ 119

Qy 116 GTTIVTVSS 123

Db 120 GTTIVTVSS 127

## RESULT 8

S46393  
Ig heavy chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 20-Jun-2000  
C;Accession: S46393  
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.  
J. Mol. Biol. 239, 68-78, 1994  
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by  
A;Reference number: S46390; MUID:94254092; PMID:8196048  
A;Accession: S46393  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-129 <FIG>  
A;Cross-references: EMBL:Z31680; NID:g509786; PIDN:CAA83485.1; PID:g1335146

C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.7%; Score 481; DB 2; Length 129;  
Best Local Similarity 72.2%; Pred. No. 1.8e-37; Mismatches 16; Indels 14; Gaps 2;  
Matches 96; Conservative 7;

Qy 1 QVOLVSGAEVKKPGASVKSCASGYTFSSYGFSGVSRQAPGQGLEWLGWISAYNGNTNY 60

Db 1 QVOLVSGAEVKKPGASVKSCASGYTFSSYGFSGVSRQAPGQGLEWLGWISAYNGNTNY 60

Qy 61 AQKQGRVTMTTDTSTAYMELSLRSDDTAVYVCARETKVRGVHYG-----M 110

Db 61 AQKQGRVTMTTDTSTAYMELSLRSDDTAVYVCARETKVRGVHYG-----M 116

Qy 111 DVWGQTTVTVSS 123

Db 117 DVWGQTTVTVSS 129

## RESULT 9

PH0961  
Ig heavy chain V region (G6+ T-L33) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
C;Accession: PH0961  
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.  
J. Exp. Med. 175, 983-991, 1992  
A;Title: Evidence for somatic selection of natural autoantibodies.  
A;Reference number: PH0952; MUID:92202880; PMID:1552291  
A;Accession: PH0961  
A;Status: nucleic acid sequence not shown  
A;Molecule type: DNA  
A;Residues: 1-119 <MAR>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;1-30/Region: framework 1  
F;15-98/Domain: immunoglobulin homology <IMM>  
F;31-35/Region: complementarity-determining 1  
F;36-50/Region: framework 2  
F;51-67/Region: complementarity-determining 2  
F;68-98/Region: framework 3  
F;99-107/Region: complementarity-determining 3

Query Match 73.5%; Score 480; DB 2; Length 119;  
Best Local Similarity 78.0%; Pred. No. 2e-37; Mismatches 5; Indels 4; Gaps 1;  
Matches 96; Conservative 5;

Qy 1 QVOLVSGAEVKKPGASVKSCASGYTFSSYGFSGVSRQAPGQGLEWLGWISAYNGNTNY 60

Db 1 QVOLVSGAEVKKPGASVKSCASGYTFSSYGFSGVSRQAPGQGLEWLGWISAYNGNTNY 60

Qy 61 AQKQGRVTMTTDTSTAYMELSLRSDDTAVYVCARETKVRGVHYGMDVWGQTTVT 120

Db 61 AQKQGRVTMTTDTSTAYMELSLRSDDTAVYVCARETKVRGVHYGMDVWGQTTVT 116

Qy 121 VSS 123

Db 117 VSS 119

## RESULT 10

S21924  
Ig heavy chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C;Accession: S21924; S21923  
R;Friedman, D.F.  
submitted to the EMBL Data Library, July 1991  
A;Reference number: S21923  
A;Accession: S21924  
A;Status: preliminary

A;Molecule type: DNA  
A;Residues: 1-131 <FRI>  
A;Cross-references: EMBL:X60505; NID:g33565; PIDN:CAA43025.1; PID:g33566; EMBL:X60504; N  
C;Genetics:  
A;Intons: 16/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;34-117/Domain: immunoglobulin homology <IMM>  
  
Query Match 73.0%; Score 477; DB 2; Length 131;  
Best Local Similarity 91.8%; Pred. No. 4.2e-37;  
Matches 90; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
  
QY 1 QVOLVSGAEVKKPGASVKVCKASGYTFSSYGFSGFVSRQAPGGLEWLGWISAYNGNTNY 60  
DB 20 QVOLVSGAEVKKPGASVKVCKASGYTFSSYGFSGFVSRQAPGGLEWLGWISAYNGNTNY 79  
  
QY 61 AOKLQGRVTMTTDTSTAYMELSLRSDDTAVVYCAR 98  
DB 80 AOKLQGRVTMTTDTSTAYMELSLRSDDTAVVYCAR 117  
  
RESULT 11  
C33548  
Ig heavy chain V-1 region (783) - human  
C;Species: Homo sapiens (man)  
C;Date: 17-Jan-1990 #sequence\_revision 17-Jan-1990 #text\_change 16-Aug-1996  
C;Accession: C33548  
R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.  
Proc. Natl. Acad. Sci. U.S.A. 86: 5913-5917, 1989  
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr  
A;Reference number: A33548; MUID:89345575; PMID:2503826  
A;Accession: C33548  
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A;Molecule type: DNA  
A;Residues: 1-133 <KIP>  
A;Experimental source: the sequence was determined from the differentiated gene  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>  
  
Query Match 73.0%; Score 477; DB 2; Length 133;  
Best Local Similarity 72.4%; Pred. No. 4.3e-37;  
Matches 97; Conservative 7; Mismatches 18; Indels 12; Gaps 2;  
  
QY 1 QVOLVSGAEVKKPGASVKVCKASGYTFSSYGFSGFVSRQAPGGLEWLGWISAYNGNTNY 60  
DB 1 QVOLVSGAEVKKPGASVKVCKASGYTFSSYGFSGFVSRQAPGGLEWLGWISAYNGNTNY 60  
  
QY 61 AOKLQGRVTMTTDTSTAYMELSLRSDDTAVVYCAR 109  
DB 61 AOKLQGRVTMTTDTSTAYMELSLRSDDTAVVYCAR 119  
  
QY 110 MDVWGQGTITVTVSS 123  
DB 120 MDVWGQGTITVTVSS 133  
  
RESULT 12  
S14683  
Ig mu chain precursor, membrane-bound (clone 201) - human  
C;Species: Homo sapiens (man)  
C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 23-Jul-1999  
C;Accession: S14683; S08047  
R;Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.  
Nucleic Acids Res. 18, 4278, 1990  
A;Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain.  
A;Reference number: S14683; MUID:90332450; PMID:2115996  
A;Accession: S14683  
A;Molecule type: mRNA  
A;Residues: 1-627 <FRI>  
A;Cross-references: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; PID:g33451  
C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: immunoglobulin; membrane protein  
F;1-15/Domain: signal sequence #status predicted <SIG>  
F;16-627/Product: Ig mu chain #status predicted <MAT>  
F;34-117/Domain: immunoglobulin homology <IMM>  
  
Query Match 73.0%; Score 477; DB 2; Length 627;  
Best Local Similarity 72.4%; Pred. No. 2.2e-36;  
Matches 97; Conservative 7; Mismatches 18; Indels 12; Gaps 2;  
  
QY 1 QVOLVSGAEVKKPGASVKVCKASGYTFSSYGFSGFVSRQAPGGLEWLGWISAYNGNTNY 60  
DB 20 QVOLVSGAEVKKPGASVKVCKASGYTFSSYGFSGFVSRQAPGGLEWLGWISAYNGNTNY 79  
  
QY 61 AOKLQGRVTMTTDTSTAYMELSLRSDDTAVVYCAR 109  
DB 80 AOKLQGRVTMTTDTSTAYMELSLRSDDTAVVYCAR 138  
  
QY 110 MDVWGQGTITVTVSS 123  
DB 139 MDVWGQGTITVTVSS 152  
  
RESULT 13  
PH0960  
Ig heavy chain V region (G6+ T-130) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
C;Accession: PH0960  
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.  
J. Exp. Med. 175, 983-991, 1992  
A;Title: Evidence for somatic selection of natural autoantibodies.  
A;Reference number: PH0952; MUID:92202880; PMID:1552291  
A;Accession: PH0960  
A;Status: nucleic acid sequence not shown  
A;Molecule type: DNA  
A;Residues: 1-136 <MAR>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;1-30/Region: framework 1  
F;15-98/Domain: immunoglobulin homology <IMM>  
F;31-35/Region: complementarity-determining 1  
F;36-50/Region: framework 2  
F;51-67/Region: complementarity-determining 2  
F;68-98/Region: framework 3  
F;99-124/Region: complementarity-determining 3  
  
Query Match 72.8%; Score 475.5; DB 2; Length 136;  
Best Local Similarity 72.8%; Pred. No. 6e-37;  
Matches 99; Conservative 6; Mismatches 18; Indels 13; Gaps 3;  
  
QY 1 QVOLVSGAEVKKPGASVKVCKASGYTFSSYGFSGFVSRQAPGGLEWLGWISAYNGNTNY 60  
DB 1 QVOLVSGAEVKKPGASVKVCKASGYTFSSYGFSGFVSRQAPGGLEWLGWISAYNGNTNY 60  
  
QY 61 AOKLQGRVTMTTDTSTAYMELSLRSDDTAVVYCAR 107  
DB 61 AOKLQGRVTMTTDTSTAYMELSLRSDDTAVVYCAR 120  
  
QY 108 YGMDVWGQGTITVTVSS 123  
DB 121 YGMDVWGQGTITVTVSS 136  
  
RESULT 14  
PH0954  
Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
C;Accession: PH0954  
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.  
J. Exp. Med. 175, 983-991, 1992  
A;Title: Evidence for somatic selection of natural autoantibodies.  
A;Reference number: PH0952; MUID:92202880; PMID:1552291



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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	501	76.7	500	2	Q6N091	Q6n091 homo sapien
2	490.5	75.1	159	2	Q96QSO	Q96q80 homo sapien
3	474	72.6	244	2	Q65ZC8	Q65zcr homo sapien
4	472.5	72.4	500	2	Q9BRV0	Q9brv0 homo sapien
5	469.5	71.9	469	2	Q727P5	Q727p5 homo sapien
6	464	71.1	125	2	Q9UL95	Q9ul95 homo sapien
7	453	69.4	119	2	Q9UL94	Q9ul94 homo sapien
8	450.5	69.0	124	2	Q9UL92	Q9ul92 homo sapien
9	449.5	68.8	147	1	HVIC HUMAN	P01744 homo sapien
10	440.5	67.5	518	2	Q6N030	Q6n030 homo sapien
11	438.5	67.2	498	2	Q6N041	Q6n041 homo sapien
12	436	66.8	119	2	Q9GY22	Q9gy22 schistosoma
13	419.5	64.2	116	2	Q9UL89	Q9ul89 homo sapien
14	417	63.9	480	2	Q6P089	Q6p089 homo sapien
15	417	63.9	480	2	Q6PJF1	Q6pjf1 homo sapien
16	416	63.7	497	2	Q8WY24	Q8wy24 homo sapien
17	415	63.6	117	1	HV1B HUMAN	P01743 homo sapien
18	412	63.1	208	2	Q62P87	Q62p87 homo sapien
19	409.5	62.7	465	2	Q6PJB2	Q6pjb2 mus musculus
20	409	62.6	120	1	HV03 MOUSE	P01747 mus musculus
21	408	62.5	140	1	HV02_MOUSE	P01746 mus musculus
22	406.5	62.3	143	2	Q924P9	Q924p9 mus musculus
23	405	62.0	120	2	Q6NSA4	Q6nsa4 homo sapien
24	404	61.9	117	1	HV1G HUMAN	P23083 homo sapien
25	403.5	61.8	145	2	Q924Q6	Q924q6 mus musculus
26	402.5	61.6	475	2	Q6N095	Q6n095 homo sapien
27	398.5	61.0	613	2	Q8VCX7	Q8vcx7 mus musculus
28	396	60.6	117	2	Q9QXE9	Q9qxe9 mus musculus
29	396	60.6	142	2	Q924Q1	Q924q1 mus musculus
30	393.5	60.3	241	2	Q921A6	Q921a6 mus musculus
31	391	59.9	134	2	Q65ZR6	Q65zr6 mus musculus

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RESULT 2
Q96QSO PRELIMINARY; PRT; 159 AA.
ID Q96QSO
AC Q96QSO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative matrix cell adhesion molecule-3.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tilson M.D.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY039025; AAK82649.1; -.
DR HSSP; P01869; IAE6
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 159 AA; 17497 MW; 5D29537B881FAF02 CRC64;

Query Match 75.1%; Score 490.5; DB 2; Length 159;
Best Local Similarity 72.3%; Pred. No. 2.1e-44;
Matches 94; Conservative 13; Mismatches 16; Indels 7; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFPSYGFVSVVRQAPGGQLEWLGWISAYNGTNY 60
D 20 QVQLVQSGAEVKKPGASVKVSKASGYTFPSYGFVSVVRQAPGGQLEWLGWISAYNGTNY 79
QY 61 AQKLQGRVTMTDTSTSTAYMELRSDDTAVVYCARETKV-----RGVHYGMDVW 113
D 80 SQKFGQLTMTDRTSTSTVYMDLSRLSDDTAVVYFCAREMEITFGGAVSKGFFYYGMDVW 139
QY 114 GQGTITVTVSS 123
D 140 GQGTITVTVSS 149

RESULT 3
Q65ZC8 PRELIMINARY; PRT; 244 AA.
ID Q65ZC8
AC Q65ZC8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name-scFv;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kontermann R.E., Wing M.G., Winter G.;
RL "Complement recruitment using bispecific diabodies.";
DR Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13057; CAA73500.1; -.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
FT NON_TER 244 244
SQ SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;

Query Match 72.6%; Score 474; DB 2; Length 244;
Best Local Similarity 71.1%; Pred. No. 6.3e-42;
Matches 91; Conservative 10; Mismatches 22; Indels 5; Gaps 1;

Best Local Similarity 75.6%; Pred. No. 2e-42;
Matches 93; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFPSYGFVSVVRQAPGGQLEWLGWISAYNGTNY 60
D 1 QVQLVQSGAEVKKPGASVKVSKASGYTFSDHYMHVVRQAPGGQLEWLGWISAYNGTNY 60
QY 61 AQKLQGRVTMTDTSTSTAYMELRSDDTAVVYCARETKVGRVHYHYGMDVWGQGTITVT 120
D 61 AQKFGQGRVTMTDRTSTISAAAYMEVRLSDDTAVVYCAREG--TGSAIYGMVDMVGQGTITVT 118
QY 121 VSS 123
D 119 VSS 121

RESULT 4
Q9BRV0 PRELIMINARY; PRT; 500 AA.
ID Q9BRV0
AC Q9BRV0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC27165 protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RL "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005951; AAK05951.1; -.
DR HSSP; P01876; IOW0.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

Query Match 72.4%; Score 472.5; DB 2; Length 500;
Best Local Similarity 71.1%; Pred. No. 6.3e-42;
Matches 91; Conservative 10; Mismatches 22; Indels 5; Gaps 1;
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QY 1 QVOLVSGAEVKKPGASVKVSCKASGYTFYFGFVSWVRQAPGQGLEWIGWISAYNGNTNY 60
|||
DB 20 QVHLVSGAEVMSFGASVRVSKTSGYAFHTYISIIWVRQAPGQGLEWIGWISPSDDTRP 79
|||
QY 61 AQKLGQVMTTDTSTSTAYMELSLRSDDTAVYYCAR-----ETKVRGVHYYGMDVWGQ 115
|||
DB 80 AKFPQGRVTLTDTSTSTVYVMEVLSRLSDDTAVYYCARRYSYSSCQNDYYYYMDVWGK 139
|||
QY 116 GTTVTVSS 123
|||
DB 140 GTTVTVSS 147
|||
RESULT 5
Q727P5 PRELIMINARY; PRT; 469 AA.
AC Q727P5
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGH1 protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051328; AAH51328.1;
DR HSSP; P01857; 1HZH.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;
Query Match 71.9%; Score 469.5; DB 2; Length 469;
Best Local Similarity 74.8%; Pred. No. 1.2e-41;
Matches 92; Conservative 9; Mismatches 19; Indels 3; Gaps 2;
QY 1 QVOLVSGAEVKKPGASVKVSCKASGYTFYFGFVSWVRQAPGQGLEWIGWISAYNGNTNY 60
|||
DB 20 QVHLVSGAEVMSFGASVRVSKTSGYAFHTYISIIWVRQAPGQGLEWIGWISPSDDTRP 79
|||
QY 61 AQKLGQVMTTDTSTSTAYMELSLRSDDTAVYYCAR-----ETKVRGVHYYGMDVWGQ 115
|||
DB 80 AKFPQGRVTLTDTSTSTVYVMEVLSRLSDDTAVYYCARRYSYSSCQNDYYYYMDVWGK 139
|||
QY 116 GTTVTVSS 123
|||
DB 140 GTTVTVSS 147
|||
RESULT 6
Q9UL95 PRELIMINARY; PRT; 125 AA.
AC Q9UL95
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035019; AAD56255.1;
DR HSSP; P01751; INQB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR NON_TER; 1
FT NON_TER 125
SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;
Query Match 71.1%; Score 464; DB 2; Length 125;
Best Local Similarity 72.8%; Pred. No. 1.1e-41;
Matches 91; Conservative 9; Mismatches 23; Indels 2; Gaps 1;
QY 1 QVOLVSGAEVKKPGASVKVSCKASGYTFYFGFVSWVRQAPGQGLEWIGWISAYNGNTNY 60
|||
DB 1 EVQLVESGAEVKKPGASVKVSCKASGYTFYFGFVSWVRQAPGQGLEWIGWISAYNGNTNY 60
|||
QY 61 AQKLGQVMTTDTSTSTAYMELSLRSDDTAVYYCAR-----ETKVRGVHYYGMDVWGQ 118
|||
DB 61 AQKLGQVMTTDTSTSTAYMELSLRSDDTAVYYCAR-----ETKVRGVHYYGMDVWGQ 118
|||
QY 119 VTVSS 123
|||
DB 121 VTVSS 125
|||
RESULT 7
Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
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RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetuses";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035020; AAD56256.1; -;  
DR HSSP; P01751; INQB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
FT NON\_TER 1 1  
FT NON\_TER 119 119  
SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345F4A16E CRC64;  
  
Query Match 69.4%; Score 453; DB 2; Length 119;  
Best Local Similarity 74.0%; Pred. No. 1.6e-40;  
Matches 91; Conservative 8; Mismatches 20; Indels 4; Gaps 2;  
  
QY 1 QVQLVSGAEVKKPGASVKVSCKASGYTFYFSGFSWVRQAPGQGLEWLGWISAYNGNTNY 60  
Db 1 EVQLVESGAEVKKPGASVKVSCKASGYTFGYTHHVRQAPGQGLEWMGWINPNSWTNY 60  
  
QY 61 AQKLGQGRVTMTTDTSTSTAYMELSLRSDTAVYVCARETKVRGVH-----YGMVDVWG 114  
Db 61 AQKFGQGRVTMTDRTSTSTAYMELSLRSDTAVYCA-----RGLVYVVVPAAPSRFDYWG 115  
  
QY 121 VSS 123  
Db 117 VSS 119

RESULT 8  
Q9UL92 PRELIMINARY; PRT; 124 AA.  
AC Q9UL92;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
(Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetuses";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035022; AAD56258.1; -;  
DR HSSP; P01751; INQB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
FT NON\_TER 1 1  
FT NON\_TER 124 124  
SQ SEQUENCE 124 AA; 13580 MW; 1BAACB9D6ACD2A2 CRC64;  
  
Query Match 69.0%; Score 450.5; DB 2; Length 124;  
Best Local Similarity 70.5%; Pred. No. 3.1e-40;  
Matches 91; Conservative 10; Mismatches 17; Indels 11; Gaps 2;  
  
QY 1 QVQLVSGAEVKKPGASVKVSCKASGYTFYFSGFSWVRQAPGQGLEWLGWISAYNGNTNY 60  
Db 1 EVQLVESGAEVKKPGASVKVSCKASGYTFSSYYHHVRQAPGQGLEWMGINPFGGTSY 60

QY 61 AQKLGQGRVTMTTDTSTSTAYMELSLRSDTAVYVCARETKVRGVH-----YGMVDVWG 114  
Db 61 AQKFGQGRVTMTDRTSTSTAYMELSLRSDTAVYCA-----RGLVYVVVPAAPSRFDYWG 115  
  
QY 115 QGTITVTSS 123  
Db 116 QGTITVTSS 124  
  
RESULT 9  
HV1C HUMAN STANDARD; PRT; 147 AA.  
ID HV1C HUMAN  
AC P01744;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ig heavy chain V-I region ND precursor (Fragments).  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83065234; PubMed=6815656;  
Kanten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,  
Bell L.O., Gould H.J.;  
RA "Cloning and sequence determination of the gene for the human  
immunoglobulin epsilon chain expressed in a myeloma cell line.";  
RT Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).  
RN [2]  
RP SEQUENCE OF 20-147.  
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;  
RL (in) Bach M.K. (eds.);  
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,  
Marcel Dekker, New York (1978).  
CC -I- MISCELLANEOUS: This epsilon chain was isolated from a myeloma  
protein.  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR HSSP; P01751; INQB.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin V region;  
KW Pyridolone carboxylic acid; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 147 Ig heavy chain V-I region ND.  
FT DOMAIN 20 131 Ig-like.  
FT MOD\_RES 20 20 Pyridolone carboxylic acid.  
FT DISULFID 41 115  
FT CONFLICT 21 21 T -> V (in Ref. 2).  
FT CONFLICT 53 54 IH -> HI (in Ref. 2).  
FT CONFLICT 67 68 IH -> GV (in Ref. 2).  
FT CONFLICT 125 125 Missing (in Ref. 2).  
FT NON\_TER 147 147  
SQ SEQUENCE 147 AA; 16491 MW; 948P9F72A5366C20 CRC64;

Query Match 68.8%; Score 449.5; DB 1; Length 147;  
Best Local Similarity 67.2%; Pred. No. 4.8e-40;  
Matches 86; Conservative 13; Mismatches 24; Indels 5; Gaps 1;  
  
QY 1 QVQLVSGAEVKKPGASVKVSCKASGYTFYFSGFSWVRQAPGQGLEWLGWISAYNGNTNY 60  
Db 20 QVQLVSGAEVKKPGASVKVSCKASGYTFIDSVIHWIRQAPGQGLEWMINPNSGNTNY 79  
  
QY 61 AQKLGQGRVTMTTDTSTSTAYMELSLRSDTAVYVCARETKVRGVH-----YGMVDVWG 115  
Db 80 APRFGQGRVTMTDASPTAYMDLSRSDSAVFYCAKSPDPSYDFSYTLDDVWG 139  
  
QY 116 GTITVTSS 123

```

Db      140 GTTIVTSS 147
|||||
RESULT 10
Q6N030 PRELIMINARY; PRT; 518 AA.
ID Q6N030
AC Q6N030;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686l15212.
GN Name=DKFZp686l15212;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640724; CAE45841.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR000005; HTHAcC.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein_
FT NON_TER 1
SQ SEQUENCE 518 AA; 57019 MW; 93B5F98613BF6382 CRC64;

Query Match 67.5%; Score 440.5; DB 2; Length 518;
Best Local Similarity 69.9%; Pred. No. 1.8e-38;
Matches 86; Conservative 13; Mismatches 23; Indels 1; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFYSGFSGVVRQAPGQGLEWLGWISAYNGNTNY 60
Db 20 QVHLVQSGAEVKKPGASVKVSCTASGYTFNHFINWVRQAPGQGLEWGWINTGNGNTKY 79
|||||
Qy 61 AQKLQGRVTMTDTSTAYMELRLSRDSDTAVVYCARETKVRG--VHYIGMDVWGQTTVT 120
Db 80 SQKFGQGVITRTDTTWTAYMDLSSLSASEDTAVVYWCARDAP-QGVTTTYFDYWGQGLT 138
|||||
Qy 121 VSS 123
Db 139 VSS 141
|||||
RESULT 11
Q6N041 PRELIMINARY; PRT; 498 AA.
ID Q6N041
AC Q6N041;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686O16217 (Fragment).
GN Name=DKFZp686O16217;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640724; CAE45841.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR000005; HTHAcC.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein_
FT NON_TER 1
SQ SEQUENCE 518 AA; 57019 MW; 93B5F98613BF6382 CRC64;

Query Match 67.5%; Score 440.5; DB 2; Length 518;
Best Local Similarity 69.9%; Pred. No. 1.8e-38;
Matches 86; Conservative 13; Mismatches 23; Indels 1; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFYSGFSGVVRQAPGQGLEWLGWISAYNGNTNY 60
Db 20 QVHLVQSGAEVKKPGASVKVSCTASGYTFNHFINWVRQAPGQGLEWGWINTGNGNTKY 79
|||||
Qy 61 AQKLQGRVTMTDTSTAYMELRLSRDSDTAVVYCARETKVRG--VHYIGMDVWGQTTVT 120
Db 80 SQKFGQGVITRTDTTWTAYMDLSSLSASEDTAVVYWCARDAP-QGVTTTYFDYWGQGLT 138
|||||
Qy 121 VSS 123
Db 139 VSS 141
|||||
SEQUENCE FROM N.A.
RP TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640710; CAE45829.1; -.
DR HSSP; P01751; IAGW.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 498 AA; 54125 MW; 40B3208A84E03B46 CRC64;

Query Match 67.2%; Score 438.5; DB 2; Length 498;
Best Local Similarity 70.4%; Pred. No. 2.8e-38;
Matches 88; Conservative 12; Mismatches 22; Indels 3; Gaps 2;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFYSGFSGVVRQAPGQGLEWLGWISAYNGNTNY 60
Db 35 QVQLVQSGADVKKPGASVKVSCKASGYTFNTPFHWVRQAPGQGPWGMINPRDGSSTKY 94
|||||
Qy 61 AQKLQGRVTMTDTSTAYMELRLSRDSDTAVVYCARETKVRG--VHYIGMDVWGQTT 118
Db 95 AQRFGQGVSMTRDTSTIYMWLSSLSASEDTAMFFCARAGPGYGTSSAY--FDYWGQGL 153
|||||
Qy 119 VTVSS 123
Db 154 VTVSS 158
|||||
RESULT 12
Q9GYZ2 PRELIMINARY; PRT; 119 AA.
ID Q9GYZ2
AC Q9GYZ2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 heavy chain variable region (Fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
SEQUENCE FROM N.A.
RP Song X.T., Feng X.O., Guan X.H.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282622; AAG01452.1; -.
DR HSSP; P01751; IAGW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13567 MW; BA893873FDSFA6AB CRC64;

Query Match 66.8%; Score 436; DB 2; Length 119;
Best Local Similarity 69.9%; Pred. No. 1.1e-38;
Matches 86; Conservative 12; Mismatches 21; Indels 4; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFYSGFSGVVRQAPGQGLEWLGWISAYNGNTNY 60
|||||

```

Db 1 QVOLVSGAEVRKPGASVVRKSCASGYTFTGYMWNVRQAPGCHLEWIGYINPSRGYTNV 60

QY 61 AQKLGQRVTMTTDTSTSTAYMELSLRSDTAVYYCARETKVRGVHYGMDVWGQGTVT 120

Db 61 NQKFKDRVTMTTDTKSFSTAYMDLSRLSADSASVVCARYVD---DHYCLDYGWQGTVT 116

QY 121 VSS 123

Db 117 VSS 119

#### RESULT 13

Q9UL89 PRELIMINARY; PRT; 116 AA.

AC Q9UL89; 05-JUL-2004 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Myosin-reactive immunoglobulin heavy chain variable region

DE (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=9827139; PubMed=9614934; DOI=10.1006/clin.1998.4531;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Bernay S.M.,

RA Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RT fetus";

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL; AF03025; AAD56261.1; -.

DR PIR; PH0870; PH0870.

DR PIR; PH1671; PH1671.

DR HSP; P01751; INQB.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig\_v.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PSS0835; IG\_LIKE; 1.

FT NON\_TER 1

FT SEQUENCE 116 AA; 12605 MW; C8F9131DE13EA898 CRC64;

Query Match 64.2%; Score 419.5; DB 2; Length 116;

Best Local Similarity 72.3%; Pred. No. 6e-37;

Matches 86; Conservative 8; Mismatches 22; Indels 3; Gaps 2;

QY 5 VQSGAEVKKPGASVKVSCKASGYTFPSYGFSSVRQAPGQGLEWLGWISAYNGNTYAOKL 64

Db 1 VQSGAEVKKPGSSVKVSCKASGDTFSSYAISSVRQAPGQGLEWGRIPILGIANYAQKF 60

QY 65 QGRVTMTTDTSTSTAYMELSLRSDTAVYYCARETKVRGVHYGMDVWGQGTVT 123

Db 61 QGRVTITADKSTSTAYMELSLRSDTAVYYCASSN--WGPIWY-PDLWGRGLTVTVSS 116

#### RESULT 14

Q6P089

AC Q6P089 PRELIMINARY; PRT; 480 AA.

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Glandular pool- thyroid;

RE MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Glandular pool- thyroid;

RA Strausberg R.;

RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC065733; AAH65733.1; -.

DR HSP; P01751; IA6W.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig\_c1.

DR InterPro; IPR003006; IG\_MHC.

DR InterPro; IPR003596; IG\_v.

DR Pfam; PF07654; C1-set; 2.

DR SMART; SM00409; IG; 4.

DR SMART; SM00407; IGC1; 3.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PSS0835; IG\_LIKE; 4.

DR PROSITE; PSS00290; IG\_MHC; UNKNOWN\_2.

KW Hypothetical protein.

SQ SEQUENCE 480 AA; 51997 MW; 2E286C57E4F0ED65 CRC64;

Query Match 63.9%; Score 417; DB 2; Length 480;

Best Local Similarity 68.3%; Pred. No. 5.3e-36;

Matches 84; Conservative 9; Mismatches 28; Indels 2; Gaps 1;

QY 1 QVOLVSGAEVRKPGASVKVSCKASGYTFPSYGFSSVRQAPGQGLEWLGWISAYNGNTNY 60

Db 20 QVOLVSGAEVRKPGASVKVSCKASGYTFPSYGFSSVRQAPGQGLEWMAIRPQNGTVS 79

QY 61 AQKLGQRVTMTTDTSTSTAYMELSLRSDTAVYYCARETKVRGVHYGMDVWGQGTVT 120

Db 80 AEKFGQVRVTITDTSNTAYMELTSLKSDDTALYYCARGHSDWSSYF--DYWGQGLTVT 137

QY 121 VSS 123

Db 138 VSS 140

#### RESULT 15

Q6PJF1

ID Q6PJF1 PRELIMINARY; PRT; 480 AA.

AC Q6PJF1; 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;

RA	MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.D., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hales S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skalsood U., Smailus D.E., Schnerch A., Schein J.E.,
RA	Jones S.J., Marra M.A.;
RA	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences.";
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RA	[2]
RA	SEQUENCE FROM N.A.
RC	TISSUE=Lung.
RA	Strausberg R.;
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RL	EMBL; BC016381; AAH16381.1; -.
DR	HSSP; P01861; 1ADQ.
DR	InterPro; IPR003599; Ig.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003597; Ig_c1.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF07654; C1-set; 3.
DR	SMART; SM00409; Ig; 2.
DR	SMART; SM00407; Igcl; 3.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS50835; IG-LIKE; 4.
DR	PROSITE; PS00290; IG MHC; UNKNOWN_2.
SW	Hypothetical protein.
SK	SEQUENCE 480 AA: 52586 MW: 64DC641AE47CD6C8 CRC64:

(also) 11/17/19 11/17/19

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:43:32 ; Search time 73.3684 Seconds  
(without alignments)  
627.306 Million cell updates/sec

Title: US-10-660-357A-25

Perfect score: 636

Sequence: 1 QVQLQESGPGLVKPSQTL...DRETAGDYWGQGLTVTVSS 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 396760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_16Dec04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003as:\*
- 7: Geneseq2003bs:\*
- 8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	636	100.0	119	7	ADQ9796 Anti-huma
2	636	100.0	119	7	ADQ9796 Anti-MUC1
3	636	100.0	119	7	ADQ9796 Human ant
4	561	88.2	117	7	ADQ9784 Anti-huma
5	561	88.2	117	7	ADQ9784 Anti-MUC1
6	561	88.2	117	7	ADQ9784 Human ant
7	558	87.7	122	4	AAB62765 Human HIV
8	554.5	87.2	123	4	AAB62745 Human HIV
9	553.5	87.0	118	7	ADQ9796 Murine-ex
10	552	86.8	123	7	ADQ9796 Murine-ex
11	551	86.6	119	7	ADQ9796 Murine-ex
12	549	86.3	123	7	ADQ9796 Murine-ex
13	549	86.3	123	7	ADQ9796 Murine-ex
14	548	86.2	120	4	AAB62775 Human HIV
15	547.5	86.1	121	7	ADQ9796 Antibody
16	547	86.0	119	7	ADQ9796 Murine-ex
17	547	86.0	446	8	ADK52356 Human ant
18	546.5	85.9	120	7	ADQ9796 Murine-ex
19	546.5	85.9	120	7	ADQ9796 Murine-ex
20	545.5	85.8	252	5	ADP45983 Human Bly
21	545.5	85.8	252	7	ADG96810 Single ch
22	545	85.7	119	2	AAR30143 MAB GAH v
23	545	85.7	119	6	ABP98691 Human GAH
24	545	85.7	119	6	ABP98683 Human GAH
25	545	85.7	119	7	ADG43869 Human pro

## ALIGNMENTS

### RESULT 1

ADQ9796  
ID ADC9796 standard; protein; 119 AA.

XX AC ADC9796;

XX AC ADC9796;

DT 01-JAN-2004 (first entry)

XX DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 25.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
KW cytotaxtic; melanoma; oesophageal; pancreatic; colorectal tumour;  
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
KW lung cancer; human.

XX OS Homo sapiens.

XX WC2003057838-A2.

XX PD 17-JUL-2003.

XX PF 26-DEC-2002; 2002MO-US041581.

XX PR 28-DEC-2001; 2001US-0346299P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J;

XX DR WPI; 2003-587113/55.

XX DR N-PSDB; ADC9798.

XX PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
or condition associated with expression of MUC18 in a patient, e.g.  
tumors, cancers, and other malignancies.

XX PS Claim 1; SEQ ID NO 25; 78pp; English.

XX CC The invention relates to a novel isolated monoclonal antibody comprising  
a heavy or light chain amino acid or a heavy or light chain variable  
domain where the antibody binds to MUC18. The monoclonal antibody of the  
invention demonstrates cytostatic activity and may be useful for treating  
a disease or condition associated with the expression of MUC18 on the  
cell surface such as tumours, specifically melanoma, oesophageal,  
pancreatic or colorectal tumours, carcinomas, particularly cervical  
carcinomas and cervical intraepithelial neoplasia and cancers including  
colorectal, breast or lung cancer, as well as other malignancies. The  
current sequence is that of the anti-human MUC18 monoclonal antibody

26	545	85.7	119	8	ADQ28266	Adq28266 Method of
27	545	85.7	127	7	ADP03874	Adp03874 Murine-ex
28	544.5	85.6	124	7	ADP03935	Adp03935 Murine-ex
29	544	85.5	123	2	AAW78433	Aaw78433 Antibody
30	544	85.5	123	5	ABB97976	Abb97976 Heavy cha
31	544	85.5	123	5	ADG88414	Adg88414 anti-Ob-R
32	542	85.2	117	7	ADC99776	Adc99776 Anti-huma
33	542	85.2	117	7	ADD05380	Add05380 Anti-MUC1
34	542	85.2	117	7	ADF09818	Adf09818 Human ant
35	542	85.2	123	7	ADP03869	Adp03869 Murine-ex
36	541.5	85.1	122	7	ADP03977	Adp03977 Murine-ex
37	541	85.1	125	7	ADP03871	Adp03871 Murine-ex
38	540	84.9	121	7	ADP03982	Adp03982 Murine-ex
39	540	84.9	125	7	ADP03868	Adp03868 Murine-ex
40	540	84.9	125	7	ADP03876	Adp03876 Murine-ex
41	540	84.9	129	5	AAU81275	Aau81275 Human trk
42	540	84.9	129	5	AAU81276	Aau81276 Human trk
43	540	84.9	251	6	ABJ19829	Abj19829 Human VEG
44	540	84.9	251	8	ADH13871	Adh13871 Human vas
45	539.5	84.8	120	7	ADP03969	Adp03969 Murine-ex

CC heavy chain protein of the invention.

XX  
SQ Sequence 119 AA;

Query Match 100.0%; Score 636; DB 7; Length 119;

Best Local Similarity 100.0%; Pred. No. 1.1e-48; Mismatches 0; Indels 0; Gaps 0;

Matches 119; Conservative 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKLEWIGIYSSGSTY 60

DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKLEWIGIYSSGSTY 60

QY 61 YNP SLKSRITLSVDTSKNQFSLKNSMTAADTAVYYCARDRETAGFDYWGQGTLTIVSS 119

DB 61 YNP SLKSRITLSVDTSKNQFSLKNSMTAADTAVYYCARDRETAGFDYWGQGTLTIVSS 119

RESULT 2

ADD05400

ID ADD05400 standard; protein; 119 AA.

XX

AC ADD05400;

DT 01-JAN-2004 (first entry)

XX

DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 25.

XX monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;

KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.

XX

OS Homo sapiens.

XX

PN WO2003057006-A2.

XX

PD 17-JUL-2003.

XX

PF 26-DEC-2002; 2002WO-US041582.

XX

PR 28-DEC-2001; 2001US-0346460P.

XX

PA (ABGE-) ABGENIX INC.

XX

PI Gudas J, Bar-Eli M;

XX

DR WPI; 2003-577496/54.

XX

DR N-PSDB; ADD05402.

XX

PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion

PT associated with melanoma, or increasing survival of an animal having a

PT metastatic tumor.

XX

PS Claim 1; SEQ ID NO 25; 87pp; English.

XX

CC The invention relates to a novel monoclonal antibody used for inhibiting

CC tumour growth in an animal. The tumour inhibition process comprises

CC selecting an animal in need of treatment for a tumour, providing a

CC monoclonal antibody comprising a heavy chain amino acid, where the

CC antibody consists of any one of 10 fully defined sequences of 117-123

CC amino acids given in the specification, and where the monoclonal antibody

CC binds MUC18, and contacting the tumour with the antibody resulting in

CC inhibited proliferation of the cells. The monoclonal antibody has

CC cytostatic and can be used in the production of a vaccine. The monoclonal

CC antibodies against the MUC18 antigen are useful for diagnosing and

CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or

CC tumour metastasis), inhibiting cell invasion associated with melanoma, or

CC increasing survival of an animal having a metastatic tumour. This

CC sequence represents an anti-MUC18 antibody heavy chain, variable region,

CC protein of the invention.

XX

XX Sequence 119 AA;

XX Query Match 100.0%; Score 636; DB 7; Length 119;

Best Local Similarity 100.0%; Pred. No. 1.1e-48; Mismatches 0; Indels 0; Gaps 0;

Matches 119; Conservative 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKLEWIGIYSSGSTY 60

DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKLEWIGIYSSGSTY 60

QY 61 YNP SLKSRITLSVDTSKNQFSLKNSMTAADTAVYYCARDRETAGFDYWGQGTLTIVSS 119

DB 61 YNP SLKSRITLSVDTSKNQFSLKNSMTAADTAVYYCARDRETAGFDYWGQGTLTIVSS 119

RESULT 3

ADF09838

ID ADF09838 standard; protein; 119 AA.

XX

AC ADF09838;

XX

DT 12-FEB-2004 (first entry)

XX

DE Human anti-MUC18 monoclonal antibody heavy chain #7.

XX

KW cell proliferation inhibition; MUC18 tumour antigen;

KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;

KW carcinoma; cancer; malignancy; heavy chain; human.

XX

OS Homo sapiens.

XX

PN WO2003057837-A2.

XX

PD 17-JUL-2003.

XX

PF 26-DEC-2002; 2002WO-US041580.

XX

PR 28-DEC-2001; 2001US-0346414P.

XX

PA (ABGE-) ABGENIX INC.

XX

PI Gudas J;

XX

DR WPI; 2003-598367/56.

DR N-PSDB; ADF09840.

XX

XX

PT Inhibiting cell proliferation associated with expression of MUC18 tumor

PT antigen, involves incubating and inhibiting cell by administering anti-

PT MUC18 monoclonal antibody.

XX

PS Claim 1; SEQ ID NO 25; 83pp; English.

XX

CC The invention comprises a method for inhibiting cell proliferation

CC associated with expression of MUC18 tumour antigen. The method involves

CC administering anti-MUC18 monoclonal antibody. The method of the invention

CC is useful for inhibiting cell (e.g. melanoma or tumour cell)

CC proliferation associated with the expression of MUC18 tumour antigen, the

CC method is preferably useful for inhibiting tumour metastasis. The method

CC is useful for inhibiting cell proliferation in patients with tumours,

CC carcinomas, cancer and other malignancies. The present amino acid

CC sequence represents a heavy chain from an MUC18 tumour antigen-specific

CC monoclonal antibody.

XX

SQ Sequence 119 AA;

XX

XX Query Match 100.0%; Score 636; DB 7; Length 119;

XX Best Local Similarity 100.0%; Pred. No. 1.1e-48;

XX Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKLEWIGIYSSGSTY 60

DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKLEWIGIYSSGSTY 60

QY 61 YNP SLKSRITLSVDTSKNQFSLKNSMTAADTAVYYCARDRETAGFDYWGQGTLTIVSS 119

DB 61 YNP SLKSRITLSVDTSKNQFSLKNSMTAADTAVYYCARDRETAGFDYWGQGTLTIVSS 119



RESULT 4  
 ID ADC99784 standard; protein; 117 AA.  
 XX  
 AC ADC99784;  
 DT 01-JAN-2004 (first entry)  
 XX  
 DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 13.  
 XX  
 KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
 KW cytosolic; melanoma; oesophageal; pancreatic; colorectal tumour;  
 KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
 KW lung cancer; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003057838-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 26-DEC-2002; 2002WO-US041581.  
 XX  
 PR 28-DEC-2001; 2001US-0346299P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Gudas J;  
 XX  
 DR WPI; 2003-587113/55.  
 DR N-PSDB; ADC99786.  
 XX  
 PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
 PT or condition associated with expression of MUC18 in a patient, e.g.  
 PT tumors, cancers, and other malignancies.  
 XX  
 PS Claim 1; SEQ ID NO 13; 78pp; English.  
 XX  
 CC The invention relates to a novel isolated monoclonal antibody comprising  
 CC a heavy or light chain amino acid or a heavy or light chain variable  
 CC domain where the antibody binds to MUC18. The monoclonal antibody of the  
 CC invention demonstrates cytostatic activity and may be useful for treating  
 CC a disease or condition associated with the expression of MUC18 on the  
 CC cell surface such as tumours, specifically melanoma, oesophageal,  
 CC pancreatic or colorectal tumours, carcinomas, particularly cervical  
 CC carcinomas and cervical intraepithelial neoplasia and cancers including  
 CC colorectal, breast or lung cancer, as well as other malignancies. The  
 CC current sequence is that of the anti-human MUC18 monoclonal antibody  
 CC heavy chain protein of the invention.  
 XX  
 SQ Sequence 117 AA;  
 Query Match 88.2%; Score 561; DB 7; Length 117;  
 Best Local Similarity 88.2%; Pred. No. 4.9e-42;  
 Matches 105; Conservative 9; Mismatches 3; Indels 2; Gaps 1;  
 QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSINSGCCYWSWIQHPKGLIEWIGFIYSGSTY 60  
 Db 1 QVQLQESGPGLVKPSQTLSTCTVSGSINSGCCYWSWIQHPKGLIEWIGFIYSGSTY 60  
 QY 61 YNPSLKSRITLSVDTSKNQPSLKLNSMTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 119  
 Db 61 YNPSLKSRVITISVDTSKNQPSLKLSSVTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 117  
 RESULT 5  
 ID ADD05388 standard; protein; 117 AA.  
 XX  
 AC ADD05388;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human anti-MUC18 monoclonal antibody heavy chain #4.  
 XX  
 KW cell proliferation inhibition; MUC18 tumour antigen;

01-JAN-2004 (first entry)  
 Anti-MUC18 antibody heavy chain variable region protein, SEQ ID NO 13.  
 monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
 antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.  
 Homo sapiens.  
 WO2003057006-A2.  
 17-JUL-2003.  
 26-DEC-2002; 2002WO-US041582.  
 28-DEC-2001; 2001US-0346460P.  
 (ABGE-) ABGENIX INC.  
 Gudas J, Bar-Eli M;  
 WPI; 2003-577496/54.  
 N-PSDB; ADD05390.  
 Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
 treating tumors, inhibiting tumor growth, inhibiting cell invasion  
 associated with melanoma, or increasing survival of an animal having a  
 metastatic tumor.  
 Claim 1; SEQ ID NO 13; 87pp; English.  
 The invention relates to a novel monoclonal antibody used for inhibiting  
 tumour growth in an animal. The tumour inhibition process comprises  
 selecting an animal in need of treatment for a tumour, providing a  
 monoclonal antibody comprising a heavy chain amino acid, where the  
 antibody consists of any one of 10 fully defined sequences of 117-123  
 amino acids given in the specification, and where the monoclonal antibody  
 binds MUC18, and contacting the tumour with the antibody resulting in  
 inhibited proliferation of the cells. The monoclonal antibody has  
 cytostatic and can be used in the production of a vaccine. The monoclonal  
 antibodies against the MUC18 antigen are useful for diagnosing and  
 treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or  
 tumour metastasis), inhibiting cell invasion associated with melanoma, or  
 increasing survival of an animal having a metastatic tumour. This  
 sequence represents an anti-MUC18 antibody heavy chain, variable region,  
 protein of the invention.  
 Sequence 117 AA;  
 Query Match 88.2%; Score 561; DB 7; Length 117;  
 Best Local Similarity 88.2%; Pred. No. 4.9e-42;  
 Matches 105; Conservative 9; Mismatches 3; Indels 2; Gaps 1;  
 QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSINSGCCYWSWIQHPKGLIEWIGFIYSGSTY 60  
 Db 1 QVQLQESGPGLVKPSQTLSTCTVSGSINSGCCYWSWIQHPKGLIEWIGFIYSGSTY 60  
 QY 61 YNPSLKSRITLSVDTSKNQPSLKLNSMTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 119  
 Db 61 YNPSLKSRVITISVDTSKNQPSLKLSSVTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 117  
 RESULT 6  
 ID ADF09826 standard; protein; 117 AA.  
 XX  
 AC ADF09826;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human anti-MUC18 monoclonal antibody heavy chain #4.  
 XX  
 KW cell proliferation inhibition; MUC18 tumour antigen;





XX SQ Sequence 123 AA;  
Query Match 86.8%; Score 552; DB 7; Length 123;  
Best Local Similarity 86.2%; Pred. No. 3.3e-41;  
Matches 106; Conservative 6; Mismatches 7; Indels 4; Gaps 1;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKGLEWIGYIYSSGSTY 60  
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKGLEWIGYIYSSGSTY 60  
QY 61 YNPSLKSRTITLSVDTSKNQFSLKNSMTAADTAVYYCARDRETAG----PDYWGQGLTVLT 116  
DB 61 YNPSLKSRTITLSVDTSKNQFSLKNSMTAADTAVYYCARDRETAG----PDYWGQGLTVLT 120  
QY 117 VSS 119  
DB 121 VSS 123  
RESULT 11  
ADP03970  
ID ADP03970 standard; protein; 119 AA.  
AC ADP03970;  
XX  
XX  
XX 29-JUL-2004 (first entry)  
XX Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 140.  
XX  
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
KW cytostatic; colorectal neoplasm; renal cell carcinoma;  
KW cervical intraepithelial squamous neoplasia;  
KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
KW gene therapy; murine; mouse; human; heavy chain variable domain.  
XX  
XX Unidentified.  
XX WO2003048328-A2.  
XX 12-JUN-2003.  
XX  
XX 02-DEC-2002; 2002WO-US038550.  
XX  
XX 03-DEC-2001; 2001US-0337275P.  
XX  
XX (ABGE-) ABGENIX INC.  
XX  
XX Gudas J, Foltz I, Handa M, Gallo M;  
XX WPI; 2003-523295/49.  
XX  
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
XX  
XX Example 2; SEQ ID NO 140; 89pp; English.  
XX  
XX The invention relates to a novel isolated monoclonal antibody (mAb)  
CC comprising a heavy chain polypeptide and light chain polypeptide having a  
CC sequence chosen from one of 53 fully defined amino acid sequences given  
CC in the specification, where the antibody specifically binds carbonic  
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
CC demonstrates cytostatic activity and may be useful for treating a tumour,  
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.  
XX  
XX Sequence 119 AA;

Query Match 86.6%; Score 551; DB 7; Length 119;  
Best Local Similarity 87.4%; Pred. No. 3.9e-41;  
Matches 104; Conservative 5; Mismatches 10; Indels 0; Gaps 0;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKGLEWIGYIYSSGSTY 60  
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKGLEWIGYIYSSGSTY 60  
QY 61 YNPSLKSRTITLSVDTSKNQFSLKNSMTAADTAVYYCARDRETAGPDYWGQGLTVTVSS 119  
DB 61 YNPSLKSRTITLSVDTSKNQFSLKNSMTAADTAVYYCARDRETAGPDYWGQGLTVTVSS 119  
RESULT 12  
ADP03879  
ID ADP03879 standard; protein; 123 AA.  
XX  
XX  
XX ADP03879;  
XX  
XX 29-JUL-2004 (first entry)  
XX  
XX Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 19.  
XX  
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
KW cytostatic; colorectal neoplasm; renal cell carcinoma;  
KW cervical intraepithelial squamous neoplasia;  
KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
KW gene therapy; murine; mouse; human; heavy chain variable domain.  
XX  
XX Unidentified.  
XX WO2003048328-A2.  
XX 12-JUN-2003.  
XX  
XX 02-DEC-2002; 2002WO-US038550.  
XX  
XX 03-DEC-2001; 2001US-0337275P.  
XX  
XX (ABGE-) ABGENIX INC.  
XX  
XX Gudas J, Foltz I, Handa M, Gallo M;  
XX WPI; 2003-523295/49.  
XX  
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
XX  
XX Claim 1; SEQ ID NO 19; 89pp; English.  
XX  
XX The invention relates to a novel isolated monoclonal antibody (mAb)  
CC comprising a heavy chain polypeptide and light chain polypeptide having a  
CC sequence chosen from one of 53 fully defined amino acid sequences given  
CC in the specification, where the antibody specifically binds carbonic  
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
CC demonstrates cytostatic activity and may be useful for treating a tumour,  
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.  
XX  
XX Sequence 123 AA;  
Query Match 86.3%; Score 549; DB 7; Length 123;  
Best Local Similarity 85.4%; Pred. No. 6e-41;  
Matches 105; Conservative 6; Mismatches 8; Indels 4; Gaps 1;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKGLEWIGYIYSSGSTY 60

Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGGYVWSWIRHPGKGLEWIGYIYSGSTY 60  
 QY 61 YNPSLKSRITLSVDTSKNQFSLKLSMTAADTAVVYCARDRET---AGFDYWGQGLT 116  
 Db 61 YNPSLKSRVLIISVDTSENQFSLKLSVTAADTAVVYCARDRET---AGFDYWGQGLT 120  
 QY 117 VSS 119  
 Db 121 VSS 123

## RESULT 13

ADP03878  
 ID ADP03878 standard; protein; 123 AA.

XX  
 AC ADP03878;

DT 29-JUL-2004 (first entry)

XX Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 18.  
 DE monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KW cytostatic; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;  
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; heavy chain variable domain.  
 XX

OS Unidentified.

XX WO2003048328-A2.

PN 12-JUN-2003.

XX 02-DEC-2002; 2002WO-US038550.

XX 03-DEC-2001; 2001US-0337275P.

XX (ABGE-) ABGENIX INC.

XX Gudas J, Foltz I, Handa M, Gallo M;

XX WPI; 2003-523295/49.

XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

PS Claim 1; SEQ ID NO 18; 89pp; English.

XX The invention relates to a novel isolated monoclonal antibody (mAb)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
 CC demonstrates cytostatic activity and may be useful for treating a tumour,  
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumour or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
 CC (heavy chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.

XX Sequence 123 AA;

Query Match 86.3%; Score 549; DB 7; Length 123;  
 Best Local Similarity 85.4%; Pred. No. 6e-41;  
 Matches 105; Conservative 6; Mismatches 8; Indels 4; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGGYVWSWIRHPGKGLEWIGYIYSGSTY 60  
 Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGGYVWSWIRHPGKGLEWIGYIYSGSTY 60

QY 61 YNPSLKSRITLSVDTSKNQFSLKLSMTAADTAVVYCARDRET---AGFDYWGQGLT 116  
 Db 61 YNPSLKSRVLIISVDTSENQFSLKLSVTAADTAVVYCARDRET---AGFDYWGQGLT 120  
 QY 117 VSS 119  
 Db 121 VSS 123

## RESULT 14

AAB62775  
 ID AAB62775 standard; protein; 120 AA.

XX  
 AC AAB62775;

DT 03-APR-2001 (first entry)

XX Human HIV-1 monoclonal antibody SEQ ID NO: 74.

XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;  
 KW envelope glycoprotein; gp120; diagnosis.

XX Homo sapiens.

PN WO200100678-A1.

XX 04-JAN-2001.

XX 23-JUN-2000; 2000WO-US017327.

XX 30-JUN-1999; 99US-0141701P.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Watkins BA, Reitz MS;

XX WPI; 2001-112438/12.

XX N-PSDB; AAF29076.

XX Novel human monoclonal antibody immunoreactive with human  
 PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1  
 PT in biological sample and providing passive immunotherapy to HIV-1  
 PT infected mammal.

XX Claim 1; Page 69; 81pp; English.

XX The present invention provides the protein and coding sequences for the  
 CC variable regions of human monoclonal antibodies which are immunoreactive  
 CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.  
 CC These can be used in diagnosis and therapy of HIV-1 infection

XX Sequence 120 AA;

Query Match 86.2%; Score 548; DB 4; Length 120;  
 Best Local Similarity 87.4%; Pred. No. 7.2e-41;  
 Matches 104; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGGYVWSWIRHPGKGLEWIGYIYSGSTY 60  
 Db 2 EVQLQESGPGLVKPSQTLSTCTVSGGINSGGYVWSWIRHPGKGLEWIGYIYSGSTY 61

QY 61 YNPSLKSRITLSVDTSKNQFSLKLSMTAADTAVVYCARDRETAGFDYWGQGLT 119  
 Db 62 YNPSLKSRVLIISVDTSKNQFSLKLSVTAADTAVVYCARDRETAGFDYWGQGLT 120

## RESULT 15

ADJ80377  
 ID ADJ80377 standard; protein; 121 AA.

XX  
 ADJ80377;

06-MAY-2004 (first entry)

Antibody variable heavy chain with homology to mouse anti-human antibody.

hybrid antibody; antibody; framework region; homology; immunogenicity.

Unidentified.

WO2003048321-A2.

12-JUN-2003.

03-DEC-2002; 2002WO-US038450.

03-DEC-2001; 2001US-0336591P.

(ALEX-) ALEXION PHARM INC.

Rother R, Wu D;

WPI; 2003-513753/48.

Producing a hybrid antibody or hybrid antibody fragment by operatively linking the selected framework sequences to one or more complementarity determining regions of the initial antibody.

Example 1: SEQ ID NO 137; 77pp; English.

The invention relates to a method of producing a hybrid antibody or hybrid antibody fragment by: (i) providing an initial antibody having specificity for a target; (ii) determining the sequence of a variable region of the initial antibody; (iii) selecting a first component of the variable region consisting of FR1, FR2, FR3 and FR4; (iv) comparing the sequence of the first component to sequencers contained in a reference database of antibody sequences or antibody fragment sequences from a target species; (v) selecting a sequence from an antibody in the database which demonstrates a high degree of homology to the first component; (vi) selecting a second component of the variable region which is different than the first component, the second component selected from the group consisting of FR1, FR2, FR3 and FR4; (vii) comparing the sequence of the second component to sequences contained in a reference database of antibody sequences or antibody fragment sequences from the target species; (viii) selecting a sequence from the database which demonstrates a high degree of homology to the second component and which is from a different antibody than the selected antibody; and (ix) operatively linking the selected framework sequences to one or more complementarity determining regions (CDRs) of the initial antibody to produce a hybrid antibody or hybrid antibody fragment. The method is useful for producing a hybrid antibody or hybrid antibody fragment (claimed). The antibody and fragments are useful for therapeutic and diagnostic purposes. The method uses entire framework regions from a single antibody variable heavy or variable light chain to receive the CDRs. This produces antibodies that are highly homologous and exhibit reduced immunogenicity while maintaining an optimum binding profile. This sequence represents an antibody variable heavy chain which has good homology to an initial murine anti-human mannose binding lectin antibody (ADJ80371). The sequence was used to generate a hybrid antibody of the invention.

Sequence 121 AA;

Very Match	86.1%;	Score 547.5;	DB 7;	Length 121;
1st Local Similarity	86.0%;	Pred. No. 8e-41;		
Matches 104;	Conservative	7;	Mismatches	7;
			Indels	3;
			Gaps	1;

2 VQLQESGPGLVKPSQTLSTCTVSGGSINSGGCYWSWIRQHPGKLEWIGIYIYSSGSTYY 61

1 VOLQESGPGLVKPSOTLSLTCTVSGSISSGGYWNIROHPGKGLEWIGIYYSGSY 60

62 NPSLKSRITLSVDTSKNQFSLKLSNMTAADTAVYCARDRETAG---FDYWGGQLVTVS 118

61 NP5LSKRVITISVDTSKNQFSLKLSSTVAADTAIVYCCARGLKWGSGNHFFDYWGQGTILVTVS 120

119 S 119

Db 121 S 121

Search completed: November 9, 2005, 12:55:29  
Job time : 74.3684 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2005, 11:29:55 ; Search time 18.4912 Seconds  
(without alignments)  
480.403 Million cell updates/sec

Title: US-10-660-357A-25

Perfect score: 636

Sequence: 1 QVQLQESGPGLVKPSQTL.....DRETAGFDYWGQTLTVSS 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	545	85.7	119	1	US-08-360-125-5
2	545	85.7	119	2	US-08-450-578-5
3	545	85.7	119	2	US-09-017-628-5
4	545	85.7	119	2	US-09-014-680-5
5	545	85.7	119	4	US-08-450-363-5
6	545	85.7	119	4	US-09-467-903-5
7	532.5	83.7	487	4	US-09-800-729-145
8	523.5	82.3	473	3	US-09-049-672A-4
9	513.5	80.7	118	3	US-09-025-769B-25
10	513.5	80.7	118	4	US-09-490-070A-25
11	513.5	80.7	118	4	US-09-490-153-25
12	513.5	80.7	118	4	US-09-490-324-25
13	506.5	79.6	172	4	US-09-472-087-7
14	506.5	79.6	172	4	US-09-472-087-86
15	503	79.1	117	4	US-09-720-493-2
16	503	79.1	119	3	US-09-025-769B-39
17	503	79.1	119	3	US-09-025-769B-65
18	503	79.1	119	4	US-09-490-070A-39
19	503	79.1	119	4	US-09-490-070A-65
20	503	79.1	119	4	US-09-490-153-39
21	503	79.1	119	4	US-09-490-153-65
22	503	79.1	119	4	US-09-490-324-39
23	503	79.1	119	4	US-09-490-324-65
24	499.5	78.5	122	1	US-08-360-125-11
25	499.5	78.5	122	2	US-08-450-578-11
26	499.5	78.5	122	2	US-09-017-628-11
27	499.5	78.5	122	2	US-09-014-680-11

28 499.5 78.5 122 4 US-08-450-363-11 Sequence 11, Appl  
29 499.5 78.5 122 4 US-09-467-903-11 Sequence 11, Appl  
30 494 77.7 118 3 US-08-545-809A-116 Sequence 116, App  
31 490 77.0 142 2 US-08-480-774A-2 Sequence 2, Appli  
32 488 76.7 155 4 US-09-471-276-888 Sequence 888, App  
33 487.5 76.7 244 3 US-08-918-148-79 Sequence 79, Appl  
34 487.5 76.7 244 4 US-09-138-091A-77 Sequence 77, Appl  
35 485.5 76.3 120 4 US-09-424-840B-20 Sequence 20, Appl  
36 478 75.2 476 3 US-08-487-550-12 Sequence 12, Appl  
37 478 75.2 476 4 US-09-526-098-12 Sequence 12, Appl  
38 478 75.2 476 4 US-09-383-916-12 Sequence 12, Appl  
39 473.5 74.4 139 4 US-09-471-276-837 Sequence 837, App  
40 468.5 73.7 278 3 US-09-260-527-3 Sequence 3, Appli  
41 465 73.1 118 3 US-08-545-809A-142 Sequence 142, App  
42 463.5 72.9 139 4 US-09-203-768A-2 Sequence 2, Appli  
43 463.5 72.9 143 4 US-09-471-276-839 Sequence 839, App  
44 459.5 72.2 118 2 US-08-652-816A-13 Sequence 13, Appl  
45 458.5 72.1 150 4 US-09-582-337-14 Sequence 14, Appl

#### ALIGNMENTS

RESULT 1  
US-08-360-125-5  
; Sequence 5, Application US/08360125  
; Patent No. 5767246  
; GENERAL INFORMATION:  
; APPLICANT: Saiko HOSOKAWA  
; APPLICANT: Toshiaki TAGAWA  
; APPLICANT: Yoko HIRAKAWA  
; APPLICANT: No. 5767246hiko ITO  
; APPLICANT: Kazuhiro NAGAIKE  
; TITLE OF INVENTION: Human Monoclonal Antibody  
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
; TITLE OF INVENTION: Cell Membrane  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/360,125  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/905,534  
; FILING DATE: June 29, 1992  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

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;
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human
; CELL TYPE: antibody GAH
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
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; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
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; US-08-360-125-5
;
; Query Match 85.7%; Score 545; DB 1; Length 119;
; Best Local Similarity 84.9%; Pred. No. 5e-47;
; Matches 101; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
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; Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCCYWSWIRQHPKGLGWIGYIYSGSTY 60
;
; Qy 61 YNPSLKSRIITLSVDTSKNQFSLKNSMTAADTAVYYCARDRETAGPDYWGQGLTVTVSS 119
; Db 61 YNPSLKSRTISLDTSKSQFSLKLSLTAADTAVYYCARSTRLRGADYWGQGLTVTVSS 119
;
; RESULT 2
; US-08-450-578-5
; Sequence 5, Application US/08450578
; Patent No. 5837845
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5837845ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
;
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,578
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human
; CELL TYPE: antibody GAH
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
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; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
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; US-08-450-578-5
;
; Query Match 85.7%; Score 545; DB 2; Length 119;
; Best Local Similarity 84.9%; Pred. No. 5e-47;
; Matches 101; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
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RESULT 4  
US-09-014-880-5  
; Sequence 5, Application US/09014880  
; Patent No. 5990297  
; GENERAL INFORMATION:  
; APPLICANT: Saiko HOSOKAWA et al.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY  
; TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
; STREET: 2033 K Street, N.W., #800  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:

RESULT 5  
US-08-450-363-5  
; Sequence 5, Application US/08450363  
; Patent No. 6436434  
; GENERAL INFORMATION:  
; APPLICANT: Saiko HOSOKAWA  
; APPLICANT: Toshiaki TAGAWA  
; APPLICANT: Yoko HIRAKAWA  
; APPLICANT: No. 6436434;hiko ITO  
; APPLICANT: Kazuhiro NAGAIKE  
; TITLE OF INVENTION: Human Monoclonal Antibody  
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
; TITLE OF INVENTION: Cell Membrane  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/450.363

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; FILING DATE: May 25, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA: 07/905,534
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; CELL TYPE: Hybridoma producing human
; CELL LINE: antibody GAH
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
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; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; US-08-450-363-5
;
; Query Match 85.7%; Score 545; DB 4; Length 119;
; Best Local Similarity 84.9%; Pred. No. 5e-47;
; Matches 101; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
;
; Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGCCYWSWIRQHPGKGLIEWIGYISGSGTY 60
; Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGCCYWSWIRQHPGKGLIEWIGYISGSGTY 60
; Qy 61 YNPSLKSRTISLDTSKSFSLKSLTAADTAVYYCARSLRGADYWGQGTMTVTVSS 119
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; Db 61 YNPSLKSRTISLDTSKSFSLKSLTAADTAVYYCARSLRGADYWGQGTMTVTVSS 119
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; RESULT 6
; US-09-467-903-5
; Sequence 5, Application US/09467903
; Patent No. 6787153
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; Toshiaki TAGAWA
; Yoko HIRAKAWA
; No. 6787153biko ITO
; Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; Specifically Binding to Surface Antigen of Cancer
; Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/467,903
; FILING DATE: 21-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/450,363
; FILING DATE: May 25, 1995
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER: JPI58859/1991
; FILING DATE: June 28, 1991
; APPLICATION NUMBER: JPI58860/1991
; FILING DATE: June 28, 1991
; APPLICATION NUMBER: JPI58861/1991
; FILING DATE: June 28, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8200
; TELEFAX: <Unknown>
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: <Unknown>
; ANTI-SENSE: <Unknown>
; ORIGINAL SOURCE:
; ORGANISM: <Unknown>
; STRAIN: <Unknown>
; INDIVIDUAL ISOLATE: <Unknown>
; DEVELOPMENTAL STAGE: <Unknown>
; HAPLOTYPE: <Unknown>
; TISSUE TYPE: <Unknown>
; CELL TYPE: Hybridoma producing human
; antibody GAH
; CELL LINE: <Unknown>
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[illegible]

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Query Match      82.3%; Score 523.5; DB 3; Length 473;
Best Local Similarity 82.3%; Pred. No. 3.6e-44;
Matches 102; Conservative 5; Mismatches 12; Indels 5; Gaps 1
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Db      20 QVQLQESGFLVKKPSQTLISLTCAVSGGSITSGGYMSWIRQPPGKLEWIGYIYSGSTL 79
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QY      61 YNPPLSKSRITLSVDTSKNQPSLKLNGMTAADTAVYVCARD-----RETACFDVWGQGLTV 115
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      80 YNPPLSKSRVTISVDTSKNQPSLKSVTAAADTAVYVCARDDDVGLRGNGYGMVDWGQGLTV 139
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QY      116 TVSS 119

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Db      140 TVSS 143
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RESULT 9
US-09-025-769B-25
; Sequence 25, Application US/09025769B
; Patent No. 630064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-25

Query Match      80.7%; Score 513.5; DB 3; Length 118;
Best Local Similarity 85.0%; Pred. No. 6.8e-44;
Matches 102; Conservative 6; Mismatches 9; Indels 3; Gaps 2;

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Db      59 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYICARGGGGVFDYWGQGTFLVTVSS 118
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RESULT 10
US-09-490-070A-25
; Sequence 25, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-25

Query Match      80.7%; Score 513.5; DB 3; Length 118;
Best Local Similarity 85.0%; Pred. No. 6.8e-44;
Matches 102; Conservative 6; Mismatches 9; Indels 3; Gaps 2;

Qy      1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPKGLIEWIGYIYSGSTY 60
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Db      1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPKGLIEWIGYIYSGSTN 58
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Qy      61 YNPSLKSRITLSVDTSKNQFSLKNSMTAADTAVYICARDRETAG-PDYWGQGTFLVTVSS 119
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Db      59 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYICARGGGGVFDYWGQGTFLVTVSS 118
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RESULT 11
US-09-490-153-25
; Sequence 25, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
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; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-070A-25

Query Match      80.7%; Score 513.5; DB 4; Length 118;
Best Local Similarity 85.0%; Pred. No. 6.8e-44;
Matches 102; Conservative 6; Mismatches 9; Indels 3; Gaps 2;

Qy      1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPKGLIEWIGYIYSGSTY 60
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Db      1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPKGLIEWIGYIYSGSTN 58
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Qy      61 YNPSLKSRITLSVDTSKNQFSLKNSMTAADTAVYICARDRETAG-PDYWGQGTFLVTVSS 119
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-153-25

Query Match      80.7%; Score 513.5; DB 4; Length 118;
Best Local Similarity 85.0%; Pred. No. 6.8e-44;
Matches 102; Conservative 6; Mismatches 9; Indels 3; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCCYMSWIRQHPGKGLIEWIGYIYSSGSTY 60
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINS--YYMSWIRQPPGKGLIEWIGIYHSGSTN 58
QY 61 YNPFLSKSRITLSVDTSKNQFSLKLSMTAADTAVYYCARDRETAG-PDYWGQGTTLTVSS 119
DB 59 YNPFLSKSRITLSVDTSKNQFSLKLSMTAADTAVYYCARDRETAG-PDYWGQGTTLTVSS 118

RESULT 12
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; Sequence 25, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckhuhn, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769

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; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-324-25

Query Match      80.7%; Score 513.5; DB 4; Length 118;
Best Local Similarity 85.0%; Pred. No. 6.8e-44;
Matches 102; Conservative 6; Mismatches 9; Indels 3; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCCYMSWIRQHPGKGLIEWIGYIYSSGSTY 60
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINS--YYMSWIRQPPGKGLIEWIGIYHSGSTN 58
QY 61 YNPFLSKSRITLSVDTSKNQFSLKLSMTAADTAVYYCARDRETAG-PDYWGQGTTLTVSS 119
DB 59 YNPFLSKSRITLSVDTSKNQFSLKLSMTAADTAVYYCARDRETAG-PDYWGQGTTLTVSS 118

RESULT 13
US-09-472-087-7
; Sequence 7, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-7

Query Match      79.6%; Score 506.5; DB 4; Length 172;
Best Local Similarity 84.2%; Pred. No. 5.3e-43;
Matches 96; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

QY 7 SGPGLVKPSQTLSTCTVSGGSINSGCCYMSWIRQHPGKGLIEWIGYIYSSGSTYYPNPSLK 66
DB 1 SGPGLVKPSQTLSTCTVSGGSINS--YYMSWIRQPPGKGLIEWIGIYIYNTYYPNPSLK 60
QY 67 SRTLSVDTSKNQFSLKLSMTAADTAVYYCARDRETAG-PDYWGQGTTLTVSS 119
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US-09-472-087-86
; Sequence 86, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-86

Query Match          79.6%; Score 506.5; DB 4; Length 172;
Best Local Similarity 84.2%; Pred. No: 5.3e-43;
Matches 96; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

QY 7 SGPLVKPSQTLSTCTVSGGINSGGCYWSWIRQHPGKLEWIGYIYSSGSTYNNPSLK 66
Db 1 SGPLVKPSQTLSTCTVSGGINSGGHYWSWIRQHPGKLEWIGYIYIGNTYNNPSLK 60

QY 67 SRITLSVDTSKNQFSLKLSMTAADTAVYYCARDR-ETAGFDYWGQGLTVTVSS 119
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RESULT 15
US-09-720-493-2
; Sequence 2, Application US/09720493
; Patent No. 6827925
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Williams, Andrew J
; APPLICANT: Tempest, Philip R
; APPLICANT: Holtet, Thor L
; APPLICANT: Main, Sarah H
; APPLICANT: Jackson, Helen
; APPLICANT: Daramola, Olalekan
; TITLE OF INVENTION: Improvements relating to antibodies
; FILE REFERENCE: AHB/CP5775333
; CURRENT APPLICATION NUMBER: US/09/720,493
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: GB 9814383.7
; PRIOR FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-720-493-2

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Best Local Similarity 83.2%; Pred. No: 7.5e-43;
Matches 99; Conservative 8; Mismatches 10; Indels 2; Gaps 2;

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Db 1 QVOLQESGPGLVKPSQTLSTCTVSGGINSGGHYWSWIRQHPGKLEWIGYIYHSGSTY 59

QY 61 YNPSLKSRITLSVDTSKNQFSLKLSMTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 119
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2005, 11:40:37 ; Search time 66.1111 Seconds  
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Title: US-10-660-357A-25  
 Perfect score: 636  
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Total number of hits satisfying chosen parameters: 1867879

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Post-processing: Minimum Match 0%
                  Maximum Match 10%
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Published Applications AA:\*\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	636	100.0	119	US-10-330-613-25	Sequence 25, Appl
2	636	100.0	119	US-10-330-530-25	Sequence 25, Appl
3	636	100.0	119	US-10-660-357-25	Sequence 25, Appl
4	561	88.2	117	US-10-330-613-13	Sequence 13, Appl
5	561	88.2	117	US-10-330-530-13	Sequence 13, Appl
6	561	88.2	117	US-10-660-357-13	Sequence 13, Appl
7	560.5	88.1	125	US-10-805-177-53	Sequence 53, Appl
8	556.5	87.5	122	US-10-984-960A-20	Sequence 20, Appl
9	554.5	87.2	136	US-11-131-648-15	Sequence 15, Appl
10	554.5	87.2	136	US-11-131-648-39	Sequence 39, Appl
11	553.5	87.0	118	US-10-309-762-138	Sequence 138, Appl

12	552	86.8	123	15	US-10-309-762-10	Sequence 10, Appl
13	551	86.6	119	15	US-10-309-762-140	Sequence 140, App
14	551	86.6	121	17	US-10-706-689-8	Sequence 8, Appl
15	551	86.6	121	18	US-10-988-360-8	Sequence 8, Appl
16	549	86.3	123	15	US-10-309-762-18	Sequence 18, Appl
17	549	86.3	123	15	US-10-309-762-19	Sequence 19, Appl
18	547.5	86.1	121	15	US-10-308-817-137	Sequence 137, App
19	547.5	86.1	121	15	US-10-453-698-137	Sequence 137, App
20	547.5	86.1	122	18	US-10-984-960A-56	Sequence 56, Appl
21	547	86.0	119	15	US-10-309-762-131	Sequence 131, App
22	547	86.0	446	17	US-10-644-277-62	Sequence 62, Appl
23	546.5	85.9	120	15	US-10-309-762-13	Sequence 13, Appl
24	546.5	85.9	120	15	US-10-309-762-144	Sequence 144, App
25	545.5	85.8	252	10	US-09-880-748-1994	Sequence 1994, Ap
26	545.5	85.8	252	15	US-10-293-418-1994	Sequence 1994, Ap
27	545	85.7	119	17	US-10-483-994-7	Sequence 7, Appl
28	545	85.7	119	17	US-10-483-993-7	Sequence 7, Appl
29	545	85.7	119	18	US-10-497-516-7	Sequence 7, Appl
30	545	85.7	127	15	US-10-309-762-14	Sequence 14, Appl
31	544.5	85.6	124	15	US-10-309-762-75	Sequence 75, Appl
32	544.5	85.6	143	15	US-10-309-762-96	Sequence 96, Appl
33	544	85.5	144	17	US-10-893-576-35	Sequence 35, Appl
34	543.5	85.5	120	18	US-10-706-689-40	Sequence 40, Appl
35	543.5	85.5	120	18	US-10-988-360-40	Sequence 40, Appl
36	542	85.2	117	14	US-10-330-613-5	Sequence 5, Appl
37	542	85.2	117	14	US-10-330-530-5	Sequence 5, Appl
38	542	85.2	117	16	US-10-660-357-5	Sequence 5, Appl
39	542	85.2	123	15	US-10-309-762-9	Sequence 9, Appl
40	542	85.2	480	17	US-10-910-901-6	Sequence 6, Appl
41	541.5	85.1	122	15	US-10-309-762-147	Sequence 147, App
42	541	85.1	125	15	US-10-309-762-11	Sequence 11, Appl
43	540	84.9	121	15	US-10-309-762-152	Sequence 152, App
44	540	84.9	125	15	US-10-309-762-8	Sequence 8, Appl
45	540	84.9	125	15	US-10-309-762-16	Sequence 16, Appl

## ALIGNMENTS

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RESULT 1
US-10-330-613-25
; Sequence 25, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudac, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-25

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Query Match	100.0%;	Score 636;	DB 14;	Length 119;
Best Local Similarity	100.0%;	Pred. No. 1.9e-48;		
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Qy	61	YNPSLKSRIITLSVDITSKNQPSLKLNSMTAADTAVYYCARDRETAGFDYWGQGLTVTVSS	119	
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; Sequence 25, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-25

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Best Local Similarity 100.0%; Pred. No. 1.9e-48;
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Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGGCYWSWIROHPGKGLEWIGYIYSSGSTY 60

Qy 61 YNPSLKSRITLSVDTSKNQFSLKLSMTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 119
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RESULT 3
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; Sequence 25, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-25

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Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGGCYWSWIROHPGKGLEWIGYIYSSGSTY 60

Qy 61 YNPSLKSRITLSVDTSKNQFSLKLSMTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 119
Db 61 YNPSLKSRITLSVDTSKNQFSLKLSMTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 119

RESULT 4
US-10-330-613-13
; Sequence 13, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-13

Query Match      88.2%; Score 561; DB 14; Length 117;
Best Local Similarity 88.2%; Pred. No. 7.5e-42;
Matches 105; Conservative 9; Mismatches 3; Indels 2; Gaps 1;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGGCYWSWIROHPGKGLEWIGYIYSSGSTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGGCYWSWIROHPGKGLEWIGYIYSSGSTY 60

Qy 61 YNPSLKSRITLSVDTSKNQFSLKLSMTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 119
Db 61 YNPSLKSRITLSVDTSKNQFSLKLSMTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 119

RESULT 5
US-10-330-530-13
; Sequence 13, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-13

Query Match      88.2%; Score 561; DB 14; Length 117;
Best Local Similarity 88.2%; Pred. No. 7.5e-42;
Matches 105; Conservative 9; Mismatches 3; Indels 2; Gaps 1;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGGCYWSWIROHPGKGLEWIGYIYSSGSTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGGCYWSWIROHPGKGLEWIGYIYSSGSTY 60

Qy 61 YNPSLKSRITLSVDTSKNQFSLKLSMTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 119
Db 61 YNPSLKSRITLSVDTSKNQFSLKLSMTAADTAVYYCARDRETAGFDYWGQGLTVTVSS 119

RESULT 6
US-10-660-357-13
; Sequence 13, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
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Db 121 VSS 123  
RESULT 13  
US-10-309-762-140  
; Sequence 140, Application US/10309762  
; Publication No. US20040018198A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; APPLICANT: Foltz, Ian  
; APPLICANT: Handa, Masahisa  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
; FILE REFERENCE: ABGENIX.027A  
; CURRENT APPLICATION NUMBER: US/10/309,762  
; PRIOR FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/337275  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 140  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-309-762-140

Query Match 86.6%; Score 551; DB 15; Length 119;  
Best Local Similarity 87.4%; Pred. No. 5.8e-41;  
Matches 104; Conservative 5; Mismatches 10; Indels 0; Gaps 0;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKGLEWIGYIYSSGSTY 60  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKGLEWIGYIYSSGSTY 60

QY 61 YNPSSLKSRITLSVDTSKNQFSLKLSNSMTAADTAVYYCARDRETAG--FDYWGQGLTVTVSS 119  
Db 61 YNPSSLKSRITLSVDTSKNQFSLKLSNSMTAADTAVYYCARDRETAG--FDYWGQGLTVTVSS 119  
QY 119 S 119  
Db 121 S 121

US-10-988-360-8  
; Sequence 8, Application US/10988360  
; Publication No. US20050147610A1  
; GENERAL INFORMATION:  
; APPLICANT: Ghayur, Tariq  
; APPLICANT: Labkovsky, Boris  
; APPLICANT: Voss, Jeffrey  
; APPLICANT: Green, Larry  
; APPLICANT: Babcock, John  
; APPLICANT: Jia, Xiao-chi  
; APPLICANT: Wieler, James  
; APPLICANT: Kang, Paul  
; APPLICANT: Hegberg, Brad  
; TITLE OF INVENTION: IL-18 Binding Proteins  
; FILE REFERENCE: BBC-085US  
; CURRENT APPLICATION NUMBER: US/10/988,360  
; CURRENT FILING DATE: 2004-11-12  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 8  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-988-360-8

Query Match 86.6%; Score 551; DB 18; Length 121;  
Best Local Similarity 86.0%; Pred. No. 5.9e-41;  
Matches 104; Conservative 9; Mismatches 6; Indels 2; Gaps 1;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKGLEWIGYIYSSGSTY 60  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKGLEWIGYIYSSGSTY 60

QY 61 YNPSSLKSRITLSVDTSKNQFSLKLSNSMTAADTAVYYCARDRETAG--FDYWGQGLTVTVSS 118  
Db 61 YNPSSLKSRITLSVDTSKNQFSLKLSNSMTAADTAVYYCARDRETAG--FDYWGQGLTVTVSS 118  
QY 119 S 119  
Db 121 S 121

US-10-706-689-8  
; Sequence 8, Application US/10706689  
; Publication No. US20050100965A1  
; GENERAL INFORMATION:  
; APPLICANT: Ghayur, Tariq  
; APPLICANT: Labkovsky, Boris  
; APPLICANT: Voss, Jeffrey  
; APPLICANT: Green, Larry  
; APPLICANT: Babcock, John  
; APPLICANT: Jia, Xiao-chi  
; APPLICANT: Wieler, James  
; APPLICANT: Kang, Paul  
; APPLICANT: Hegberg, Brad  
; TITLE OF INVENTION: IL-18 Binding Proteins  
; FILE REFERENCE: BBC-085  
; CURRENT APPLICATION NUMBER: US/10/706,689  
; CURRENT FILING DATE: 2003-11-12  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 8  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-706-689-8

Query Match 86.6%; Score 551; DB 17; Length 121;  
Best Local Similarity 86.0%; Pred. No. 5.9e-41;  
Matches 104; Conservative 9; Mismatches 6; Indels 2; Gaps 1;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKGLEWIGYIYSSGSTY 60  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKGLEWIGYIYSSGSTY 60

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Job time : 66.1111 secs

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F;41-125/Domain: immunoglobulin homology <IMM>

Query Match 81.0%; Score 515; DB 2; Length 147;  
Best Local Similarity 82.6%; Pred. No. 3.6e-39;  
Matches 100; Conservative 7; Mismatches 12; Indels 2; Gaps 1;  
  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKLEWIGYIYSGSTY 60  
Db QQLQLQESGPGLVKPSQTLSTCTVSGGSISSSYYWGWIRQPPGKLEWIGSIYSGSTY 86  
QY 61 YNPSLKSRITLSVDTSKNQFSLKNSMTAADTAVVYCARDRETAG--FDYWGQGLTVTVS 118  
Db YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVVYCARPLLWFGELFDYWGQGLTVTVS 146  
QY 119 S 119  
Db 147 S 147

RESULT 3  
I37782  
Ig variable region (VDJ) (clone T23-9) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999  
C:Accession: I37782; S25476  
R:Demaision, C.; Chastagner, P.; Theze, J.; Zouali, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994  
A:Title: Somatic diversification in the heavy chain variable region genes expressed by B  
A:Reference number: A36876; MUID:94119917; PMID:8290556  
A:Accession: I37782  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140 <RES>  
A:Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F;46-128/Domain: immunoglobulin homology <IMM>

Query Match 80.7%; Score 513; DB 2; Length 140;  
Best Local Similarity 82.1%; Pred. No. 5.2e-39;  
Matches 101; Conservative 8; Mismatches 8; Indels 6; Gaps 2;  
  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKLEWIGYIYSGSTY 60  
Db QVQLQESGPGLVKPSQTLSTCTVSGGSISS--YYWSWIRQPPGKLEWIGIYIYSGSTN 77  
QY 61 YNPSLKSRITLSVDTSKNQFSLKNSMTAADTAVVYCARDRETAG---FDYWGQGLTVT 116  
Db YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVVYCARHNSSSWYGRYFDYWGQGLTVT 137  
QY 117 VSS 119  
Db 138 VSS 140

RESULT 4  
S31690  
Ig heavy chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S31690  
R:Quisnir, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.  
submitted to the EMBL Data Library, June 1992  
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A:Reference number: S31585  
A:Accession: S31690  
A:Molecule type: mRNA  
A:Residues: 1-130 <CUI>  
A:Cross-references: EMBL:Z14199; NID:g30984; PIDN:CAA78568.1; PID:g30985  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;20-102/Domain: immunoglobulin homology <IMM>

Query Match 78.6%; Score 500; DB 2; Length 130;  
Best Local Similarity 78.7%; Pred. No. 7e-38;  
Matches 100; Conservative 6; Mismatches 11; Indels 10; Gaps 2;  
  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKLEWIGYIYSGSTY 60  
Db QVQLQESGPGLVKPSQTLSTCTVSGGSISS--YYWSWIRQPPGKLEWIGIYIYSGSTN 63  
QY 61 YNPSLKSRITLSVDTSKNQFSLKNSMTAADTAVVYCARDRETA-----GFDYWGQ 112  
Db YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVVYCARSSVLLWFGELLYYFDYWGQ 123  
QY 113 TLVTVSS 119  
Db 124 TLVTVSS 130

RESULT 5  
S69912  
Ig V-D-J region (ND) - human  
C:Species: Homo sapiens (man)  
C>Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 21-Jan-2000  
C:Accession: S69912  
R:Sahota, S.; Hamblin, T.; Oscier, D.G.; Stevenson, F.K.  
Leukemia 8, 1285-1289, 1994  
A:Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of multi-  
A:Reference number: S69909; MUID:94335315; PMID:8057663  
A:Accession: S69912  
A>Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-122 <SAH>  
A:Cross-references: EMBL:Z33398; NID:9871347; PIDN:CAA83849.1; PID:g987460  
A>Note: the sequence of residues 108-122 and the corresponding nucleic acid sequence at-  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 78.5%; Score 499.5; DB 2; Length 122;  
Best Local Similarity 78.7%; Pred. No. 7.3e-38;  
Matches 96; Conservative 12; Mismatches 11; Indels 3; Gaps 1;  
  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKLEWIGYIYSGSTY 60  
Db RVQLQESGPGLVKPSQTLSTCTVSGGSISSDGHFWNIHQHPGKLEWIGNIYFSGSSY 60  
QY 61 YNPSLKSRITLSVDTSKNQFSLKNSMTAADTAVVYCARD---RETAGFDYWGQGLTVTV 117  
Db YNPSLKSRITISVDTSKNQFSLRLKSVTAADTAVVFCARGFFFRGTGLDTWGQGLTVRL 120  
QY 118 SS 119  
Db 121 SS 122

RESULT 6  
S78051  
Ig heavy chain precursor V-D-J region (clone mAb 61VH) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 19-Nov-1997 #sequence\_revision 05-Dec-1997 #text\_change 23-Jul-1999  
C:Accession: S78051; S23716  
R:Harindranath, N.  
submitted to the EMBL Data Library, August 1990  
A:Reference number: S78051  
A:Accession: S78051  
A:Molecule type: mRNA  
A:Residues: 1-135 <HAR>  
A:Cross-references: EMBL:X54437; NID:g37814; PIDN:CAA38306.1; PID:g930117  
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Nockin,  
inc. Immunol. 3, 865-875, 1991  
A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and  
patient.  
A:Reference number: S23716; MUID:92031262; PMID:1718404  
A:Accession: S23716  
A:Molecule type: mRNA

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A;Residues: 13-111 <HAW>
A;Cross-references: EMBL:X54437
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-13/Domain: signal sequence (fragment) #status predicted <SIG>
F;14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;27-111/Domain: immunoglobulin homology <IMM>

Query Match      78.3%; Score 498; DB 2; Length 135;
Best Local Similarity 78.0%; Pred. No. 1.1e-37;
Matches 96; Conservative 9; Mismatches 14; Indels 4; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGCCYWSWIRQHPGKGLEWIGYIYSSGSTY 60
DB 13 QQLQESGPGLVKPSQTLSTCTVSGGINSRGSHYWGWIQPPGKGLEWIGSIYSGNTY 72
QY 61 YNPFLSKRITLSVDTSKNQFSLKNSMTAADTAVYYCAR----DRETAGDYWGQGLT 116
DB 73 FNEFLSKRVITISVDTSKNQFSLKSSVTAADTAVYYCARLGPDDYTLDGMDVWGQGLT 132
QY 117 VSS 119
DB 133 VSS 135

RESULT 7
S31514
IG heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31514
R;Chastagner, P.; Dematison, C.; Theze, J.; Zouali, M.
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A;Reference number: S31509
A;Accession: S31514
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-128 <CHA>
A;Cross-references: EMBL:X69862; NID:g33086; PIDN:CAA49496.1; PID:g33087
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;22-106/Domain: immunoglobulin homology <IMM>

Query Match      78.0%; Score 496; DB 2; Length 128;
Best Local Similarity 79.3%; Pred. No. 1.6e-37;
Matches 96; Conservative 8; Mismatches 15; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGCCYWSWIRQHPGKGLEWIGYIYSSGSTY 60
DB 8 QVQLQESGPGLVKPSQTLSTCTVSGGINSRGSHYWGWIQPPGKGLEWIAHYIYPSGSTY 67
QY 61 YNPFLSKRITLSVDTSKNQFSLKNSMTAADTAVYYCARDRET--AGFDYWGQGLT 118
DB 68 YNPFLSKRVITISVDTSENQFSLRSTVTPADTAVYYCARIGNFYGFDPWGQGLT 127
QY 119 S 119
DB 128 S 128

RESULT 8
S26801
IG heavy chain V region (DP-65) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 25-Oct-1996 #text_change 20-Jun-2000
C;Accession: S26801; S26900
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A;Reference number: S26800; MUID:92201299; PMID:1348029
A;Accession: S26801
A;Status: preliminary
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A;Molecule type: DNA
A;Residues: 1-99 <WEN>
A;Cross-references: EMBL:Z14237; NID:g37706; PIDN:CAA78606.1; PID:gl335372
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
F;14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;27-111/Domain: immunoglobulin homology <IMM>

Query Match      77.7%; Score 494; DB 2; Length 99;
Best Local Similarity 92.9%; Pred. No. 1.8e-37;
Matches 92; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGCCYWSWIRQHPGKGLEWIGYIYSSGSTY 60
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSRGSHYWGWIQPPGKGLEWIGYIYSSGSTY 60
QY 61 YNPFLSKRITLSVDTSKNQFSLKNSMTAADTAVYYCAR 99
DB 61 YNPFLSKRVITISVDTSKNQFSLKSSVTAADTAVYYCAR 99

RESULT 9
S37456
IG mu chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37456
R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.
A;Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from
A;Reference number: S37453
A;Accession: S37456
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-116 <MCI>
A;Cross-references: EMBL:X75024; NID:g404313; PIDN:CAA52932.1; PID:g758095
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;8-90/Domain: immunoglobulin homology <IMM>

Query Match      77.5%; Score 493; DB 2; Length 116;
Best Local Similarity 81.0%; Pred. No. 2.6e-37;
Matches 94; Conservative 8; Mismatches 8; Indels 6; Gaps 1;

QY 10 GLVKPSQTLSTCTVSGGINSGCCYWSWIRQHPGKGLEWIGYIYSSGSTYNNPSLKSR 69
DB 1 GLVKPSQTLSTCTVSGGINSRGSHYWGWIQPPGKGLEWIGYIYSSGSTYNNPSLKSRV 60
QY 70 TLSVDTSKNQFSLKNSMTAADTAVYYCARDRETAGF-----DYWGQGLT 119
DB 61 TISVDTSKNQFSLKSSVTAADTAVYYCARGYSYGYIYNDVWGKGT 116

RESULT 10
S44113
IG heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44113
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable
A;Reference number: S44105
A;Accession: S44113
A;Status: preliminary
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.  
OM protein - protein search, using sw model  
Run on: November 9, 2005, 11:46:52 ; Search time 61.4386 Seconds  
(without alignments)  
991.843 Million cell updates/sec  
Title: US-10-660-357A-25  
Perfect score: 636  
Sequence: 1 QVQLQESGPGLVKPSQTL...DRETAGFDYWGQGLTVTVSS 119

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Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : UniProt\_03:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	522	82.1	476	2	Q6GMX1	Q6gm1 homo sapien
2	507.5	79.8	465	2	Q6GMX6	Q6gm6 homo sapien
3	503.5	79.2	478	2	Q72379	Q72379 homo sapien
4	490.5	77.1	477	2	Q6GMX7	Q6gm7 homo sapien
5	489.5	77.0	620	2	Q96EY0	Q96ey0 homo sapien
6	486	76.4	119	2	Q9UL73	Q9ul73 homo sapien
7	476.5	74.9	150	2	Q95973	Q95973 homo sapien
8	475.5	74.8	496	2	Q96KX8	Q96kx8 homo sapien
9	466.5	73.3	576	2	Q6P418	Q6p418 homo sapien
10	461	72.5	492	2	Q72374	Q72374 homo sapien
11	457.5	71.9	130	2	Q81ZD7	Q81zd7 homo sapien
12	455	71.5	139	2	Q86SX2	Q86sx2 homo sapien
13	444	69.8	129	1	HV2F_HUMAN	HV2f human
14	432.5	68.0	122	2	Q9UL75	Q9ul75 homo sapien
15	429	67.5	478	2	Q6NVH3	Q6nvh3 homo sapien
16	425	66.8	595	2	Q8WUX4	Q8wux4 homo sapien
17	425	66.8	537	2	Q6GMX5	Q6gm5 homo sapien
18	425	66.8	597	2	Q9BU10	Q9bu10 homo sapien
19	425	66.8	625	2	Q96AA6	Q96aa6 homo sapien
20	419	65.9	597	2	Q9BQB8	Q9bqb8 homo sapien
21	417.5	65.6	146	1	HV2I_HUMAN	HV2i human
22	414.5	65.2	473	2	Q8TC63	Q8tc63 homo sapien
23	409	64.3	479	2	Q99M22	Q99m22 mus musculus
24	407.5	64.1	136	2	Q6LBO5	Q6lbq5 mus musculus
25	407	64.0	137	1	HV46_MOUSE	HV46 mouse
26	407	64.0	262	2	Q652I1	Q652i1 mus musculus
27	406	63.8	113	1	HV47_MOUSE	HV47 mouse
28	405	63.7	117	1	HV2C_HUMAN	HV2c human
29	387	60.8	476	2	Q6MZX7	Q6mzx7 homo sapien
30	385	60.5	116	2	Q723Y6	Q723y6 homo sapien
31	369.5	58.1	482	2	Q91X92	Q91x92 mus musculus

RESULT 1

ID	Q6GMX1	PRELIMINARY;	PRT;	476 AA.
AC	Q6GMX1;			
DT	05-JUL-2004 (TrEMBLrel. 27, Created)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)			
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Splicein;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.C., Smailus U., Smailus D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Splicein;			
RA	Strausberg R.;			
RL	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC073773; AAH73773.1; -.			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003597; IG-cl.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; IG_v.			
DR	Pfam; PF07654; C1-set; 3.			
DR	Pfam; PF00047; IG; 4.			
DR	SMART; SM00409; IG; 2.			
DR	SMART; SM00409; IGcl; 3.			
DR	SMART; SM00406; IGv; 1.			
DR	PROSITE; PS00835; IG LIKE; 4.			
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.			

P18533 mus musculus  
P18531 mus musculus  
P01819 mus musculus  
P18532 mus musculus  
Q99NG4 mus musculus  
Q9ul96 homo sapien  
Q811u5 mus musculus  
P20957 xenopus lae  
Q9ul72 homo sapien  
P01816 homo sapien  
Q6in78 homo sapien  
Q6pja4 homo sapien  
Q9ul74 homo sapien  
P01817 homo sapien

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KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match      82.1%; Score 522; DB 2; Length 476;
Best Local Similarity 80.3%; Pred. No. 1.1e-45;
Matches 102; Conservative 9; Mismatches 8; Indels 8; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKGLEWIGYIYSGSTY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLQESGPGLVKPSQTLSTCTVSGGSISGSDYYWMIQPPGKGLEWIGYIYSGSTY 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 YNPISLKSRIITLSVDTSKNQFSLKNSMTAADTAATVAVYCARD-----RETA--CFDYWGOG 112
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 YNPISLKSRIITLSVDTSKNQFSLKNSMTAADTAATVAVYCARDAGVWGSFRSWAIDGFNIWGOG 139
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 113 TLTVTSS 119
   |||||
Db 140 TWTVTSS 146
   |||||

RESULT 2
Q6GMX6 PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Strapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Skaleka J., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]

SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC073766; AAH73766.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00407; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
```

```
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match      79.8%; Score 507.5; DB 2; Length 465;
Best Local Similarity 84.9%; Pred. No. 3.3e-44;
Matches 101; Conservative 7; Mismatches 8; Indels 3; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKGLEWIGYIYSGSTY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLQESGPGLVKPSQTLSTCTVSGGSIS--GYWSMIQPPGKGLEWIGRIYTSNSTN 77
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 YNPISLKSRIITLSVDTSKNQFSLKNSMTAADTAATVAVYCARDTAGFDYWGOGTLTVTSS 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 78 YNPISLKSRIITLSVDTSKNQFSLKNSMTAADTAATVAVYCARDGRFTY--FDYWGOGTLTVTSS 135
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
Q7Z379 PRELIMINARY; PRT; 478 AA.
AC Q7Z379;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFP686K04218 (Fragment).
GN Name=DKFP686K04218;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Human rectum tumor;
RA Bloeker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; BX538066; CAD97996.1; -.
DR HSSP; P01820; IG7U.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON_TER 1
FT SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;

Query Match      79.2%; Score 503.5; DB 2; Length 478;
Best Local Similarity 79.2%; Pred. No. 8.9e-44;
Matches 95; Conservative 12; Mismatches 12; Indels 1; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYWSWIRQHPGKGLEWIGYIYSGSTY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 19 QVQLQESGPGLVKPSQTLSTCTVSGGSIGSDYFWSWIRQPPGKGLEWIGYIYSGSTY 78
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 YNPISLKSRIITLSVDTSKNQFSLKNSMTAADTAATVAVYCARDRET--AGFDYWGOGTLTVTSS 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 79 YNPISLKSRIITLSVDTSKNQFSLKNSMTAADTAATVAVYCARDGLGTAFDIWGOGTVTVTSS 138
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
Q6GMX7 PRELIMINARY; PRT; 477 AA.
AC Q6GMX7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX Strausberg R.;  
 RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073765; AAH73765.1; -;  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 2.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00409; IG; 4.  
 DR SMART; SM00407; IGcl; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
 KW Hypothetical protein\_  
 SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CFFB5 CRC64;  
 Query Match 77.1%; Score 490.5; DB 2; Length 477;  
 Best Local Similarity 81.7%; Pred. No. 2e-42;  
 Matches 98; Conservative 6; Mismatches 13; Indels 3; Gaps 2;  
 QY 1 QVQLQESGPGLVKPSOTLSLTCTVSGGSINSGGYWSWIRQHPGKGLWIGYISGSGSTY 60  
 Db 20 QVQLQESGPGLVKPSOTLSLTCTVSGGSINS--YYWSWIRQHPGKGLWIGYISGSGST 77  
 QY 61 YNPSLKSRITLSVDTSKNQPSLKNMTAADTAVYYCARDRE-TAGFDYWGQGTLLTVSS 119  
 Db 78 YNPSLKSRITLSVDTSKNQPSLKNMTAADTAVYYCARDRE-TAGFDYWGQGTLLTVSS 137  
 RESULT 5  
 Q96EYO PRELIMINARY; PRT; 620 AA.  
 AC Q96EYO;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE IGHM protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX Strausberg R.;  
 RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC011857; AAH11857.2; -;  
 DR PIR; S15590; S15590.  
 DR HSP; P01820; IG7J.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 4.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 4.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 3.  
 SQ SEQUENCE 620 AA; 68125 MW; 990A1A4A6E8FF27B CRC64;  
 Query Match 77.0%; Score 489.5; DB 2; Length 620;  
 Best Local Similarity 80.3%; Pred. No. 3.4e-42;  
 Matches 98; Conservative 8; Mismatches 11; Indels 5; Gaps 2;  
 QY 1 QVQLQESGPGLVKPSOTLSLTCTVSGGSINSGGYWSWIRQHPGKGLWIGYISGSGSTY 60  
 Db 27 QVQLQESGPGLVKPSOTLSLTCTVSGGSINS--YYWSWIRQHPGKGLWIGYISGSGSTN 84  
 QY 61 YNPSLKSRITLSVDTSKNQPSLKNMTAADTAVYYCARDRE-TAGFDYWGQGTLLTV 117  
 Db 85 YNPSLKSRITLSVDTSKNQPSLKNMTAADTAVYYCARDRE-TAGFDYWGQGTLLTV 144  
 QY 118 SS 119  
 Db 145 SS 146  
 RESULT 6  
 Q9UL73 PRELIMINARY; PRT; 119 AA.  
 ID Q9UL73;  
 AC Q9UL73;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035041; AAD56277.1; -.
DR PIR; PH0876; PH0876.
DR PIR; S12416; S12416.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13219 MW; 1BD86B6420EA0BE CRC64;

Query Match 76.4%; Score 486; DB 2; Length 119;
Best Local Similarity 81.0%; Pred. No. 1.2e-42;
Matches 98; Conservative 5; Mismatches 14; Indels 4; Gaps 2;

QY 1 OVQLQESGGLVKPSTLSCTVSGGSINSGCYWSWIROHPGKLEWIGIYSSGSTY 60
DB 1 OVQLQESGGLVKPSETLSCTVSGGSISSTYYWGWIRQPPKLEWIGISLHNSGSDY 58
QY 61 YNPSLKSRITLSVDTSKNOFSLKNSMTAADTAVVYCARDRETAG--PDYWGQGLTVTVS 118
DB 59 YTPSLKSRVTISVDRSKNOFSLKLTSLTAADTAVYFCARLSNWNQPYFYDWGQGLTVTVS 118
QY 119 S 119
DB 119 S 119

RESULT 7
O95973 PRELIMINARY; PRT; 150 AA.
AC O95973;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE VH4 heavy chain variable region precursor (Fragment).
GN Names=IGM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF103795; AAC79084.1; -.
DR PIR; S31673; S31673.
DR HSSP; S78056; S78056.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 >150 VH4 heavy chain variable region.
FT NON_TER 150
SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;

Query Match 74.9%; Score 476.5; DB 2; Length 150;
Best Local Similarity 75.6%; Pred. No. 1.6e-41;
Matches 90; Conservative 14; Mismatches 14; Indels 1; Gaps 1;

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QY 1 OVQLQESGGLVKPSTLSCTVSGGSINSGCYWSWIROHPGKLEWIGIYSSGSTY 60
DB 20 OVQLQESGGLVKPSETLSCTVSGGSISSTYYWGWIRQPPKLEWIGISLHNSGSDY 79
QY 61 YNPSLKSRITLSVDTSKNOFSLKNSMTAADTAVVYCARDRETAGFDYWGQGLTVTVSS 119
DB 80 YNPSLKSRVTISVDTSKNOFSLKLSVTAADTAVVYCAR-LGMGAFDFWGHGTMVTVSS 137

RESULT 8
O96KX8 PRELIMINARY; PRT; 496 AA.
AC O96KX8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC27165 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Ziegler B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016369; AAHL6369.1; -.
DR HSSP; P01876; IOWO.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;

Query Match 74.8%; Score 475.5; DB 2; Length 496;
Best Local Similarity 74.2%; Pred. No. 7.6e-41;
Matches 92; Conservative 8; Mismatches 19; Indels 5; Gaps 1;

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Qy 116 TVSS 119
Db 140 TVSS 143

RESULT 9
Q6P418 PRELIMINARY; PRT; 576 AA.
AC Q6P418;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGH protein.
GN Name=IGH;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063384; AAH63384.1; -
DR HSSP; P01820; 1A7N.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;

Query Match 73.3%; Score 466.5; DB 2; Length 576;
Best Local Similarity 77.7%; Pred. No. 7.9e-40;
Matches 94; Conservative 7; Mismatches 17; Indels 3; Gaps 2;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYKSWIRQHPKGLIEWIYSSGSTY 60
Db 27 QVQLQESGPGLVKPSQTLSTCTVSGGSINSSN-WWSVWRQPPKGLIEWIYHSGSTN 85
Qy 61 YNPFLSKSRITLSVDTSKNPSLKNMTAADTAAYVCAR--DRETAGFDYWGQGLTVTS 118

us-10-660-357a-25.rup

Db 86 YNPFLSKSRITLSVDTSKNPSLKNMTAADTAAYVCASLGDIVYGVNDVWGQGLTVTS 145
Qy 119 S 119
Db 146 S 146

RESULT 10
Q7Z374 PRELIMINARY; PRT; 492 AA.
AC Q7Z374;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686C02218 (Fragment).
GN Name=DKFZp686C02218;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloembergen H., Boscher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX338077; CAD98001.1; -
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;

Query Match 72.5%; Score 461; DB 2; Length 492;
Best Local Similarity 73.6%; Pred. No. 2.4e-39;
Matches 89; Conservative 12; Mismatches 18; Indels 2; Gaps 1;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCYKSWIRQHPKGLIEWIYSSGSTY 60
Db 32 QVQLQESGPGLVKPSQTLSTCTVSGGSVSNRNYWGWIRQPPKGLIEWIYSSGSTY 91
Qy 61 YNPFLSKSRITLSVDTSKNPSLKNMTAADTAAYVCAR--TAGFDYWGQGLTVTS 118
Db 92 YNPFLSKSRITLSVDTSKNPSLKNMTAADTAAYVCVRHVEGPGYGFDPWGQGLTVTS 151
Qy 119 S 119
Db 152 S 152

RESULT 11
Q81ZD7 PRELIMINARY; PRT; 130 AA.
AC Q81ZD7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-thyroglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jang Y.-J., Chung J., Park J.-Y.;

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RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY145445; AAN64329.1; -.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 130
SQ SEQUENCE 130 AA; 13901 MW; 036131FC6EC1551E CRC64;

Query Match 71.9%; Score 457.5; DB 2; Length 130;
Best Local Similarity 69.2%; Pred. No. 1.3e-39;
Matches 90; Conservative 12; Mismatches 17; Indels 11; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCCYMSWIRQHPGKLEWIGIYSSGST- 59
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLQSGPGLVKPSQTLSTCTVSGGSISSSSYWGWIRQSPGKLEWIGSIYSSGSTY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 60 ----YNPISLKRITLSVDTSKNQFSLKLSMTAADTAVVYCARDRETAG-----FDYW 109
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SGSPYAPSLRSRVITISVDTSKNQLSLRLSSVTAADTAVVYCASPTHCSGGCGYAFQHW 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 110 GQGLTVTVSS 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 GQGLTVTVSS 130
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 12
Q86SX2 PRELIMINARY; PRT; 139 AA.
AC Q86SX2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Full-length cDNA clone CS0DL004YM19 of B cells (Ramos cell line) of
DE Homo sapiens (human) (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Li W.B., Gruber C., Jesse J., Polayes D.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX248300; CAD62627.1; -.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 139
SQ SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;

Query Match 71.5%; Score 455; DB 2; Length 139;
Best Local Similarity 88.0%; Pred. No. 2.5e-39;
Matches 88; Conservative 6; Mismatches 4; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCCYMSWIRQHPGKLEWIGIYSSGSTY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 33 QVQLQESGPGLVKPSQTLSTCTVSGGSISS--YVMSWIRQHPGKLEWIGIYSSGSTN 90
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 YNPISLKRITLSVDTSKNQFSLKLSMTAADTAVVYCARD 100
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 91 YNPISLKRVTISVDTSKNQFSLKLSVTAADTAVVYCARD 130
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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RESULT 13
HV2F HUMAN STANDARD; PRT; 129 AA.
AC P01824;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-II region WAH.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82222325; PubMed=6806818;
RA Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;
RT "Complete amino acid sequence of the delta heavy chain of human
   immunoglobulin D.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
CC -!- MISCELLANEOUS: This chain was isolated from an IgD myeloma
   protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02099; D2HUWA.
DR HSSP; P01820; IG7J.
DR GlycoSuiteDB; P01824; -.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig, 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 113
FT NON_TER 129 129
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Query Match 69.8%; Score 444; DB 1; Length 129;
Best Local Similarity 65.9%; Pred. No. 3.2e-38;
Matches 85; Conservative 11; Mismatches 23; Indels 10; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSINSGCCYMSWIRQHPGKLEWIGIYSSGSTY 60
   ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 RLQLQESGPGLVKPSQTLSTCTVSGGPIRRGTGWIQHPGKLEWIGIYSSGSTY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 YNPISLKRITLSVDTSKNQFSLKLSMTAADTAVVYCARDR-----ETAGFDYWG 110
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 YNPISLGRVTISVDTSRNQFSLNLRMSAADTAVVYCARGNPPYYDICTGSDGIDVWG 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 111 QGTLTVTVSS 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 QGTLTVTVSS 129
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 14
Q9UL75 PRELIMINARY; PRT; 122 AA.
AC Q9UL75;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
   (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cclin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
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RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RT Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035039; AAD56275.1; -.
DR PIR; D36006; D36006.
DR PIR; PH1674; PH1674.
DR PIR; PLO117; PLO117.
DR PIR; PLO160; PLO160.
DR PIR; PS0089; PS0089.
DR PIR; PS0090; PS0090.
DR PIR; PS0091; PS0091.
DR PIR; S12433; S12433.
DR PIR; S24700; S24700.
DR HSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 122 122
FT SEQUENCE 122 AA; 13719 MW; 56CB0612586A6529 CRC64;
Query Match 68.0%; Score 432.5; DB 2; Length 122;
Best Local Similarity 68.9%; Pred. No. 4.7e-37;
Matches 84; Conservative 12; Mismatches 23; Indels 3; Gaps 2;
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGGCYMSWIRHPKGLGIEWIGYVSSGSTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTCAISGDSVSSNSAANNWIRQSPSRGLEWIGRYYSKWY 60
QY 61 --YNPSLKSRITLSVDTSKNQFSLKNSMTAATAVYYCARDRETAG-PDYWGQGLTVTV 117
Db 61 NDYRVSVKSRITINPTDSKQFSLQNSVTPEDTAVYYCARDLELLQPDYWGQGLTVTV 120
QY 118 SS 119
Db 121 SS 122
RESULT 15
Q6NYH3 PRELIMINARY; PRT; 478 AA.
AC Q6NYH3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
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RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL EMBL; BC066594; AAH66594.1; -.
DR HSP; P01820; IA7N.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGc1; 3.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein_
SQ SEQUENCE 478 AA; 51856 MW; 5F8B98F6F0F077256 CRC64;
Query Match 67.5%; Score 429; DB 2; Length 478;
Best Local Similarity 69.4%; Pred. No. 5e-36;
Matches 84; Conservative 16; Mismatches 17; Indels 4; Gaps 2;
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGINSGGCYMSWIRHPKGLGIEWIGYVSSGSTY 60
Db 20 QVDLQESGPGLVKPSQTLSTCTCSVSGDSIAS--YYSWIRKSPQGGMEWIGYIFHSGTLL 77
QY 61 YNPISLKSRITLSVDTSKNQFSLKNSMTAATAVYYCAR--DRETAGDYWGQGLTVTVS 118
Db 78 YNPISLESRTVMSVDTSKDQFSMKLTSTVAADTAIYYCARGYGGKSRFYDLWGRGVPVTVS 137
QY 119 S 119
Db 138 S 138
Search completed: November 9, 2005, 13:05:50
Job time : 62.4386 secs
```

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:43:32 ; Search time 73.985 Seconds  
(without alignments)  
627.306 Million cell updates/sec

Title: US-10-660-357A-29

Perfect score: 629

Sequence: 1 QVQLVESGGGVQPGKSLRL.....FGVVIDYGMVDMVGQGTITTV 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 segs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	629	100.0	120	7	Adc99800 Anti-huma
2	629	100.0	120	7	AdD05404 Anti-MUC1
3	629	100.0	120	7	Adf09842 Human ant
4	580.5	92.3	123	8	AdS84372 Human ant
5	580.5	92.3	123	8	Adr68514 Anti-EPO-
6	577.5	91.8	123	8	AdS84396 Human ant
7	576.5	91.7	123	8	Adr68538 Anti-EPO-
8	576.5	91.7	123	8	AdS84376 Human ant
9	576.5	91.7	123	8	AdS84368 Human ant
10	576.5	91.7	123	8	Adr68518 Anti-EPO-
11	576.5	91.7	123	8	Adr68510 Anti-EPO-
12	576	91.6	118	5	Aam51167 Human DP-
13	571.5	90.9	144	6	Aae37209 Human AB-
14	571	90.8	122	8	Adp22128 Human ant
15	571	90.8	126	7	Adk18593 Anti-huma
16	571	90.8	126	7	Adk18785 Anti-huma
17	571	90.8	126	7	Adk18858 Anti-huma
18	571	90.8	126	8	AdL25404 Human mAb
19	569.5	90.5	121	7	AdP03979 Murine-ex
20	569.5	90.5	121	7	AdP03962 Murine-ex
21	569	90.5	126	7	AdP03963 Murine-ex
22	567.5	90.2	451	3	Aay93734 The heavy
23	567.5	90.2	451	6	Aae35889 Human 11.
24	565.5	89.9	125	8	Adp22316 Human ant
25	565	89.8	121	8	Adp47227 Human pho

ALIGNMENTS

RESULT 1

ADC99800

ID ADC99800 standard; protein; 120 AA.

AC ADC99800;

DT 01-JAN-2004 (first entry)

DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 29.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
KW lung cancer; human.

OS Homo sapiens.

XX WO2003057838-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

PI Gudas J;

DR WPI; 2003-587113/55.

XX N-PSDB; ADC99802.

XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
PT or condition associated with expression of MUC18 in a patient, e.g.  
PT tumors, cancers, and other malignancies.

XX Claim 1; SEQ ID NO 29; 78pp; English.

XX The invention relates to a novel isolated monoclonal antibody comprising  
CC a heavy or light chain amino acid or a heavy or light chain variable  
CC domain where the antibody binds to MUC18. The monoclonal antibody of the  
CC invention demonstrates cytostatic activity and may be useful for treating  
CC a disease or condition associated with the expression of MUC18 on the  
CC cell surface such as tumours, specifically melanoma, oesophageal,  
CC pancreatic or colorectal tumours, carcinomas, particularly cervical  
CC carcinomas and cervical intraepithelial neoplasia and cancers including  
CC colorectal, breast or lung cancer, as well as other malignancies. The  
CC current sequence is that of the anti-human MUC18 monoclonal antibody



## RESULT 4

ADS84372 standard; protein; 123 AA.

XX ADS84372;

DT 18-NOV-2004 (first entry)

XX Human anti-EPO-R antibody heavy chain variable region SEQ ID NO:11.

XX human; erythropoietin receptor; EPO receptor;  
 KW erythropoietin receptor binding antibody; EPO receptor binding antibody;  
 KW antianemic; neuroprotective; vulnary; gene therapy; aplasia; anaemia;  
 KW wound healing; neural cell damage protection;  
 KW neural tissue damage protection; brain injury; spinal cord injury;  
 KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.

XX Homo sapiens.

XX WO2004035603-A2.

XX 29-APR-2004.

XX 14-OCT-2003; 2003WO-US032243.

XX 14-OCT-2002; 2002US-00269711.

XX 10-OCT-2003; 2003US-00684109.

XX (ABBO ) ABBOTT LAB.

XX Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;

XX WPI; 2004-348433/32.

XX N-PSDB; ADS84371.

XX New antibodies that bind to or activate an endogenous human  
 PT erythropoietin receptor, useful for diagnosing, preventing or treating  
 PT disorders associated with dysfunctional erythropoietin receptor, e.g.  
 PT anemia.

XX Claim 9; SEQ ID NO 11; 192pp; English.

XX The present invention describes an antibody or its fragment that binds to  
 CC or activates an endogenous activity of a human erythropoietin (EPO)  
 CC receptor in a mammal, but does not interact with a peptide having a  
 CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)  
 CC methods of modulating or activating an endogenous activity of a human EPO  
 CC receptor in a mammal, comprising administering to the mammal a  
 CC therapeutic amount of the above antibody or its fragment to modulate or  
 CC activate the receptor; (2) a method of treating a mammal suffering from  
 CC aplasia, comprising administering to the mammal a therapeutic amount of  
 CC the above antibody or its fragment to modulate or activate the receptor;  
 CC (3) a pharmaceutical composition comprising a therapeutic amount of the  
 CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)  
 CC an isolated and purified polynucleotide sequence, and their fragments,  
 CC complements and degenerate codon equivalents; and (5) an isolated and  
 CC purified amino acid sequence, and their fragments. The EPO receptor  
 CC binding antibody has antianemic, neuroprotective and vulnary  
 CC activities, and can be used in gene therapy. The compositions and methods  
 CC from the present invention can be used for modulating an endogenous  
 CC activity of a human EPO receptor or for treating mammals suffering from  
 CC aplasia or anaemia. They may also be used for identifying mammals having  
 CC a dysfunctional EPO receptor. The composition may also be used in  
 CC promoting wound healing or in protecting against neural cell and/or  
 CC tissue damage resulting from brain/spinal cord injury, stroke and the  
 CC like. The present sequence represents a human anti-EPO-R antibody heavy  
 CC chain variable region, which is given in the exemplification of the  
 CC present invention.

XX Sequence 123 AA;

Query Match 92.3%; Score 580.5; DB 8; Length 123;  
 Best Local Similarity 93.4%; Pred. No. 5.7e-43;  
 Matches 113; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
 DB 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
 QY 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCARSIFFGVVDYGHVQGGTTVT 119  
 DB 61 ADSVKGRFTISRDNKNTLYLQWNSLRVEDTAIVYCARDHGRYVYVDYGHVQGGTTVT 120  
 QY 120 V 120  
 DB 121 V 121

## RESULT 5

ADR68514

ID ADR68514 standard; protein; 123 AA.

XX ADR68514;

XX 02-DEC-2004 (first entry)

XX Anti-EPO-R antibody heavy chain variable region seqid 11.

XX antianemic; respiratory; vulnary; gene therapy; vaccine;  
 KW erythropoietin receptor; EPO-R; anti-EPO-R antibody; aplasia; anaemia;  
 KW hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;  
 KW wound healing; neural cell damage; tissue damage; brain injury;  
 KW spinal cord injury; stroke; anti-EPO-R antibody; heavy chain;  
 KW variable region.

XX Homo sapiens.

XX US2004175379-A1.

XX 09-SEP-2004.

XX 10-OCT-2003; 2003US-00684109.

XX 14-OCT-2002; 2002US-0418031P.

XX (DEVV/) DEVRIES P J.

XX (OSTR/) OSTROW D H.

XX (REIL/) REILLY E B.

XX (GREE/) GREEN L L.

XX (WIEL/) WIELER J.

XX Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;

XX WPI; 2004-661369/64.

XX N-PSDB; ADR68513.

XX New antibody or its antibody fragment that activates an endogenous  
 PT activity or is capable of binding to a human erythropoietin receptor in a  
 PT mammal, useful for treating a mammal suffering aplasia or anemia.

XX Claim 9; SEQ ID NO 11; 156pp; English.

XX The invention describes an antibody or its fragment that activates an  
 CC endogenous activity or capable of binding to a human erythropoietin  
 CC receptor in a mammal, or that comprises at least one heavy or light chain  
 CC variable region having a sequence comprising 116 or 107 amino acids (SEQ  
 CC ID NO: 3 or 5) given in the specification or its fragment, but does not  
 CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also  
 CC given in the specification. Also described are: a method of activating or  
 CC modulating an endogenous activity of a human erythropoietin receptor in a  
 CC mammal; a pharmaceutical composition comprising a therapeutic amount of  
 CC an antibody or antibody fragment above and a pharmaceutical excipient;  
 CC isolated and purified polynucleotide sequence selected from 28 sequences  
 CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in

CC the specification, and their fragments, complements, and degenerate codon  
 CC equivalents; and an isolated and purified amino acid sequence selected  
 CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between  
 CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or  
 CC their fragments. The antibody or its antibody fragment that activates or  
 CC modulates the activity of the receptor is useful in a method of treating  
 CC a mammal suffering aplasia or anaemia. The antibodies are also useful for  
 CC treating disorders characterised by decreased or subnormal levels of  
 CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue  
 CC hypoxia and/or diseases characterised by inadequate blood circulation or  
 CC reduced blood flow. They are also useful for promoting wound healing or  
 CC for protecting against neural cell and/or tissue damage, resulting from  
 CC brain/spinal cord injury, stroke and the like. The antibodies are also  
 CC useful for identifying or diagnosing mammals having dysfunctional  
 CC erythropoietin receptor. This is the amino acid sequence of an anti-EPO-R  
 CC -antibody heavy chain variable region.

XX  
 SQ Sequence 123 AA;

Query Match 92.3%; Score 580.5; DB 8; Length 123;  
 Best Local Similarity 93.4%; Pred. No. 5.7e-43;  
 Matches 113; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWAVISYDGSNKYY 60  
 DB 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWAVISYDGSNKYY 60  
 QY 61 ADSVKGRTISRDNKNTLYLQMNSLRVEDTAVYICARSIFFG-VVIDYGMVWGOGTTVT 119  
 DB 61 ADSVKGRTISRDNKNTLYLQMNSLRVEDTAVYICARSIFFG-VVIDYGMVWGOGTTVT 120  
 QY 120 V 120  
 DB 121 V 121

RESULT 6  
 ADS84396  
 ID ADS84396 standard; protein; 123 AA.  
 AC ADS84396;  
 DT 18-NOV-2004 (first entry)  
 DE Human anti-EPO-R antibody heavy chain variable region SEQ ID NO:35.  
 KW human; erythropoietin receptor; EPO receptor;  
 KW erythropoietin receptor binding antibody; EPO receptor binding antibody;  
 KW antianaemic; neuroprotective; vulnerary; gene therapy; aplasia; anaemia;  
 KW wound healing; neural cell damage protection;  
 KW neural tissue damage protection; brain injury; spinal cord injury;  
 KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.  
 OS Homo sapiens.  
 XX  
 XX WO2004035603-A2.  
 XX  
 XX 29-APR-2004.  
 XX  
 XX 14-OCT-2003; 2003WO-US032243.  
 XX  
 XX 14-OCT-2002; 2002US-00269711.  
 XX 10-OCT-2003; 2003US-00684109.  
 XX (ABBO ) ABBOTT LAB.  
 XX Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;  
 XX WPI; 2004-348433/32.  
 XX N-PSDB; ADS84395.  
 XX  
 XX New antibodies that bind to or activate an endogenous human  
 XX erythropoietin receptor, useful for diagnosing, preventing or treating

PT disorders associated with dysfunctional erythropoietin receptor, e.g.  
 PT anemia.

XX Claim 9; SEQ ID NO 35; 192pp; English.

CC The present invention describes an antibody or its fragment that binds to  
 CC or activates an endogenous activity of a human erythropoietin (EPO)  
 CC receptor in a mammal, but does not interact with a peptide having a  
 CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)  
 CC methods of modulating or activating an endogenous activity of a human EPO  
 CC receptor in a mammal, comprising administering to the mammal a  
 CC therapeutic amount of the above antibody or its fragment to modulate or  
 CC activate the receptor; (2) a method of treating a mammal suffering from  
 CC aplasia, comprising administering to the mammal a therapeutic amount of  
 CC the above antibody or its fragment to modulate or activate the receptor;  
 CC (3) a pharmaceutical composition comprising a therapeutic amount of the  
 CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)  
 CC an isolated and purified polynucleotide sequence, and their fragments;  
 CC complements and degenerate codon equivalents; and (5) an isolated and  
 CC purified amino acid sequence, and their fragments. The EPO receptor  
 CC binding antibody has antianaemic, neuroprotective and vulnerary  
 CC activities, and can be used in gene therapy. The compositions and methods  
 CC from the present invention can be used for modulating an endogenous  
 CC activity of a human EPO receptor or for treating mammals suffering from  
 CC aplasia or anaemia. They may also be used for identifying mammals having  
 CC a dysfunctional EPO receptor. The composition may also be used in  
 CC promoting wound healing or in protecting against neural cell and/or  
 CC tissue damage resulting from brain/spinal cord injury, stroke and the  
 CC like. The present sequence represents a human anti-EPO-R antibody heavy  
 CC chain variable region, which is given in the exemplification of the  
 CC present invention.

XX  
 SQ Sequence 123 AA;

Query Match 91.8%; Score 577.5; DB 8; Length 123;  
 Best Local Similarity 92.6%; Pred. No. 1e-42;  
 Matches 112; Conservative 1; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWAVISYDGSNKYY 60  
 DB 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWAVISYDGSNKYY 60  
 QY 61 ADSVKGRTISRDNKNTLYLQMNSLRVEDTAVYICARSIFFG-VVIDYGMVWGOGTTVT 119  
 DB 61 ADSVKGRTISRDNKNTLYLQMNSLRVEDTAVYICARSIFFG-VVIDYGMVWGOGTTVT 120  
 QY 120 V 120  
 DB 121 V 121

RESULT 7  
 ADR68538  
 ID ADR68538 standard; protein; 123 AA.  
 XX  
 XX ADR68538;  
 XX  
 XX 02-DEC-2004 (first entry)  
 XX  
 XX Anti-EPO-R-antibody heavy chain variable region seqid 35.  
 XX antianaemic; respiratory; vulnerary; gene therapy; vaccine;  
 KW erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;  
 KW hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;  
 KW wound healing; neural cell damage; tissue damage; brain injury;  
 KW spinal cord injury; stroke; anti-EPO-R-antibody; heavy chain;  
 KW variable region.  
 XX  
 XX Homo sapiens.  
 OS  
 XX US2004175379-A1.  
 XX  
 XX 09-SEP-2004.  
 PD



Db 1 QVQLVESGGGVQPGKSLRSLSCAASGFTSSYGMHWVRQAPGKLEWVWVISYDGSNKYY 60  
QY 61 ADSVKGRFTISRDNKNTLYLQNSLRRAEDTAVYYCARSIFG-VVIDYGMVWVGQTTT 119  
Db 61 ADSVKGRFTISRDNKNTLYLQNSLRVEDTAVYYCARDHGGRYVVDYGMVWVGQTTT 120  
QY 120 V 120  
Db 121 V 121

RESULT 9  
ADS84368  
ID ADS84368 standard; protein; 123 AA.  
XX AC ADS84368;  
XX DT 18-NOV-2004 (first entry)  
XX DE Human anti-EPO-R antibody heavy chain variable region SEQ ID NO:7.  
XX KW human; erythropoietin receptor; EPO receptor;  
KW erythropoietin receptor binding antibody; EPO receptor binding antibody;  
KW antianaemic; neuroprotective; vulnerary; gene therapy; aplasia; anaemia;  
KW wound healing; neural cell damage protection;  
KW neural tissue damage protection; brain injury; spinal cord injury;  
KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.  
XX OS Homo sapiens.  
XX PN WO2004035603-A2.  
XX PD 29-APR-2004.  
XX PF 14-OCT-2003; 2003WO-US032243.  
XX PR 14-OCT-2002; 2002US-00269711.  
XX PR 10-OCT-2003; 2003US-00684109.  
XX PA (ABBO ) ABBOTT LAB.  
XX PI Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;  
XX WPI; 2004-348433/32.  
XX DR N-PSDB; ADS84367.  
XX PT New antibodies that bind to or activate an endogenous human  
XX erythropoietin receptor, useful for diagnosing, preventing or treating  
XX disorders associated with dysfunctional erythropoietin receptor, e.g.  
XX anemia.  
XX PS Claim 6; SEQ ID NO 7; 192pp; English.  
XX CC The present invention describes an antibody or its fragment that binds to  
XX or activates an endogenous activity of a human erythropoietin (EPO)  
XX receptor in a mammal, but does not interact with a peptide having a  
XX sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)  
XX methods of modulating or activating an endogenous activity of a human EPO  
XX receptor in a mammal, comprising administering to the mammal a  
XX therapeutic amount of the above antibody or its fragment to modulate or  
XX activate the receptor; (2) a method of treating a mammal suffering from  
XX aplasia, comprising administering to the mammal a therapeutic amount of  
XX the above antibody or its fragment to modulate or activate the receptor;  
XX (3) a pharmaceutical composition comprising a therapeutic amount of the  
XX above antibody or antibody fragment, and a pharmaceutical excipient; (4)  
XX an isolated and purified polynucleotide sequence, and their fragments,  
XX complements and degenerate codon equivalents; and (5) an isolated and  
XX purified amino acid sequence, and their fragments. The EPO receptor  
XX binding antibody has antianaemic, neuroprotective and vulnerary  
XX activities, and can be used in gene therapy. The compositions and methods  
XX from the present invention can be used for modulating an endogenous  
XX activity of a human EPO receptor or for treating mammals suffering from

CC aplasia or anaemia. They may also be used for identifying mammals having  
CC a dysfunctional EPO receptor. The composition may also be used in  
CC promoting wound healing or in protecting against neural cell and/or  
CC tissue damage resulting from brain/spinal cord injury, stroke and the  
CC like. The present sequence represents a human anti-EPO-R antibody heavy  
CC chain variable region, which is given in the exemplification of the  
CC present invention.  
XX XX  
SQ Sequence 123 AA;  
Query Match 91.7%; Score 576.5; DB 8; Length 123;  
Best Local Similarity 92.6%; Pred. No. 1.3e-42;  
Matches 112; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
QY 1 QVQLVESGGGVQPGKSLRSLSCAASGFTSSYAMHWVRQAPGKLEWVWVISYDGSNKYY 60  
Db 1 QVQLVESGGGVQPGKSLRSLSCVAGSFTSSYGMHWVRQAPGKLEWVWVISYDGSNKYY 60  
QY 61 ADSVKGRFTISRDNKNTLYLQNSLRRAEDTAVYYCARSIFG-VVIDYGMVWVGQTTT 119  
Db 61 ADSVKGRFTISRDNKNTLYLQNSLRVEDTAVYYCARDHGGRYVVDYGMVWVGQTTT 120  
QY 120 V 120  
Db 121 V 121

RESULT 10  
ADR68518  
ID ADR68518 standard; protein; 123 AA.  
XX AC ADR68518;  
XX DT 02-DEC-2004 (first entry)  
XX DE Anti-EPO-R-antibody heavy chain variable region seqid 15.  
XX KW antianaemic; respiratory; vulnerary; gene therapy; vaccine;  
KW erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;  
KW hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;  
KW wound healing; neural cell damage; tissue damage; brain injury;  
KW spinal cord injury; stroke; anti-EPO-R-antibody; heavy chain;  
KW variable region.  
XX OS Homo sapiens.  
XX PN US2004175379-A1.  
XX PD 09-SEP-2004.  
XX PF 10-OCT-2003; 2003US-00684109.  
XX PR 14-OCT-2002; 2002US-0418031P.  
XX PA (DEVV/) DEVRIES P J.  
XX (OSTR/) OSTROW D H.  
XX (REIL/) REILLY E B.  
XX (GREE/) GREEN L L.  
XX (WIEL/) WIELER J.  
XX PI Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;  
XX WPI; 2004-661369/64.  
XX DR N-PSDB; ADR68517.  
XX PT New antibody or its antibody fragment that activates an endogenous  
XX activity or is capable of binding to a human erythropoietin receptor in a  
XX mammal, useful for treating a mammal suffering aplasia or anemia.  
XX PS Claim 9; SEQ ID NO 15; 156pp; English.  
XX CC The invention describes an antibody or its fragment that activates an  
XX endogenous activity or capable of binding to a human erythropoietin



CC receptor in a mammal, or that comprises at least one heavy or light chain  
 CC variable region having a sequence comprising 116 or 107 amino acids (SEQ  
 CC ID NO: 3 or 5) given in the specification or its fragment, but does not  
 CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also  
 CC given in the specification. Also described are: a method of activating or  
 CC modulating an endogenous activity of a human erythropoietin receptor in a  
 CC mammal; a pharmaceutical composition comprising a therapeutic amount of  
 CC an antibody or antibody fragment above and a pharmaceutical excipient; an  
 CC isolated and purified polynucleotide sequence selected from 28 sequences  
 CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in  
 CC the specification, and their fragments, complements, and degenerate codon  
 CC equivalents; and an isolated and purified amino acid sequence selected  
 CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between  
 CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or  
 CC their fragments. The antibody or its antibody fragment that activates or  
 CC modulates the activity of the receptor is useful in a method of treating  
 CC a mammal suffering aplasia or anaemia. The antibodies are also useful for  
 CC treating disorders characterised by decreased or subnormal levels of  
 CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue  
 CC hypoxia and/or diseases characterised by inadequate blood circulation or  
 CC reduced blood flow. They are also useful for promoting wound healing or  
 CC for protecting against neural cell and/or tissue damage, resulting from  
 CC brain/spinal cord injury, stroke and the like. The antibodies are also  
 CC useful for identifying or diagnosing mammals having dysfunctional  
 CC erythropoietin receptor. This is the amino acid sequence of an anti-EPO-R  
 CC -antibody heavy chain variable region.

XX Sequence 123 AA;

Query Match 91.7%; Score 576.5; DB 8; Length 123;

Best Local Similarity 92.6%; Pred. No. 1.3e-42;

Matches 112; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTSSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
 DB 1 QVQLVESGGGVQPGKSLRLSCAASGFTSSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
 QY 61 ADSVKGRFTISRDNKNTLYLQMSLRVEDTAVYYCARSIFFG-VVIDYGMVWGQGTIVT 119  
 DB 61 ADSVKGRFTISRDNKNTLYLQMSLRVEDTAVYYCARSIFFG-VVIDYGMVWGQGTIVT 120  
 QY 120 V 120  
 DB 121 V 121

RESULT 11

ADR68510  
 ID ADR68510 standard; protein; 123 AA.

XX ADR68510;

XX 02-DEC-2004 (first entry)

DE Anti-EPO-R-antibody heavy chain variable region seqid 7.

XX antianaemic; respiratory; vulnery; gene therapy; vaccine;  
 KW erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;  
 KW hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;  
 KW wound healing; neural cell damage; tissue damage; brain injury;  
 KW spinal cord injury; stroke; anti-EPO-R-antibody; heavy chain;  
 KW variable region.

XX Homo sapiens.

XX US2004175379-A1.

XX 09-SEP-2004.

XX 10-OCT-2003; 2003US-00684109.

XX 14-OCT-2002; 2002US-0418031P.

XX

PA (DEVV/) DEVRIES P J.  
 PA (OSTR/) OSTROW D H.  
 PA (REIL/) REILLY E B.  
 PA (GREE/) GREEN L L.  
 PA (WIEL/) WIELER J.

PI Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;

DR WPI: 2004-661369/64.

DR N-PSDB; ADR68509.

XX New antibody or its antibody fragment that activates an endogenous  
 PT activity or is capable of binding to a human erythropoietin receptor in a  
 PT mammal, useful for treating a mammal suffering aplasia or anemia.

PS Claim 6; SEQ ID NO 7; 156pp; English.

XX The invention describes an antibody or its fragment that activates an  
 CC endogenous activity or capable of binding to a human erythropoietin  
 CC receptor in a mammal, or that comprises at least one heavy or light chain  
 CC variable region having a sequence comprising 116 or 107 amino acids (SEQ  
 CC ID NO: 3 or 5) given in the specification or its fragment, but does not  
 CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also  
 CC given in the specification. Also described are: a method of activating or  
 CC modulating an endogenous activity of a human erythropoietin receptor in a  
 CC mammal; a pharmaceutical composition comprising a therapeutic amount of  
 CC an antibody or antibody fragment above and a pharmaceutical excipient; an  
 CC isolated and purified polynucleotide sequence selected from 28 sequences  
 CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in  
 CC the specification, and their fragments, complements, and degenerate codon  
 CC equivalents; and an isolated and purified amino acid sequence selected  
 CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between  
 CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or  
 CC their fragments. The antibody or its antibody fragment that activates or  
 CC modulates the activity of the receptor is useful in a method of treating  
 CC a mammal suffering aplasia or anaemia. The antibodies are also useful for  
 CC treating disorders characterised by decreased or subnormal levels of  
 CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue  
 CC hypoxia and/or diseases characterised by inadequate blood circulation or  
 CC reduced blood flow. They are also useful for promoting wound healing or  
 CC for protecting against neural cell and/or tissue damage, resulting from  
 CC brain/spinal cord injury, stroke and the like. The antibodies are also  
 CC useful for identifying or diagnosing mammals having dysfunctional  
 CC erythropoietin receptor. This is the amino acid sequence of an anti-EPO-R  
 CC -antibody heavy chain variable region.

XX Sequence 123 AA;

Query Match 91.7%; Score 576.5; DB 8; Length 123;

Best Local Similarity 92.6%; Pred. No. 1.3e-42;

Matches 112; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTSSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
 DB 1 QVQLVESGGGVQPGKSLRLSCAASGFTSSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
 QY 61 ADSVKGRFTISRDNKNTLYLQMSLRVEDTAVYYCARSIFFG-VVIDYGMVWGQGTIVT 119  
 DB 61 ADSVKGRFTISRDNKNTLYLQMSLRVEDTAVYYCARSIFFG-VVIDYGMVWGQGTIVT 120  
 QY 120 V 120  
 DB 121 V 121

RESULT 12

AAW51167

ID AAW51167 standard; protein; 118 AA.

XX AAW51167;

XX 10-JUN-2002 (first entry)

XX

DE Human DP-46 heavy chain variable region.

XX Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;

KW complementarity determining region; antirheumatic; antiarthritic;

KW antiulcer; antiasthmatic; anti allergic; antiinflammatory; antischlicking;

KW antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotickling;

KW antianginal; cardiant; antibacterial; virucide; fungicide; antileprotic;

KW protozoacide; cyostatic; neuroprotective; antiparkinsonian; nootropic;

KW human; diagnosis; therapy; DP-46.

XX Homo sapiens.

XX Key Location/Qualifiers

FT 1..30

FT /label= FR1

FT 31..35

FT /label= CDR1

FT 36..49

FT /label= FR2

FT 50..66

FT /label= CDR2

FT 67..98

FT /label= FR3

FT 99..107

FT /label= CDR3

FT 108..118

FT /label= J6

XX WO200212502-A2.

XX 14-FEB-2002.

XX 07-AUG-2001; 2001WO-US024785.

XX 07-AUG-2000; 2000US-0223360P.

XX 29-SEP-2000; 2000US-0236826P.

XX 01-AUG-2001; 2001US-00920137.

XX (CENZ ) CENTOCOR INC.

XX Giles-Komar J, Knight DM, Heavner G, Scallion B, Shealy D;

XX WPI; 2002-217194/27.

XX N-PSDB; ABL53507.

XX Novel isolated mammalian anti-tumor necrosis factor antibody, useful for

PT treating sickle cell anemia, diabetes, atherosclerosis, restenosis,

PT angina pectoris, myocardial infarction, leprosy.

XX Example 3; Fig 4; 131pp; English.

PS The present sequence is that of a human DP-46 heavy chain variable region

XX encoded by a human germline DP-46 gene in a transgenic mouse used in

CC human monoclonal antibody (mAb) construction. A GENTV fusion was

CC performed using spleen cells from a hybrid mouse containing human

CC variable and constant region antibody transgenes that was immunised with

CC recombinant human tumour necrosis factor (TNF) alpha. Human mAbs were

CC obtained that bound immobilised human TNF alpha with apparently high

CC avidity. These mAbs had a totally human IgG1, kappa isotype. Their heavy

CC chain variable region deduced amino acid sequences (see AAM51168-72)

CC showed high similarity to the DP-46 sequence. The invention provides

CC isolated human, primate, rodent, mammalian, chimeric, humanised and/or

CC complementarity determining region (CDR)-grafted anti-TNF antibodies,

CC immunoglobulins, and cleavage products and variants, as well as anti-TNF

CC antibody compositions, encoding or complementary nucleic acids, vectors,

CC host cells, compositions, formulations, devices, transgenic animals,

CC transgenic plants, and methods of making and using them. The anti-TNF

CC antibody comprises at least a portion of an immunoglobulin molecule,

CC especially the heavy chain and/or light chain variable regions given in

CC the present sequence and in AAM51165, or either all of the CDRs of the

CC heavy chain (see AAM51158-60) or all of the CDRs of the light chain (see

CC AAM51161-63). The antibodies may inhibit TNF-induced cell adhesion

CC molecules, inhibit TNF binding to receptor, or provide Arthritic Index

CC improvement in a mouse model. They are useful for diagnosing or treating

CC a TNF related condition in a cell, tissue, organ or animal (claimed) such

CC as rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis,

CC Crohn's pathology, sickle cell anaemia, diabetes, a cardiovascular

CC disease such as arteriosclerosis, atherosclerosis, restenosis, angina

CC pectoris or myocardial infarction, an infectious disease in a cell such

CC as bacterial, viral, and fungal infections, pneumonia, leprosy and

CC malaria, a malignant disease such as leukaemia, chronic myelocytic

CC leukaemia, Burkitt's lymphoma and multiple myeloma, or a neurological

CC disease such as multiple sclerosis, Parkinson's disease, spinal ataxia,

CC Alzheimer's disease and Creutzfeldt-Jakob disease

XX Sequence 118 AA;

XX Query Match 91.6%; Score 576; DB 5; Length 118;

XX Best Local Similarity 93.3%; Pred. No. 1.4e-42;

XX Matches 112; Conservative 1; Mismatches 3; Indels 4; Gaps 1;

QY 1 QVQLVESGGGVOPGRSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60

DB 1 QVQLVESGGGVOPGRSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYVCARSIFGVVYIDYGMVWGQTTVTV 120

DB 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYVCARYYY----YYGMDVWGQTTVTV 116

RESULT 13

AAE37209

ID AAE37209 standard; protein; 144 AA.

XX AAE37209;

XX 07-AUG-2003 (first entry)

XX Human AB-PG1-XG1-077 PSMA antibody heavy chain variable region (VH).

XX Human; Prostate specific membrane antigen; carcinoma; sarcoma; cancer;

KW PSMA; melanoma; therapy; N-acetylated alpha-linked acidic dipeptidase;

KW folate hydrolase; dipeptidyl dipeptidase IV; gamma-glutamyl hydrolase;

KW NAALADase; antibody; heavy chain variable region; VH.

XX Homo sapiens.

XX WO2003034903-A2.

XX 01-MAY-2003.

XX 23-OCT-2002; 2002WO-US033944.

XX 23-OCT-2001; 2001US-0335215P.

PR 07-MAR-2002; 2002US-0362747P.

PR 20-SEP-2002; 2002US-0412618P.

XX (PSMA-) PSMA DEV CO LLC.

XX Maddon PJ, Donovan GP, Olson WC, Schuelke N, Gardner J, Ma D;

XX WPI; 2003-403281/38.

XX N-PSDB; AAE56224.

XX Novel isolated antibody which binds to epitope on prostate specific

PT membrane antigen, and competitively inhibits binding of second antibody

PT to its target epitope on the antigen, useful for treating prostate

XX cancer.

XX Claim 26; Page 236; 238pp; English.

XX The invention relates to an antibody or its antigen-binding fragment

CC which specifically binds to epitope on prostate specific membrane antigen

CC (PSMA), and competitively inhibits the specific binding of a second

CC antibody to its target epitope on PSMA. The invention is useful for

CC diagnosing, treating or preventing PSMA-mediated disease such as prostate

CC cancer or non-prostate cancer bladder chosen from cancer including  
 CC transitional cell carcinoma, pancreatic cancer including pancreatic duct  
 CC carcinoma, lung cancer including non-small cell lung carcinoma, kidney  
 CC cancer including conventional renal cell carcinoma, sarcoma including  
 CC soft tissue sarcoma, breast cancer including breast carcinoma, brain  
 CC cancer including glioblastoma multiforme, neuroendocrine carcinoma, colon  
 CC cancer including colonic carcinoma, testicular cancer including  
 CC testicular embryonal carcinoma, or melanoma including malignant melanoma.  
 CC The invention is useful also for inhibiting or enhancing folate hydrolase  
 CC activity of a folate hydrolase polypeptide, N-acetylated alpha-linked  
 CC acidic dipeptidase (NAALADase) activity of a NAALADase polypeptide,  
 CC dipeptidyl dipeptidase IV activity of a dipeptidyl dipeptidase IV  
 CC polypeptide, gamma-glutamyl hydrolase activity of a gamma-glutamyl  
 CC hydrolase polypeptide. The present sequence is human PSMA antibody heavy  
 CC chain variable region (VH)  
 XX  
 XX Sequence 144 AA;

Query Match 90.9%; Score 571.5; DB 6; Length 144;  
 Best Local Similarity 90.2%; Pred. No. 4.1e-42;  
 Matches 111; Conservative 2; Mismatches 7; Indels 3; Gaps 1;  
 QY 1 QVQLVESGGGVQPGRSRLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 60  
 DB 20 QVQLVESGGGVQPGRSRLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 79  
 QY 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCARSLVGLYNYNYGMVWGQGT 117  
 DB 80 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCARSLVGLYNYNYGMVWGQGT 139  
 QY 118 VTV 120  
 DB 140 VTV 142

RESULT 14  
 ADP22128  
 ID ADP22128 standard; protein; 122 AA.

XX  
 AC ADP22128;  
 DT 09-SEP-2004 (first entry)

DE Human anti-TNFA antibody heavy chain variable region SEQ ID NO:34.

XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;  
 KW anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;  
 KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;  
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;  
 KW neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;  
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;  
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
 KW prostate cancer; immuno-mediated inflammatory disease;  
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
 KW septic shock; cachexia; anorexia; multiple sclerosis.

OS Homo sapiens.

XX WO2004050683-A2.

XX 17-JUN-2004.

XX 02-DEC-2003; 2003WO-US038281.

XX 02-DEC-2002; 2002US-0430729P.

XX (ABGE-) ABGENIX INC.

XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;  
 PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;  
 PI Manchulenchko K, Faggioni R, Senaldi G, Qiaojuan JS;

XX WPI; 2004-480601/45.  
 DR N-PSDB; ADP22127.

XX New recombinant human monoclonal antibody that specifically binds to  
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such  
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid  
 PT arthritis.

XX Example 10; SEQ ID NO 34; 213pp; English.

XX The present invention describes a human monoclonal antibody (I) that  
 CC specifically binds to tumour necrosis factor-alpha (TNFA) and comprises:  
 CC (a) a heavy chain complementarity determining region 1 (CDRI) having the  
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
 CC and (b) a light chain CDRI having the two fully defined 11 amino acid  
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
 CC (M1) the level of TNFA in a patient sample, comprising contacting with  
 CC (I), and detecting the level of binding between the antibody and TNFA in  
 CC the sample; (2) a composition comprising the antibody or its functional  
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a  
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
 CC animal in need of treatment for the disease by administering the human  
 CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFA induced  
 CC apoptosis in an animal by selecting an animal in need of treatment for  
 CC TNFA induced apoptosis by administering the human monoclonal antibody of  
 CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,  
 CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-  
 CC disorders, immunomodulatory, immunosuppressive, nephrotropic,  
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used  
 CC as a TNFA antagonist. The antibody (I) is useful in the preparation of  
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
 CC diseases such as rheumatoid arthritis, glomerulonephritis,  
 CC atherosclerosis, psoriasis, restenosis, septic shock, cachexia, and  
 CC disease, graft-host reactions, immunosuppressive, nephrotropic, and  
 CC multiple sclerosis. The present sequence represents a human anti-TNFA  
 CC antibody heavy chain variable region, which is used in the  
 CC exemplification of the present invention.

XX Sequence 122 AA;

Query Match 90.8%; Score 571; DB 8; Length 122;  
 Best Local Similarity 92.5%; Pred. No. 3.8e-42;  
 Matches 111; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGRSRLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 60

DB 1 QVQLVESGGGVQPGRSRLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCARSLVGLYNYNYGMVWGQGT 120

DB 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCARSLVGLYNYNYGMVWGQGT 120

RESULT 15

ADK18593

ID ADK18593 standard; protein; 126 AA.

XX ADK18593;

XX 06-MAY-2004 (first entry)

XX Anti-human PDGF-D antibody heavy chain protein sequence.

XX antiinflammatory; immunomodulator; cytostatic; gene therapy.

XX Homo sapiens.

XX WO2003057857-A2.

PD	17-JUL-2003.
XX	
XX	06-JAN-2003; 2003WO-US000398.
XX	
XX	07-JAN-2002; 2002US-00041860.
XX	(ABGE-) ABGENIX INC.
PA	
PI	Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI	Bezabeh B;
XX	
DR	WPI; 2003-587119/55.
XX	
PT	New human monoclonal antibody that binds to platelet-derived growth
PT	factor-D (PDGF-D), useful for treating chronic and recurrent human
PT	diseases, such as inflammation, autoimmunity and cancer.
XX	
PS	Disclosure; SEQ ID NO 17; 255pp; English.
XX	
CC	The invention relates to a human monoclonal antibody that binds to
CC	platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC	treating chronic and recurrent human diseases, such as inflammation,
CC	autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC	useful for modulating collagen formation, and for staging various
CC	cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC	generated using an active protein fragment of the gene product from the
CC	clone 30664188.0.99 arising in the conditioned medium obtained when
CC	HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC	sequence corresponds to a protein used in the invention.
XX	
SQ	Sequence 126 AA;
	Query Match 90.8%; Score 571; DB 7; Length 126;
	Best Local Similarity 89.5%; Pred. No. 3.9e-42;
	Matches 111; Conservative 1; Mismatches 8; Indels 4; Gaps 1
Qy	1 QVQLVESGGGVQPGRSLRLSCAASGFTFSYAMHWVRQAPEGLEWAVIYDGSNKYY 60
Db	1 QVQLVESGGGVQPGRSKLRLSCAASGFTFSSYGMHWRQAEPKGLEWAVVIWDGSNKYY 60
Qy	61 ADSVKRGFTTTRSDNSKNTLYLOMNSLRADETAVVYCARS----IFGVVIDYGMVDVGOGT 116
Db	61 ADSVKRGFTTTRSDNSKNTLYLOMNSLRADETAVVYCARDQGVRVAGYYTYDGMVDVGOGT 120
Qy	117 TVTV 120
Db	121 TVTV 124

Search completed: November 9, 2005, 12:55:30  
Job time : 74.985 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:29:55 ; Search time 18.6466 Seconds  
(without alignments)  
480.403 Million cell updates/sec

Title: US-10-660-357A-29

Perfect score: 629

Sequence: 1 QVQLVSGGGVQPGKSLRL.....FGVVIDYGMVWGQTTTV 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/6CTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	567.5	90.2	451	4	US-09-472-087-70
2	559	88.9	123	3	US-08-983-607-38
3	550	87.4	248	4	US-09-315-926A-80
4	549.5	87.4	123	4	US-09-424-840B-6
5	546.5	86.9	120	1	US-07-942-245-35
6	544.5	86.6	119	1	US-08-331-398A-46
7	544.5	86.6	119	2	US-08-331-397B-46
8	544.5	86.6	119	2	US-08-759-804A-46
9	544.5	86.6	119	3	US-09-227-693-46
10	542.5	86.2	123	4	US-09-560-198A-2
11	538	85.5	124	4	US-09-424-840B-16
12	530	84.3	126	3	US-09-240-274-26
13	529	84.1	310	3	US-09-079-029-11
14	527.5	83.9	115	4	US-09-726-219A-167
15	526.5	83.7	123	4	US-09-560-198A-4
16	526.5	83.7	225	4	US-09-456-090A-60
17	526.5	83.7	225	4	US-09-456-090A-92
18	526.5	83.7	225	4	US-09-456-090A-108
19	526.5	83.7	225	4	US-09-453-234-60
20	526.5	83.7	225	4	US-09-453-234-92
21	526.5	83.7	225	4	US-09-453-234-108
22	526	83.6	126	3	US-09-240-274-152
23	524.5	83.4	123	4	US-09-560-198A-10
24	524.5	83.4	167	4	US-09-472-087-80
25	524	83.3	126	3	US-09-240-274-153
26	522	83.0	126	3	US-09-240-274-25
27	522	83.0	174	4	US-09-472-087-12

28	521.5	82.9	225	4	US-09-456-090A-102	Sequence 102, App
29	521.5	82.9	225	4	US-09-453-234-102	Sequence 102, App
30	520.5	82.8	117	3	US-09-025-769B-24	Sequence 24, Appl
31	520.5	82.8	117	4	US-09-490-070A-24	Sequence 24, Appl
32	520.5	82.8	117	4	US-09-490-153-24	Sequence 24, Appl
33	520.5	82.8	117	4	US-09-490-324-24	Sequence 24, Appl
34	520.5	82.8	225	4	US-09-456-090A-106	Sequence 106, App
35	520.5	82.8	225	4	US-09-453-234-106	Sequence 106, App
36	520	82.7	463	4	US-09-472-087-4	Sequence 4, Appli
37	520	82.7	463	4	US-09-472-087-68	Sequence 68, Appl
38	519.5	82.6	116	1	US-08-211-202-141	Sequence 141, App
39	519.5	82.6	225	4	US-09-456-090A-110	Sequence 110, App
40	519.5	82.6	225	4	US-09-453-234-110	Sequence 110, App
41	519.5	82.6	287	3	US-08-862-124-17	Sequence 17, Appl
42	519.5	82.6	304	3	US-08-862-124-14	Sequence 14, Appl
43	518.5	82.4	125	3	US-09-240-274-24	Sequence 24, Appl
44	518.5	82.4	225	4	US-09-456-090A-56	Sequence 56, Appl
45	518.5	82.4	225	4	US-09-453-234-56	Sequence 56, Appl

ALIGNMENTS

RESULT 1  
US-09-472-087-70  
; Sequence 70, Application US/09472087  
; Patent No. 6682736  
; GENERAL INFORMATION:  
; APPLICANT: HANSON, DOUGLAS C.  
; APPLICANT: NEVEU, MARK J.  
; APPLICANT: MUELLER, EILLEN E.  
; APPLICANT: HANKE, JEFFREY H.  
; APPLICANT: GILMAN, STEVEN C.  
; APPLICANT: DAVIS, C. GEOPFREY  
; APPLICANT: CORVALAN, JOSE R.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
; FILE REFERENCE: ABX-PFI  
; CURRENT APPLICATION NUMBER: US/09/472,087  
; CURRENT FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/113,647  
; PRIOR FILING DATE: 1998-12-23  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 70  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-472-087-70

Query Match 90.2%; Score 567.5; DB 4; Length 451;  
Best Local Similarity 90.2%; Pred.No. 6.7e+49;  
Matches 111; Conservative 1; Mismatches 8; Indels 3; Gaps 1;  
  
QY 1 QVQLVSGGGVQPGKSLRLSCAASGFTFSVAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
Db 1 QVQLVSGGGVQPGKSLRLSCAASGFTFSVAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
  
QY 61 ADSVKGRFTISRDNKNTLYLQNSLRABDTAVYYCARSIFGVVI---DYGMVWGQGT 117  
Db 61 ADSVKGRFTISRDNKNTLYLQNSLRABDTAVYYCARSIFGVVI---DYGMVWGQGT 120

QY 118 VTV 120  
Db 121 VTV 123

RESULT 2  
US-08-983-607-38  
; Sequence 38, Application US/08983607  
; Patent No. 6140470  
; GENERAL INFORMATION:  
; APPLICANT: Alan Garen  
; APPLICANT: Xiaohong Cai

;; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-  
;; TITLE OF INVENTION: bodies  
;; NUMBER OF SEQUENCES: 51  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Department of Molecular Biophysics  
;; ADDRESSEE: and Biochemistry, Yale University  
;; STREET: 266 Whitney Avenue  
;; CITY: New Haven  
;; STATE: Connecticut  
;; COUNTRY: United States of America  
;; ZIP: 06520-8114  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" 1.44 Mb diskette  
;; COMPUTER: IBM PC  
;; OPERATING SYSTEM: MS DOS  
;; SOFTWARE: Word Processing  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/983,607  
;; FILING DATE: April 27, 1998  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/IB96/01032  
;; FILING DATE: June 28, 1996  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mary M. Krinsky  
;; REGISTRATION NUMBER: 32423  
;; REFERENCE/DOCKET NUMBER: OCR-679  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 203-773-9544  
;; TELEFAX: 203-773-1183  
;; INFORMATION FOR SEQ ID NO: 38:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 123 residues  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE:  
;; DESCRIPTION: polypeptide  
;; ORIGINAL SOURCE:  
;; ORGANISM: Homo sapiens (melanoma patient  
;; ORGANISM: immunized with autologous tumor cells)  
;; INDIVIDUAL ISOLATE: peripheral blood lympho-  
;; INDIVIDUAL ISOLATE: cytes  
;; IMMEDIATE SOURCE:  
;; LIBRARY: DM414 scFv antibodies obtained from  
;; LIBRARY: fuses fusion phage construct  
;; CLONE: V575  
;; FEATURE:  
;; NAME/KEY: heavy chain  
;; US-08-983-607-38

Query Match 88.9%; Score 559; DB 3; Length 123;  
Best Local Similarity 91.0%; Pred. No. 1.le-48;  
Matches 111; Conservative 1; Mismatches 8; Indels 2; Gaps 2;  
Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAISYDGSNKYY 60  
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAISYDGSNKYY 60  
Qy 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYICARSI--FGVVIDYGMVWGQTTV 118  
Db 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYICARSI--FGVVIDYGMVWGQTTV 120  
Qy 119 TV 120  
Db 121 TV 122

RESULT 3  
US-09-315-926A-80  
; Sequence 80, Application US/09315926A  
; Patent No. 6498027

;; GENERAL INFORMATION:  
;; APPLICANT: Es van, Helmut  
;; APPLICANT: Havenga, Menzo  
;; APPLICANT: Verlingen, Stefan  
;; TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER  
;; FILE REFERENCE: 2183-4080US  
;; CURRENT APPLICATION NUMBER: US/09/315,926A  
;; CURRENT FILING DATE: 1999-05-20  
;; PRIOR APPLICATION NUMBER: EP 99201593.3  
;; PRIOR FILING DATE: 1999-05-20  
;; PRIOR APPLICATION NUMBER: EP 98201693.3  
;; PRIOR FILING DATE: 1998-05-20  
;; NUMBER OF SEQ ID NOS: 81  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 80  
;; LENGTH: 248  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; OTHER INFORMATION: Description of Artificial Sequence: phase  
;; NAME/KEY: PEPTIDE  
;; LOCATION: (1)..(248)  
;; OTHER INFORMATION: /note="hCAT1 amino acid sequence"  
;; US-09-315-926A-80

Query Match 87.4%; Score 550; DB 4; Length 248;  
Best Local Similarity 90.0%; Pred. No. 1.9e-47;  
Matches 108; Conservative 1; Mismatches 9; Indels 2; Gaps 1;  
Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAISYDGSNKYY 60  
Db 23 QVQLVQSGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAISYDGSNKYY 82  
Qy 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYICARSI--FGVVIDYGMVWGQTTV 120  
Db 83 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYICARSI--TVTKSRFDYWGQTLTV 140

RESULT 4  
US-09-424-840B-6  
; Sequence 6, Application US/09424840B  
; Patent No. 6790938  
;; GENERAL INFORMATION:  
;; APPLICANT: Berchtold, Peter  
;; APPLICANT: Escher, Robert F. A.  
;; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES  
;; FILE REFERENCE: 100564-09049  
;; CURRENT APPLICATION NUMBER: US/09/424,840B  
;; CURRENT FILING DATE: 1999-12-03  
;; PRIOR APPLICATION NUMBER: DE 19820663.1  
;; PRIOR FILING DATE: 1998-05-08  
;; PRIOR APPLICATION NUMBER: DE 19755227.7  
;; PRIOR FILING DATE: 1997-12-12  
;; PRIOR APPLICATION NUMBER: DE 19723904.8  
;; PRIOR FILING DATE: 1997-06-06  
;; NUMBER OF SEQ ID NOS: 128  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 6  
;; LENGTH: 123  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; US-09-424-840B-6

Query Match 87.4%; Score 549.5; DB 4; Length 123;  
Best Local Similarity 88.5%; Pred. No. 9.9e-48;  
Matches 108; Conservative 7; Mismatches 4; Indels 3; Gaps 2;  
Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAISYDGSNKYY 60  
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAISYDGSNKYY 60  
Qy 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYICARSI--FGVVIDYGMVWGQTTV 118

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Db      ||||| ||||| ||||| ||||| ||||| : | : ||||| : |||  
61 ADSVKGRFAISRDNSKNTLYQMNLSLRADETAVYYCARALGSWG-GWDHYVNDWVGRTTV 119
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Qy	119	TV	120
Db	120	TV	121

RESULT 5  
US-07-942-245-35  
; Sequence 35, Application US/07942245  
; Patent NO. 5639641  
; GENERAL INFORMATION:  
; APPLICANT: PEDERSEN, Jan T.  
; APPLICANT: SEARLE, Stephen M.J.  
; APPLICANT: REES, Anthony R.  
; APPLICANT: ROGUSKA, Michael A.  
; APPLICANT: GUILD, Braydon C.  
; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT  
; TITLE OF INVENTION: ANTIBODIES  
; NUMBER OF SEQUENCES: 522  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.

Query Match	86.9%;	Score 546.5;	DB 1;	Length 120;
Best Local Similarity	88.6%;	Pred. No. 1.9e-47;		
Matches 109; Conservative	1;	Mismatches 6;	Indels 7;	Gaps 2

[illegible]

**Qy**

61 ADSVKGRFTISRNSKNTLYLQWNSLR AEDTAVYVCARSIFGVVIDG---MDVWGQGTT 117  
|||||  
|||||

**Dd**

61 ADSVKGRFTISRNSKNTLYLQWNSLR AEDTAVYVCARD----RKDWGHALFDYWGQGTLL 116  
|||||  
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Qy	118	VTV	120
Db	117	VTV	119

RESULT 6  
US-08-331-398A-46  
; Sequence 46, Application US/08331398A  
; Patent No. 5608039  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira  
; APPLICANT: Willingham, Mark

```

1  APPLICANT: FitzGerald, David
2  APPLICANT: Brinkmann, Ulrich
3  APPLICANT: Pai, Lee
4  TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
5  TITLE OF INVENTION: and Their Uses (as amended)
6  NUMBER OF SEQUENCES: 68
7  CORRESPONDENCE ADDRESS:
8  ADDRESSEE: Townsend and Townsend and Crew
9  STREET: One Market Plaza, Steuart Street Plaza
10 CITY: San Francisco
11 STATE: California
12 COUNTRY: USA
13 ZIP: 94103-1492
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC Compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: Patentin Release #1.0, Version #1.30
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/08/331,398A
21 FILING DATE: 28-OCT-1994
22 CLASSIFICATION: 435
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: US 07/767,331
25 FILING DATE: 30-SEP-1991
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: US 07/596,289
28 FILING DATE: 12-OCT-1990
29 ATTORNEY/AGENT INFORMATION:
30 NAME: Hunter, Tom
31 REGISTRATION NUMBER: 38,498
32 REFERENCE/DOCKET NUMBER: 015280-126110US
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: (415) 543-9600
35 TELEFAX: (415) 543-5043
36 INFORMATION FOR SEQ ID NO: 46:
37 SEQUENCE CHARACTERISTICS:
38 LENGTH: 119 amino acids
39 TYPE: amino acid
40 STRANDEDNESS:
41 TOPOLOGY: linear
42 MOLECULE TYPE: protein
43 FEATURES:
44 NAME/KEY: Protein
45 LOCATION: 1..119
46 OTHER INFORMATION: /note= "Human fetal immunoglobulin
47 OTHER INFORMATION: 56P1'CL Variable'Heavy chain (V-H)"
48 US-08-331-398A-46

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Query Match		86.6%	Score 544.5;	DB 1;	Length 119;	
Best Local Similarity		89.3%;	Pred. No. 3e-47;			
Matches 107; Conservative		1;	Mismatches	9;	Indels	3; Gaps 1;

  

Qy	1	QVQLVSGGCVGFGRSLRLSCAASGFTFSSYAMHWVRQAPGKLEWVAIVSYDGSNKYY	60
	:	:    :	
Db	1	QVELVSGGVQFGFRSLRLSCAASGFTFSSYAMHWVRQAPGKLEWVAIVSYDGSNKYY	60

  

Qy	61	ADSVKGRTILSRNSKNLTLYLWNLSRAEDATAVYICARSIPIGVVIDYGMDMVGOGTITVT	120
	:	:    :	
Db	61	ADSVKGRFTILSRNSKNLTLYLWNLSRAEDATAVYICARR---SARTYFFDVWGOGTLTVT	117

## RESULT 7

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US-08-331-397B-46
; Sequence 46, Application US/08331397B
; Patent No. 5981726
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; TITLE OF INVENTION: Chimeric and N
; TITLE OF INVENTION: Specific Anti
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 68

```

3



COUNTRY: US  
ZIP: 94105-1493  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/227,693  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/331,396  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/767,331  
FILING DATE: 30-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/596,289  
FILING DATE: 12-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 15280-126-1-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..119  
OTHER INFORMATION: /note= "Human fetal immunoglobulin  
US-09-227-693-46

Query Match 86.6%; Score 544.5; DB 3; Length 119;  
Best Local Similarity 89.2%; Pred. No. 3e-47;  
Matches 107; Conservative 1; Mismatches 9; Indels 3; Gaps 1;  
QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
DB 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYCARSIYGVVYDYGMDVWGQGLTVTV 120  
DB 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYCARSIYGVVYDYGMDVWGQGLTVTV 117

RESULT 10  
US-09-560-198A-2  
Sequence 2, Application US/09560198A  
Patent No. 6492497  
GENERAL INFORMATION:  
APPLICANT: Thompson, Julia E  
APPLICANT: Lennard, Simon N  
APPLICANT: Wilton, Alison J  
APPLICANT: Braddock, Peta SH  
APPLICANT: Du Fou, Sarah L  
APPLICANT: McCafferty, John G  
APPLICANT: Conroy, Louise A  
APPLICANT: Tempest, Philip R  
TITLE OF INVENTION: Specific binding members for TGFbeta1  
FILE REFERENCE: 28111/35620A  
CURRENT APPLICATION NUMBER: US/09/560,198A  
CURRENT FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/131,983  
PRIOR FILING DATE: 1999-04-30  
NUMBER OF SEQ ID NOS: 25

SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 123  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-560-198A-2  
Query Match 86.2%; Score 542.5; DB 4; Length 123;  
Best Local Similarity 87.0%; Pred. No. 5e-47;  
Matches 107; Conservative 5; Mismatches 6; Indels 5; Gaps 2;  
QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
DB 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYCARSIYGVVYDYGMDVWGQGLTVTV 117  
DB 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYCARSIYGVVYDYGMDVWGQGLTVTV 118  
QY 118 TVTV 120  
DB 119 TVTV 121

RESULT 11  
US-09-424-840B-16  
Sequence 16, Application US/09424840B  
Patent No. 6790938  
GENERAL INFORMATION:  
APPLICANT: Berchtold, Peter  
APPLICANT: Escher, Robert F. A.  
TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES  
FILE REFERENCE: 100564-09049  
CURRENT APPLICATION NUMBER: US/09/424,840B  
CURRENT FILING DATE: 1999-12-03  
PRIOR APPLICATION NUMBER: DE 19820663.1  
PRIOR FILING DATE: 1998-05-08  
PRIOR APPLICATION NUMBER: DE 19755227.7  
PRIOR FILING DATE: 1997-12-12  
PRIOR APPLICATION NUMBER: DE 19723904.8  
PRIOR FILING DATE: 1997-06-06  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 16  
LENGTH: 124  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-424-840B-16

Query Match 85.5%; Score 538; DB 4; Length 124;  
Best Local Similarity 85.5%; Pred. No. 1.4e-46;  
Matches 106; Conservative 4; Mismatches 8; Indels 6; Gaps 2;  
QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
DB 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60  
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYCARSIYGVVYDYGMDVWGQGLTVTV 116  
DB 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYCARSIYGVVYDYGMDVWGQGLTVTV 118  
QY 117 TVTV 120  
DB 119 TVTV 122

RESULT 12  
US-09-240-274-26  
Sequence 26, Application US/09240274  
Patent No. 6255455  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

```
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D31
US-09-240-274-26

Query Match      84.3%; Score 530; DB 3; Length 126;
Best Local Similarity 81.2%; Pred. No. 9.1e-46;
Matches 104; Conservative 7; Mismatches 5; Indels 12; Gaps 2;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTPSVYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db 1 EVQLLESGGGVQPGKSLRLSCAASGFTPSVYGMHWVRQAPGKLEWVAIVSYDGSNKHY 60

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCAR-----SIFGWIDYGMVW 112
Db 61 SDSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCARERNFRSGYSRY----YYGMDVW 116

QY 113 GGGTTTVV 120
Db 117 GPGTTTVV 124

RESULT 13
US-09-079-029-11
; Sequence 11, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: Amino Acid
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; TOPOLOGY: Linear
US-09-079-029-11

Query Match      84.1%; Score 529; DB 3; Length 310;
Best Local Similarity 85.4%; Pred. No. 3.1e-45;
Matches 105; Conservative 2; Mismatches 6; Indels 10; Gaps 2;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTPSVYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db 40 QVQLVQSGGGVQPGKSLRLSCAASGFTPSVYGMHWVRQAPGKLEWVAGIFYDGGNKYY 99

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCARSIKFGVVID---YGMVDVMGQGT 117
Db 100 ADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCAR-----DRGIYYMDVMGKGIT 152

QY 118 VTV 120
Db 153 VTV 155

RESULT 14
US-09-726-219A-167
; Sequence 167, Application US/09726219A
; Patent No. 6806079
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clarkson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 213839-00013
; CURRENT APPLICATION NUMBER: US/09/726,219A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 167
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-726-219A-167

Query Match      83.9%; Score 527.5; DB 4; Length 115;
Best Local Similarity 88.0%; Pred. No. 1.5e-45;
Matches 103; Conservative 4; Mismatches 7; Indels 3; Gaps 2;
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Qy 1 QVQLVESGGGVVQPGSRRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60  
Db 1 QVQLVQSGGGVQPGSRRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60  
Qy 61 ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARSIFGVVIDYG-MDVWGQGT 116  
Db 61 ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKT--GYSSGMGYFDYWGQGT 115

RESULT 15

US-09-560-198A-4  
; Sequence 4, Application US/09560198A  
; Patent No. 6492497  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Julia E  
; APPLICANT: Lennard, Simon N  
; APPLICANT: Wilton, Alison J  
; APPLICANT: Braddock, Peta SH  
; APPLICANT: Du Fou, Sarah L  
; APPLICANT: McCafferty, John G  
; APPLICANT: Conroy, Louise A  
; APPLICANT: Tempest, Philip R  
; TITLE OF INVENTION: Specific binding members for TGFbeta1  
; FILE REFERENCE: 2811/35620A  
; CURRENT APPLICATION NUMBER: US/09/560,198A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/131,983  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-560-198A-4

Query Match 83.7%; Score 526.5; DB 4; Length 123;  
Best Local Similarity 86.2%; Pred. No. 2e-45;  
Matches 106; Conservative 2; Mismatches 10; Indels 5; Gaps 2;

Qy 1 QVQLVESGGGVVQPGSRRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60  
Db 1 EVQLVESGGGVVQPGSRRLSCAASGFTFSSYGMHWVRQAPGKLEWVAVISYDGSIKYY 60  
Qy 61 ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARSIFGVVIDYCMD---VWGQGT 117  
Db 61 ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCART--GEYSGYDTPQYSWGQGT 118  
Qy 118 VTV 120  
Db 119 VTV 121

Search completed: November 9, 2005, 11:46:41  
Job time : 19.6466 secs

THIS BOOK BELONGS TO

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:40:37 ; Search time 66.6667 Seconds  
(without alignments)  
753.137 Million cell updates/sec

Title: US-10-660-357A-29

Perfect score: 629  
Sequence: 1 QVQLVSGGVPGRSLRL.....FGVVIDYGMVWGQTTVT 120

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
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7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	629	100.0	120	14	US-10-330-613-29
2	629	100.0	120	14	US-10-330-530-29
3	629	100.0	120	16	US-10-660-357-29
4	580.5	92.3	123	15	US-10-269-711-11
5	580.5	92.3	123	15	US-10-269-711-23
6	580.5	92.3	123	15	US-10-269-711-27
7	580.5	92.3	123	15	US-10-269-711-31
8	580.5	92.3	123	15	US-10-269-711-35
9	580.5	92.3	123	16	US-10-684-109-11
10	578	91.9	124	15	US-10-292-088-106
11	577.5	91.8	123	15	US-10-269-711-43
					Sequence 29, Appl
					Sequence 29, Appl
					Sequence 11, Appl
					Sequence 23, Appl
					Sequence 27, Appl
					Sequence 31, Appl
					Sequence 35, Appl
					Sequence 11, Appl
					Sequence 106, Appl
					Sequence 43, Appl

12	577.5	91.8	123	16	US-10-684-109-35	Sequence 35, Appl
13	577	91.7	141	17	US-10-858-855-11	Sequence 11, Appl
14	576.5	91.7	123	15	US-10-269-711-7	Sequence 7, Appl
15	576.5	91.7	123	15	US-10-269-711-15	Sequence 15, Appl
16	576.5	91.7	123	16	US-10-684-109-7	Sequence 7, Appl
17	576.5	91.7	123	16	US-10-684-109-15	Sequence 15, Appl
18	574.5	91.3	122	20	US-11-031-485-116	Sequence 116, App
19	574.5	91.3	123	15	US-10-292-088-115	Sequence 115, App
20	572.5	91.0	123	15	US-10-292-088-117	Sequence 117, App
21	571.5	90.9	144	15	US-10-395-894-31	Sequence 31, Appl
22	571.5	90.9	144	16	US-10-695-667-31	Sequence 31, Appl
23	571.5	90.9	144	18	US-10-976-352-31	Sequence 31, Appl
24	571	90.8	122	17	US-10-727-155-34	Sequence 34, Appl
25	571	90.8	126	14	US-10-041-860-17	Sequence 17, Appl
26	571	90.8	126	14	US-10-041-860-209	Sequence 209, Appl
27	571	90.8	126	14	US-10-041-860-282	Sequence 282, App
28	571	90.8	126	16	US-10-665-383-14	Sequence 14, Appl
29	569.5	90.5	121	15	US-10-309-762-132	Sequence 132, App
30	569.5	90.5	121	15	US-10-309-762-133	Sequence 133, App
31	569	90.5	126	15	US-10-309-762-133	Sequence 133, App
32	568.5	90.4	123	15	US-10-292-088-116	Sequence 116, App
33	567.5	90.2	117	20	US-11-009-731-47	Sequence 47, Appl
34	567.5	90.2	451	14	US-10-153-382-17	Sequence 17, Appl
35	567.5	90.2	451	16	US-10-612-497-70	Sequence 70, Appl
36	567.5	90.2	451	16	US-10-776-649-70	Sequence 70, Appl
37	567.5	90.2	451	20	US-11-085-368-17	Sequence 17, Appl
38	566.5	90.1	125	15	US-10-292-088-107	Sequence 107, App
39	565.5	89.9	125	17	US-10-727-155-222	Sequence 222, App
40	565	89.8	121	17	US-10-726-332-142	Sequence 142, App
41	565	89.8	124	15	US-10-371-942-82	Sequence 82, Appl
42	564	89.7	117	20	US-11-031-485-115	Sequence 115, App
43	563.5	89.6	252	10	US-09-880-748-1731	Sequence 1731, Ap
44	563.5	89.6	252	15	US-10-293-418-1731	Sequence 1731, Ap
45	563	89.5	122	9	US-09-144-886-69	Sequence 69, Appl

ALIGNMENTS

RESULT 1  
US-10-330-613-29  
; Sequence 29, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; PRIOR FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 120  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-29

Query Match 100.0%; Score 629; DB 14; Length 120;  
Best Local Similarity 100.0%; Pred. No. 3.6e-53;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	QVQLVSGGVPGRSLRLSCAASGFTSSYAMHWVRQAPGKLEWVAIVSDGSKYY	60
Db	1	QVQLVSGGVPGRSLRLSCAASGFTSSYAMHWVRQAPGKLEWVAIVSDGSKYY	60
Qy	61	ADSVKGRFTISRDNSKNTLYLQNSLRRAEDTAVYVCARSIFGVVIDYGMVWGQTTVT	120
Db	61	ADSVKGRFTISRDNSKNTLYLQNSLRRAEDTAVYVCARSIFGVVIDYGMVWGQTTVT	120

RESULT 2

```
US-10-330-530-29
; Sequence 29, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-29

Query Match          100.0%; Score 629; DB 14; Length 120;
Best Local Similarity 100.0%; Pred. No. 3.6e-53;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYYCARSI FGVVVDYGMVWGQGTITV 120
Db 61 ADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYYCARSI FGVVVDYGMVWGQGTITV 120

RESULT 3
US-10-660-357-29
; Sequence 29, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-29

Query Match          100.0%; Score 629; DB 16; Length 120;
Best Local Similarity 100.0%; Pred. No. 3.6e-53;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYYCARSI FGVVVDYGMVWGQGTITV 120
Db 61 ADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYYCARSI FGVVVDYGMVWGQGTITV 120

RESULT 4
US-10-269-711-11
; Sequence 11, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Devries, Peter J.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Ostrow, Dave
; APPLICANT: Weiler, James
; APPLICANT: Green, Larry
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 6989.US.O1
; CURRENT APPLICATION NUMBER: US/10/269,711
; CURRENT FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-711-11

Query Match          92.3%; Score 580.5; DB 15; Length 123;
Best Local Similarity 93.4%; Pred. No. 1.9e-48;
Matches 113; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYYCARSI FG-VVVDYGMVWGQGTITV 119
Db 61 ADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYYCARSI FG-VVVDYGMVWGQGTITV 120

120 V 120
121 V 121

RESULT 5
US-10-269-711-23
; Sequence 23, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Devries, Peter J.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Ostrow, Dave
; APPLICANT: Weiler, James
; APPLICANT: Green, Larry
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 6989.US.O1
; CURRENT APPLICATION NUMBER: US/10/269,711
; CURRENT FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-711-23

Query Match          92.3%; Score 580.5; DB 15; Length 123;
Best Local Similarity 93.4%; Pred. No. 1.9e-48;
Matches 113; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYYCARSI FG-VVVDYGMVWGQGTITV 119
Db 61 ADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYYCARSI FG-VVVDYGMVWGQGTITV 120

120 V 120
121 V 121
```

```
Db      121 V 121
RESULT 6
US-10-269-711-27
; Sequence 27, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: DeVries, Peter J.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Ostrow, Dave
; APPLICANT: Weiler, James
; APPLICANT: Green, Larry
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
; FILE REFERENCE: 6989 US 01
; CURRENT APPLICATION NUMBER: US/10/269,711
; CURRENT FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-711-27

Query Match      92.3%; Score 580.5; DB 15; Length 123;
Best Local Similarity 93.4%; Pred. No. 1.9e-48;
Matches 113; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY      1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db      1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAIVSYDGSNKYY 60
QY      61 ADSVKGRFTISRDNKNTLYLQNSLRVEDTAVYICARDHGGRYVYDYGMDVMVGQGTTVT 119
Db      61 ADSVKGRFTISRDNKNTLYLQNSLRVEDTAVYICARDHGGRYVYDYGMDVMVGQGTTVT 120
QY      120 V 120
Db      121 V 121

RESULT 8
US-10-269-711-35
; Sequence 35, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: DeVries, Peter J.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Ostrow, Dave
; APPLICANT: Weiler, James
; APPLICANT: Green, Larry
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
; FILE REFERENCE: 6989 US 01
; CURRENT APPLICATION NUMBER: US/10/269,711
; CURRENT FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-711-35

Query Match      92.3%; Score 580.5; DB 15; Length 123;
Best Local Similarity 93.4%; Pred. No. 1.9e-48;
Matches 113; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY      1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db      1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAIVSYDGSNKYY 60
QY      61 ADSVKGRFTISRDNKNTLYLQNSLRVEDTAVYICARDHGGRYVYDYGMDVMVGQGTTVT 119
Db      61 ADSVKGRFTISRDNKNTLYLQNSLRVEDTAVYICARDHGGRYVYDYGMDVMVGQGTTVT 120
QY      120 V 120
Db      121 V 121

RESULT 9
US-10-684-109-11
; Sequence 11, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Weiler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: 6989 US 02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11

Query Match      92.3%; Score 580.5; DB 15; Length 123;
Best Local Similarity 93.4%; Pred. No. 1.9e-48;
Matches 113; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY      1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db      1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAIVSYDGSNKYY 60
QY      61 ADSVKGRFTISRDNKNTLYLQNSLRVEDTAVYICARDHGGRYVYDYGMDVMVGQGTTVT 119
Db      61 ADSVKGRFTISRDNKNTLYLQNSLRVEDTAVYICARDHGGRYVYDYGMDVMVGQGTTVT 120
QY      120 V 120
Db      121 V 121
```

```
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-11

Query Match      92.3%; Score 580.5; DB 16; Length 123;
Best Local Similarity 93.4%; Pred. No. 1.9e-48;
Matches 113; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAVISYDGSNKYY 60
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAVISYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQWNSLRVEDTAVYYCARDHGGRYVVDYGMVWGQGTTVT 119
Db 61 ADSVKGRFTISRDNKNTLYLQWNSLRVEDTAVYYCARDHGGRYVVDYGMVWGQGTTVT 120

QY 120 V 120
Db 121 V 121
```

```
RESULT 10
US-10-292-088-106
; Sequence 106, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 106
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-106

Query Match      91.9%; Score 578; DB 15; Length 124;
Best Local Similarity 91.8%; Pred. No. 3.3e-48;
Matches 112; Conservative 1; Mismatches 7; Indels 2; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAVISYDGSNKYY 60
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAVISYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQWNSLRVEDTAVYYCAR--SIFGVVDYGMVWGQGTTV 118
Db 61 ADSVKGRFTISRDNKNTLYLQWNSLRVEDTAVYYCARGHQLLYGYYVYGMVWGQGTTV 120

QY 119 TV 120
Db 121 TV 122
```

```
RESULT 11
US-10-269-711-43
; Sequence 43, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: DeVries, Peter J.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Ostrow, Dave
; APPLICANT: Weiler, James
```

```
; APPLICANT: Green, Larry
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
; FILE REFERENCE: ANTIBODIES
; FILE REFERENCE: 6989.US.O1
; CURRENT APPLICATION NUMBER: US/10/269,711
; CURRENT FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-711-43
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```
Query Match      91.8%; Score 577.5; DB 15; Length 123;
Best Local Similarity 92.6%; Pred. No. 3.6e-48;
Matches 112; Conservative 1; Mismatches 7; Indels 1; Gaps 1;
```

```
QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAVISYDGSNKYY 60
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAVISYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQWNSLRVEDTAVYYCARSIFFG-VVIDYGMVWGQGTTVT 119
Db 61 ADSVKGRFTISRDNKNTLYLQWNSLRVEDTAVYYCAKDHGGRYVVDYGMVWGQGTTVT 120

QY 120 V 120
Db 121 V 121
```

```
RESULT 12
US-10-684-109-35
; Sequence 35, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6989.US.O2
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-35
```

```
Query Match      91.8%; Score 577.5; DB 16; Length 123;
Best Local Similarity 92.6%; Pred. No. 3.6e-48;
Matches 112; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAVISYDGSNKYY 60
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAVISYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQWNSLRVEDTAVYYCARSIFFG-VVIDYGMVWGQGTTVT 119
Db 61 ADSVKGRFTISRDNKNTLYLQWNSLRVEDTAVYYCAKDHGGRYVVDYGMVWGQGTTVT 120

QY 120 V 120
Db 121 V 121
```



```
RESULT 13
US-10-858-855-11
; Sequence 11, Application US/10858855
; Publication No. US20050118651A1
; GENERAL INFORMATION:
; APPLICANT: BASI, Gurik
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE BETA
; FILE REFERENCE: ELN-028
; CURRENT APPLICATION NUMBER: US/10/858,855
; PRIOR FILING DATE: 2004-06-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-858-855-11

Query Match          91.7%; Score 577; DB 17; Length 141;
Best Local Similarity 93.3%; Pred. No. 4.7e-48;
Matches 112; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db 20 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 79
QY 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVVYCARSIFGVVVDYGMVWGQGTITV 120
Db 80 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVVYCARDHSSWYGMVWGQGTITV 139

RESULT 14
US-10-269-711-7
; Sequence 7, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: DeVries, Peter J.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Ostrow, Dave
; APPLICANT: Weiler, James
; APPLICANT: Green, Larry
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
; FILE REFERENCE: 6989 US.O1
; CURRENT APPLICATION NUMBER: US/10/269,711
; CURRENT FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-711-7

Query Match          91.7%; Score 576.5; DB 15; Length 123;
Best Local Similarity 92.6%; Pred. No. 4.6e-48;
Matches 112; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db 1 QVQLVESGGGVQPGKSLRLSCVASGFTFSYGMHWVRQAPGKLEWVAIVSYDGSNKYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVVYCARSIFG-VVIDYGMVWGQGTITV 119
Db 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVVYCARDHGGRYVVDYGMVWGQGTITV 120
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QY 120 V 120
Db 121 V 121

RESULT 15
US-10-269-711-15
; Sequence 15, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: DeVries, Peter J.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Ostrow, Dave
; APPLICANT: Weiler, James
; APPLICANT: Green, Larry
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
; FILE REFERENCE: 6989 US.O1
; CURRENT APPLICATION NUMBER: US/10/269,711
; CURRENT FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-711-15

Query Match          91.7%; Score 576.5; DB 15; Length 123;
Best Local Similarity 92.6%; Pred. No. 4.6e-48;
Matches 112; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAIVSYDGSNKYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVVYCARSIFG-VVIDYGMVWGQGTITV 119
Db 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVVYCARDHGGRYVVDYGMVWGQGTITV 120
QY 120 V 120
Db 121 V 121

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Job time : 67.6667 secs
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Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
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Db 1 EVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
|||||

Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVVYCARSI FGVIDYGMVWGQGT VTV 120
|||||
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVVYCAR-----DWG-DYWGQGT LTV 112

RESULT 7
G36005
Ig heavy chain V region (M74) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
C;Accession: G36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: G36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-121 <SCH>
A;Cross-references: UNIPROT:Q8WUK1; GB:M34031
C;Genetics:
A;Gene: GDB:IGH@; IGHDI1
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.9%; Score 546.5; DB 2; Length 121;
Best Local Similarity 88.6%; Pred. No. 2e-42;
Matches 109; Conservative 1; Mismatches 6; Indels 7; Gaps 2;

Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
:|||||
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
|||||

Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVVYCARSI FGVIDYGMVWGQGT TTV 117
|||||
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVVYCAR-----RKDWGWLFDYWGQGT L 116
|||||
Qy 118 VTV 120
|||
Db 117 VTV 119
|||

RESULT 8
F36005
Ig heavy chain V region (M49) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
C;Accession: F36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: F36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <SCH>
A;Cross-references: UNIPROT:Q8WUK1; GB:M34026
C;Genetics:
A;Gene: GDB:IGH@; IGHDI1
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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```
Query Match 86.7%; Score 545.5; DB 2; Length 119;
Best Local Similarity 89.2%; Pred. No. 2.4e-42;
Matches 107; Conservative 1; Mismatches 9; Indels 3; Gaps 1;

Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
:|||||
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
|||||

Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVVYCARSI FGVIDYGMVWGQGT VTV 120
|||||
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVVYCAR---RKASDAFDYWGQGT VTV 117

RESULT 9
S38493
Ig heavy chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S38493
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe,
submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a
A;Reference number: S38488
A;Accession: S38493
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-123 <MAR>
A;Cross-references: EMBL:Z23036; NID:g414033; PIDN:CAA80571.1; PID:g414034
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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```
Query Match 86.4%; Score 543.5; DB 2; Length 123;
Best Local Similarity 89.3%; Pred. No. 3.7e-42;
Matches 108; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
:|||||
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
|||||

Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVVYCARSI FG-VVIDYGMVWGQGT TTV 119
|||||
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVVYCARARSNWNYYYMDVWGKGT TTV 120
|||||
Qy 120 V 120
|||
Db 121 V 121
|||
```

```
RESULT 10
S31117
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31117
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurma
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31117
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-122 <RAA>
A;Cross-references: EMBL:X62967
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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Query Match 86.2%; Score 542; DB 2; Length 122;
Best Local Similarity 88.3%; Pred. No. 5.1e-42;
Matches 106; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
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Qy	1	OQVLVESGGGVQVQGRSLRLSCAASGFTFSYAMHWVRQAPCKGLEWAVI	60
Db	1	OQVLVESGGGVQVQGRSLRLSCAASGFTFSYAMHWVRQAPCKGLEWAVI	60
Qy	61	ADSVKGRFTISRDNSKNTLIYLGQMSLRADETAVYVCARSIFGVVIDYGM	120
Db	61	ADSVKGRFTISRDNSKNTLIYLGQMSLRADETAVYCARDFAPPNWSHF	120

RESULT 11  
S31116  
Ig heavy chain - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 09-Jul-2004  
C:Accession: S31116  
P:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman  
Eur. J. Immunol. 22, 247-251, 1992  
A>Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple  
A:Reference number: S31104; MUID:92111633; PMID:1730252  
A:Accession: S31116  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-118 <RAA>  
A:Cross-references: UNIPROT:Q8WUK1; EMBL:X62966  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain; immunoglobulin homology <IMW>

Query Match	85.9%;	Score 540;	DB 2;	Length 118;
Best Local Similarity	87.0%;	Pred. No. 7.4e-42;		
Matches 107;	Conservative 1;	Mismatches 5;	Indels 10;	Gaps 2
Qy	1	QVQLVESGGGVQPGESLFLSCAASGFTFSSYAMHWVRQAPGKLEWAVISYDGSNKYY	60	
Db	1	QVQLVESGGGVQPGKSLFLSCAASGFTFSSYGMHWVRQAPGKLEWAVISYDGSNKYY	60	
Qy	61	ADSVKGRFTISRDNSKNTLYLQMNISRAEDTAVYYCARISFGVVIDYG---MDVWVGQGT	117	
Db	61	ADSVKGRFTISRDNSKNTLYLQMNISRAEDTAVYYCA-----TDGKAAPFIWGQGT	113	
Qy	118	VTV	120	
Db	114	VTV	116	

```

RESULT 12
Sl9866
Ig heavy chain V region (VH3DJH4) - human
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C:Accession: Sl9866
R:Marks, J.D.; Hooqenboom, H.R.; Bonnett, T.P.; McCafferty, J.; Griffiths, A.D.

```

Db 61 ADSVGRFTISRDN SKNTLYLQMNSLRADTAVYCAKT--GVSSGNGYEDYWGQGTLT 118  
Qy 120 V 120  
Db 119 V 119

RESULT 13

S46392

Ig heavy chain V region (VH-28) - human

C/Species: Homo sapiens (man)

C/Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 20-Jun-2000

C/Accession: S46392

R/Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.

J. Mol. Biol. 239, 68-78, 1994

A>Title: In vitro assembly of repertoires of antibody chains on the surface of phage by

A/Reference number: S46390; MUID:94254092; PMID:8196048

A/Accession: S46392

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-114 <FTG>

A/Cross-references: EMBL:Z31688; NID:g499306; PIDN:CAA83493.1; PID:g1335145

C/Superfamily: immunoglobulin v region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

RESULT 14

S31601

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C:Date: 03-Mar-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C:Accession: S31601

R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

A:Submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31595

A:Accession: S31601

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-130 <CUI>

A:Cross-references: EMBL:Z14192; NID:G31018; PIDN:CAA78561.1; PID:G31019

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

E:30-113/Domain: immunoglobulin homology <IMM>

RESULT 15

S31701  
Ig heavy chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S31701  
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.  
submitted to the EMBL Data Library, June 1992  
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A;Reference number: S31585  
A;Accession: S31701  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-137 <CUI>  
A;Cross-references: EMBL:Z14177; NID:G31020; PIDN:CAA78546.1; PID:G31021  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 85.1%; Score 535; DB 2; Length 137;  
Best Local Similarity 86.7%; Pred. NO. 2.4e-41;  
Matches 104; Conservative 4; Mismatches 8; Indels 4; Gaps 1;  
  
Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSKYY 60  
Db |||||  
20 QVQLVESGGGVQPGKSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSKYY 79  
Qy |||||  
61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARSI FGVVVDYGMVWGQGTTVTV 120  
Db |||||  
80 PDSVKGRFTITRDNSKNTLYLQMNSLRAEDTAVYYCATPNW----NDAFDIWGGGTWTV 135

Search completed: November 9, 2005, 13:08:04  
Job time : 12.9323 secs

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500 5TH AVENUE NEW YORK 17, N.Y.



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:46:52 ; Search time 61.9549 Seconds  
(without alignments)  
991.843 Million cell updates/sec

Title: US-10-660-357A-29

Perfect score: 629

Sequence: 1 QVQLVSGGGVQPGSRSLR.....FGVVIDYGMVQGGTTVTV 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	541	86.0	613	2 Q8WU1	Q8WU1 homo sapien
2	531.5	84.5	240	2 Q652C9	Q652C9 homo sapien
3	529.5	84.2	116	2 Q9UL93	Q9UL93 homo sapien
4	517.5	82.3	113	2 Q9UL90	Q9UL90 homo sapien
5	514	81.7	122	1 HV3G_HUMAN	P01768 homo sapien
6	499	79.3	573	2 Q8WU38	Q8WU38 homo sapien
7	495	78.7	122	2 Q9UL84	Q9UL84 homo sapien
8	494.5	78.6	472	2 Q6N089	Q6N089 homo sapien
9	493.5	78.5	478	2 Q6PI81	Q6PI81 homo sapien
10	493	78.4	122	1 HV3H_HUMAN	P01769 homo sapien
11	490.5	78.0	121	2 Q9UL71	Q9UL71 homo sapien
12	489	77.7	147	2 Q9Y509	Q9Y509 homo sapien
13	482.5	76.7	121	1 HV3J_HUMAN	P01771 homo sapien
14	481	76.5	606	2 Q6GMV2	Q6GMV2 homo sapien
15	480.5	76.4	119	1 HV3I_HUMAN	P01770 homo sapien
16	476	75.7	126	1 HV3K_HUMAN	P01772 homo sapien
17	472.5	75.1	470	2 Q6PUA4	Q6PUA4 homo sapien
18	470	74.7	544	2 Q6PJ95	Q6PJ95 homo sapien
19	467.5	74.3	464	2 Q6MZU6	Q6MZU6 homo sapien
20	466.5	74.2	597	2 Q96BB9	Q96BB9 homo sapien
21	465.5	74.0	519	2 Q6N092	Q6N092 homo sapien
22	463.5	73.7	433	2 Q6GMX2	Q6GMX2 homo sapien
23	463	73.6	118	2 Q9UL91	Q9UL91 homo sapien
24	460.5	73.2	482	2 Q7Z351	Q7Z351 homo sapien
25	459	73.0	118	2 Q9UL72	Q9UL72 homo sapien
26	454	72.2	112	2 Q9HCC1	Q9HCC1 homo sapien
27	454	72.2	494	2 Q96K68	Q96K68 homo sapien
28	453	72.0	136	1 HV16_MOUSE	P01783 mus musculus
29	453	72.0	479	2 Q6MZV6	Q6MZV6 homo sapien
30	451.5	71.8	119	1 HV3L_HUMAN	P01773 homo sapien
31	450.5	71.6	499	2 Q8N5K4	Q8N5K4 homo sapien

#### RESULT 1

ID	Q8WU1	PRELIMINARY;	PRT;	613 AA.
AC	Q8WU1;			
DT	01-MAR-2002 (TrEMBLrel. 20, Created)			
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	IGHM protein.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
ON	NCBI_TaxID=9606;			
RX	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Primary B-Cells;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Primary B-Cells;			
RA	Strausberg R.;			
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL, BC020240; AAH0240.1; -			
DR	PIR, F36005; F36005.			
DR	PIR, G36005; G36005.			
DR	PIR, PH1642; PH1642.			
DR	PIR, PH1643; PH1643.			
DR	PIR, PH1645; PH1645.			
DR	PIR, PH1646; PH1646.			
DR	PIR, PL0098; PL0098.			
DR	PIR, PL0120; PL0120.			
DR	PIR, S15590; S15590.			
DR	PIR, S31116; S31116.			
DR	PIR, S31119; S31119.			
DR	PIR, S70442; S70442.			

#### ALIGNMENTS

32	449	71.4	473	2	Q91205
33	447.5	71.1	493	2	Q68CN4
34	447	71.1	475	2	Q6MZQ6
35	446.5	71.0	493	2	Q8NCL6
36	445.5	70.8	485	2	Q6PDB8
37	445	70.7	473	2	Q6MZV7
38	444.5	70.7	466	2	Q6IN78
39	443	70.4	475	2	Q6GMW7
40	442	70.3	117	1	HV3C_HUMAN
41	440	70.0	116	1	HV3T_HUMAN
42	440	70.0	483	2	Q6MZK9
43	439	69.8	487	2	Q99KA4
44	438	69.6	465	2	Q6P6C4
45	434	69.0	114	1	HV3B_HUMAN

```
DR HSSP; P01861; 1ADQ.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 5.
DR PROSITE; PS00290; IG MHC; UNKNOWN 3.
SQ SEQUENCE 613 AA; 57295 MW; 60C7F5950671E315 CRC64;

Query Match      86.0%; Score 541; DB 2; Length 613;
Best Local Similarity 84.8%; Pred. No. 5.7e-48;
Matches 106; Conservative 3; Mismatches 4; Indels 12; Gaps 2;

QY 1 QVQLVSGGVPQGRSLRLSCAASGFTSSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db 20 QVQLVSGGVPQGRSLRLSCAASGFTSSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 79

QY 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVVYCARSIFGVVIDYG-----MDVWGQG 115
Db 80 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVVYCAK-----DWSEGVETFDINGQG 132

QY 116 TVTVTV 120
Db 133 TVTVTV 137

RESULT 2
Q65ZC9 PRELIMINARY; PRT; 240 AA.
AC Q65ZC9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=97362799; PubMed=9219263;
RX STRAIN=C1q/7;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13056; CAA73499.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON_TER 1_1
FT NON_TER 240 240
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Query Match      84.5%; Score 531.5; DB 2; Length 240;
Best Local Similarity 85.2%; Pred. No. 1.9e-47;
Matches 104; Conservative 5; Mismatches 4; Indels 9; Gaps 2;

QY 1 QVQLVSGGVPQGRSLRLSCAASGFTSSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db 1 QVQLVSGGVLQPGGSLRLSCAASGFTSSYGMHWVRQAPGKLEWVAIVSYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVVYCARSIFGVVIDYG--MDVWGQGTTV 118
Db 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVVYCAR-----DWGSLDPWGKTLV 113

QY 119 TV 120
Db 114 TV 115
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RESULT 3
Q9UL93 PRELIMINARY; PRT; 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RP MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RX Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035021; AAD56257.1; -.
DR PIR; PH1644; PH1644.
DR PIR; PL0120; PL0120.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1_1
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12434 MW; ODA0348154DD6061 CRC64;

Query Match      84.2%; Score 529.5; DB 2; Length 116;
Best Local Similarity 87.4%; Pred. No. 1.3e-47;
Matches 104; Conservative 2; Mismatches 8; Indels 5; Gaps 1;

QY 2 VOLVESGGGVQGRSLRLSCAASGFTSSYAMHWVRQAPGKLEWVAIVSYDGSNKYYA 61
Db 1 VOLVESGGGVQGRSLRLSCAASGFTSSYAMHWVRQAPGKLEWVAIVSYDGSNKYYA 60

QY 62 DSVKGRFTISRDNKNTLYLQNSLRAEDTAVVYCARSIFGVVIDYGMVWGQGTTVTV 120
Db 61 DSVKGRFTISRDNKNTLYLQNSLRAEDTAVVYCAAG-----GGLGLGWGQGTTLTV 114

RESULT 4
Q9UL93 PRELIMINARY; PRT; 113 AA.
AC Q9UL93;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RP MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RX Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -.
DR PIR; S78486; S78486.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
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ID OSUL84 PRELIMINARY; PRT; 122 AA.
AC Q9UL84;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035030; AAD56266.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

Query Match 78.7%; Score 495; DB 2; Length 122;
Best Local Similarity 80.0%; Pred. No. 5.7e-44;
Matches 96; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 1 QVQLVSGGCVQPGKSLRLSCLCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVSGGCVQPGKSLRLSCLCAASRFTFSYGMHWVRQAPGKLEWVAISNDGSKFY 60

QY 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCARSIFFGVV--VIDYGMVWGQTTVV 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCARSIFFGVV--VIDYGMVWGQTTVV 120

RESULT 8
ID Q9N089 PRELIMINARY; PRT; 472 AA.
AC Q9N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686P15220.
GN Names=DKFZp686P15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAB45781.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.

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DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 78.6%; Score 494.5; DB 2; Length 472;
Best Local Similarity 79.5%; Pred. No. 3.1e-43;
Matches 97; Conservative 9; Mismatches 13; Indels 3; Gaps 2;

QY 1 QVQLVSGGCVQPGKSLRLSCLCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 EVQLVSGGCVQPGKSLRLSCLCAASGFTFDDYAMHWVRQAPGKLEWVSGISWNSGIAY 79

QY 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCARSIFFGV--VIDYGMVWGQTTVV 118
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCAKEI-GAHNFYFYGYMDVWGQTTV 138

QY 119 TV 120
Db 139 TV 140

RESULT 9
ID Q6PI81 PRELIMINARY; PRT; 478 AA.
AC Q6PI81;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Primary B-Cells;
RG MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041037; AAH41037.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.

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DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match 78.5%; Score 493.5; DB 2; Length 478;
Best Local Similarity 78.7%; Pred. No. 4e-43;
Matches 100; Conservative 7; Mismatches 13; Indels 7; Gaps 2;

QY 1 QVQLVESGGGVQVQGRSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 EVQLVESGGGVQVQGRSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 79
QY 61 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYICARSIFGVVYDYGMDVWGQGTITV 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
80 VDSVKGRFTISRDNKNTLYQMNSLRAEDTAVYICARSIFGVVYDYGMDVWGQGTITV 139
QY 114 QGTTT 120
Db :|||||:
140 KGT 146

RESULT 10
HV3H HUMAN STANDARD; PRT; 122 AA.
AC P01769;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-III region GA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN MISCHELANEUS: This chain was isolated from a Waldenström's
CC macroglobulin.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02052; M3HUGA.
DR HSSP; P01772; 2F84.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
FT Pyridolone carboxylic acid.
FT DOMAIN 1 112 Ig-like
FT MOD RES 1 122 Pyridolone carboxylic acid.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13166 MW; 74E5B695E84100A CRC64;

Query Match 78.4%; Score 493; DB 1; Length 122;
Best Local Similarity 72.5%; Pred. No. 9.3e-44;
Matches 87; Conservative 20; Mismatches 13; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQVQGRSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 QVQLVZSGGAVZPGRSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
QY 61 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYICARSIFGVVYDYGMDVWGQGTITV 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 AASVKGRFTISRDNKNTLYQMNSLRAEDTAVYICARSIFGVVYDYGMDVWGQGTITV 120

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RESULT 11
Q9UL71 PRELIMINARY; PRT; 121 AA.
ID Q9UL71;
AC Q9UL71;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035043; AAD56279.1; -.
DR HSSP; P01852; INF0.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 1.
FT NON_TER 1 121
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match 78.0%; Score 490.5; DB 2; Length 121;
Best Local Similarity 78.3%; Pred. No. 1.7e-43;
Matches 94; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQVQGRSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 EVQLVESGGGVQVQGRSLRLSCAASGFTFDGYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
QY 61 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYICARSIFGVVYDYGMDVWGQGTITV 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYICAKGVKVTIYD-RFDIWGGGTWTV 119

RESULT 12
Q9Y509 PRELIMINARY; PRT; 147 AA.
ID Q9Y509;
AC Q9Y509;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH3 protein (Fragment).
GN Name=VH3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
Cao J., Vesic R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers.";
Leukemia 9:1948-1953(1995).
DR EMBL; S80860; AAD14339.1; -.
DR HSSP; P01842; 1AQK.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGv; 1.

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RESULT 15
HV3I HUMAN
ID HV3I HUMAN STANDARD; PRT; 119 AA.
AC P01770;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-III region NIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77070269; PubMed=826475;
RA Ponstingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic
RT peptides of the H-chain, alignment of the tryptic peptides and
RT discussion of the complete structure."
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie). I: purification and
RT characterization of the protein, the L- and H-chains, the cyanogen
RT bromide cleavage products, and the disulfide bridges."
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
CC -I- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
CC protein.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A91668; GIKUNI.
DR HSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Direct protein sequencing; Immunoglobulin V region;
KW Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 Ig-like.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT DISULFID 22 96
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13242 MW; C96935A6E55E165B CRC64;

Query Match 76.4%; Score 480.5; DB 1; Length 119;
Best Local Similarity 77.0%; Pred. No. 1.8e-42;
Matches 94; Conservative 9; Mismatches 12; Indels 7; Gaps 2;

QY 1 QVQLVSGGGVQVQGRSLRSLCAASGFTSSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
DB 1 QVQLVQSGGGVQVQGRSLRSLCAASGFTSKYTHHWVRQAPGKLEWVAIVSYBGBKKHY 60

QY 61 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVVYCARSIFGVVIDYGMV--WGQGTTV 118
DB 61 ADSVNGRFTISRDNKNTLYMNSLRLPDTAVVYCAR-----IRDTAMFFAHWGQGTLV 115

QY 119 TV 120
DB 116 TV 117

```

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:43:32 ; Search time 72.1353 Seconds  
(without alignments)  
627.306 Million cell updates/sec

Title: US-10-660-357A-33

Perfect score: 626

Sequence: 1 QVQLSGSGFLVKPSTLSL.....ARGGDGYRWGQTLTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 segs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:.\*  
1: Geneseq1980s:.\*  
2: Geneseq1990s:.\*  
3: Geneseq2000s:.\*  
4: Geneseq2001s:.\*  
5: Geneseq2002s:.\*  
6: Geneseq2003as:.\*  
7: Geneseq2003bs:.\*  
8: Geneseq2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	626	100.0	117	7	ADC99804 Anti-huma
2	626	100.0	117	7	ADD05408 Anti-MUC1
3	626	100.0	117	7	ADF09846 Human ant
4	604	96.5	117	7	ADC99776 Anti-huma
5	604	96.5	117	7	ADD05380 Anti-MUC1
6	604	96.5	117	7	ADF09818 Human ant
7	568	90.7	117	7	ADC99784 Anti-huma
8	568	90.7	117	7	ADD05388 Anti-MUC1
9	568	90.7	117	7	ADF09826 Human ant
10	552	88.3	118	7	ADP03968 Murine-ex
11	552	88.2	123	7	ADP03870
12	549.5	87.8	120	7	ADP03974
13	549.5	87.8	120	7	ADP03873
14	548	87.5	123	7	ADP03869
15	542	86.6	120	4	AAB62775
16	541	86.4	119	7	ADP03970
17	540.5	86.3	121	7	ADJ80377
18	539	86.1	122	4	AAB62765
19	539	86.1	123	2	AAW78433
20	539	86.1	123	5	ABB97976 Heavy cha
21	539	86.1	123	7	ADG88414 anti-Ob-R
22	537.5	85.9	110	7	ADP03934
23	537.5	85.9	123	4	AAB62745
24	537.5	85.9	124	7	ADP03935
25	536.5	85.7	122	7	ADP03977

26	536	85.6	121	7	ADP03981	Adp03981 Murine-ex
27	536	85.6	129	5	AAU81276	Aau81276 Human trk
28	535	85.5	125	7	ADP03871	Adp03871 Murine-ex
29	534.5	85.4	246	3	AAV15126	Aav15126 Anti-muri
30	534	85.3	125	7	ADP03868	Adp03868 Murine-ex
31	534	85.3	125	7	ADP03876	Adp03876 Murine-ex
32	533.5	85.2	122	7	ADP03875	Adp03875 Murine-ex
33	533.5	85.2	221	7	ADJ32126	Adj32126 Human int
34	533	85.1	127	8	ADQ91396	Adq91396 Amino aci
35	532.5	85.1	110	8	ADP22366	Adp22366 Human ant
36	532.5	85.1	252	5	ABP45983	Abp45983 Human Bly
37	532.5	85.1	252	7	ADG96810	Adg96810 Single ch
38	532	85.0	123	7	ADP03872	Adp03872 Murine-ex
39	531	84.8	119	7	ADP03961	Adp03961 Murine-ex
40	531	84.8	121	7	ADP03982	Adp03982 Murine-ex
41	531	84.8	253	5	ABP45608	Abp45608 Human Bly
42	531	84.8	253	7	ADG96435	Adg96435 Single ch
43	530.5	84.7	120	7	ADP03969	Adp03969 Murine-ex
44	530	84.7	119	2	AAW27554	Aaw27554 Human Ab
45	530	84.7	119	6	ABJ18676	Abj18676 Antibody

ALIGNMENTS

RESULT 1

ADC99804

ID ADC99804 standard; protein; 117 AA.

AC ADC99804;

DT 01-JAN-2004 (first entry)

DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 33.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
KW lung cancer; human.

XX Homo sapiens.

XX WO2003057838-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

XX Gudas J;

XX WPI; 2003-587113/55.

XX N-PSDB; ADC99806.

XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
or condition associated with expression of MUC18 in a patient, e.g.  
tumors, cancers, and other malignancies.

XX Claim 1; SEQ ID NO 33; 78pp; English.

XX The invention relates to a novel isolated monoclonal antibody comprising  
a heavy or light chain amino acid or a heavy or light chain variable  
domain where the antibody binds to MUC18. The monoclonal antibody of the  
invention demonstrates cytostatic activity and may be useful for treating  
a disease or condition associated with the expression of MUC18 on the  
cell surface such as tumours, specifically melanoma, oesophageal,  
pancreatic or colorectal tumours, carcinomas, particularly cervical  
carcinomas and cervical intraepithelial neoplasia and cancers including  
colorectal, breast or lung cancer, as well as other malignancies. The  
current sequence is that of the anti-human MUC18 monoclonal antibody

CC heavy chain protein of the invention.

XX  
SQ Sequence 117 AA;  
  
Query Match 100.0%; Score 626; DB 7; Length 117;  
Best Local Similarity 100.0%; Pred. No. 1.8e-46;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60  
Db 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60  
  
QY 61 HNPSTKSRITISVDTSKNQFSLKSSVTAADTAVYYCARGDGYRWGGTTLTVSS 117  
Db 61 HNPSTKSRITISVDTSKNQFSLKSSVTAADTAVYYCARGDGYRWGGTTLTVSS 117

## RESULT 2

ADDF09846  
ID ADD05408 standard; protein; 117 AA.  
XX  
AC ADD05408;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 33.  
XX  
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.  
XX  
OS Homo sapiens.  
XX  
PN WO2003057006-A2.  
XX  
PD 17-JUL-2003.  
XX  
PF 26-DEC-2002; 2002WO-US041582.  
XX  
PR 28-DEC-2001; 2001US-0346460P.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Gudas J, Bar-Eli M;  
XX  
WPI; 2003-577496/54.  
DR N-PSDB; ADD05410.  
XX

PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
PT associated with melanoma, or increasing survival of an animal having a  
PT metastatic tumor.

XX Claim 1; SEQ ID NO 33; 87pp; English.

XX The invention relates to a novel monoclonal antibody used for inhibiting  
CC tumour growth in an animal. The tumour inhibition process comprises  
CC selecting an animal in need of treatment for a tumour, providing a  
CC monoclonal antibody comprising a heavy chain amino acid, where the  
CC antibody consists of any one of 10 fully defined sequences of 117-123  
CC amino acids given in the specification, and where the monoclonal antibody  
CC binds MUC18, and contacting the tumour with the antibody resulting in  
CC inhibited proliferation of the cells. The monoclonal antibody has  
CC cytostatic and can be used in the production of a vaccine. The monoclonal  
CC antibodies against the MUC18 antigen are useful for diagnosing and  
CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or  
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or  
CC increasing survival of an animal having a metastatic tumour. This  
CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
CC protein of the invention.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 626; DB 7; Length 117;

Best Local Similarity 100.0%; Pred. No. 1.8e-46;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60  
Db 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60  
  
QY 61 HNPSTKSRITISVDTSKNQFSLKSSVTAADTAVYYCARGDGYRWGGTTLTVSS 117  
Db 61 HNPSTKSRITISVDTSKNQFSLKSSVTAADTAVYYCARGDGYRWGGTTLTVSS 117

## RESULT 3

ADDF09846  
ID ADF09846 standard; protein; 117 AA.  
XX  
AC ADF09846;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Human anti-MUC18 monoclonal antibody heavy chain #9.  
XX  
KW cell proliferation inhibition; MUC18 tumour antigen;  
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
KW carcinoma; cancer; malignancy; heavy chain; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2003057837-A2.  
XX  
PD 17-JUL-2003.  
XX  
PF 26-DEC-2002; 2002WO-US041580.  
XX  
PR 28-DEC-2001; 2001US-0346414P.  
XX  
PA (ABGE-) ABGENIX INC.

XX Gudas J;

XX WPI; 2003-598367/56.  
DR N-PSDB; ADF09848.

XX Inhibiting cell proliferation associated with expression of MUC18 tumour  
PT antigen, involves incubating and inhibiting cell by administering anti-  
PT MUC18 monoclonal antibody.

XX Claim 1; SEQ ID NO 33; 83pp; English.

XX The invention comprises a method for inhibiting cell proliferation  
CC associated with expression of MUC18 tumour antigen. The method involves  
CC administering anti-MUC18 monoclonal antibody. The method of the invention  
CC is useful for inhibiting cell (e.g. melanoma or tumour cell)  
CC proliferation associated with the expression of MUC18 tumour antigen, the  
CC method is preferably useful for inhibiting tumour metastasis. The method  
CC is useful for inhibiting cell proliferation in patients with tumours,  
CC carcinomas, cancer and other malignancies. The present amino acid  
CC sequence represents a heavy chain from an MUC18 tumour antigen-specific  
CC monoclonal antibody.

XX Sequence 117 AA;

Query Match 100.0%; Score 626; DB 7; Length 117;  
Best Local Similarity 100.0%; Pred. No. 1.8e-46;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60  
Db 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60

QY 61 HNPSTKSRITISVDTSKNQFSLKSSVTAADTAVYYCARGDGYRWGGTTLTVSS 117  
Db 61 HNPSTKSRITISVDTSKNQFSLKSSVTAADTAVYYCARGDGYRWGGTTLTVSS 117



KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
KW carcinoma; cancer; malignancy; heavy chain; human.  
XX Homo sapiens.  
XX OS  
XX WO2003057837-A2.  
XX 17-JUL-2003.  
XX  
XX 26-DEC-2002; 2002WO-US041580.  
XX  
XX 28-DEC-2001; 2001US-0346414P.  
XX  
XX (ABGE-) ABGENIX INC.  
XX  
XX Gudas J;  
XX PI  
XX  
XX WPI; 2003-598367/56.  
XX N-PSDB; ADF09820.  
XX  
XX Inhibiting cell proliferation associated with expression of MUC18 tumor  
XX antigen, involves incubating and inhibiting cell by administering anti-  
XX MUC18 monoclonal antibody.  
XX  
XX Claim 1; SEQ ID NO 5; 83pp; English.  
XX  
XX The invention comprises a method for inhibiting cell proliferation  
XX associated with expression of MUC18 tumour antigen. The method involves  
XX administering anti-MUC18 monoclonal antibody. The method of the invention  
XX is useful for inhibiting cell (e.g. melanoma or tumour cell)  
XX proliferation associated with the expression of MUC18 tumour antigen, the  
XX method is preferably useful for inhibiting tumour metastasis. The method  
XX is useful for inhibiting cell proliferation in patients with tumours,  
XX carcinomas, cancer and other malignancies. The present amino acid  
XX sequence represents a heavy chain from an MUC18 tumour antigen-specific  
XX monoclonal antibody.  
XX  
XX Sequence 117 AA;  
SQ  
Query Match 96.5%; Score 604; DB 7; Length 117;  
Best Local Similarity 94.0%; Pred. No. 1.4e-44;  
Matches 110; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISGGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60  
Db 1 QVQLQESGPGLVKPSQTLSLTCTVSGSISGGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60  
Qy 61 HNPSLKSRITISVDTSKNQFSLKLSVTAADTAVYYCARGDGYRYWGQGLTVTVSS 117  
Db 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGDGYRYWGQGLTVTVSS 117  
RESULT 7  
ADC99784  
ID ADC99784 standard; protein; 117 AA.  
XX  
XX AC ADC99784;  
XX  
XX 01-JAN-2004 (first entry)  
XX  
XX Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 13.  
XX  
XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
KW cytosolic; melanoma; oesophageal; pancreatic; colorectal tumour;  
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
KW lung cancer; human.  
XX  
XX Homo sapiens.  
XX  
XX WO2003057838-A2.  
XX  
XX 17-JUL-2003.  
XX

PF 26-DEC-2002; 2002WO-US041581.  
XX  
XX 28-DEC-2001; 2001US-0346299P.  
XX  
XX (ABGE-) ABGENIX INC.  
XX  
XX Gudas J;  
XX  
XX WPI; 2003-587113/55.  
XX N-PSDB; ADC99786.  
XX  
XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
XX or condition associated with expression of MUC18 in a patient, e.g.  
XX tumors, cancers, and other malignancies.  
XX  
XX Claim 1; SEQ ID NO 13; 78pp; English.  
XX  
XX The invention relates to a novel isolated monoclonal antibody comprising  
XX a heavy or light chain amino acid or a heavy or light chain variable  
XX domain where the antibody binds to MUC18. The monoclonal antibody of the  
XX invention demonstrates cytostatic activity and may be useful for treating  
XX a disease or condition associated with the expression of MUC18 on the  
XX cell surface such as tumours, specifically melanoma, oesophageal,  
XX pancreatic or colorectal tumours, carcinomas, particularly cervical  
XX carcinomas and cervical intraepithelial neoplasia and cancers including  
XX colorectal, breast or lung cancer, as well as other malignancies. The  
XX current sequence is that of the anti-human MUC18 monoclonal antibody  
XX heavy chain protein of the invention.  
XX  
XX Sequence 117 AA;  
SQ  
Query Match 90.7%; Score 568; DB 7; Length 117;  
Best Local Similarity 88.9%; Pred. No. 1.8e-41;  
Matches 104; Conservative 10; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISGGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60  
Db 1 QVQLQESGPGLVKPSQTLSLTCTVSGSISGGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60  
Qy 61 HNPSLKSRITISVDTSKNQFSLKLSVTAADTAVYYCARGDGYRYWGQGLTVTVSS 117  
Db 61 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGDGYRYWGQGLTVTVSS 117  
RESULT 8  
ADD05388  
ID ADD05388 standard; protein; 117 AA.  
XX  
XX AC ADD05388;  
XX  
XX 01-JAN-2004 (first entry)  
XX  
XX Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 13.  
XX  
XX monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.  
XX  
XX Homo sapiens.  
XX  
XX WO2003057006-A2.  
XX  
XX 17-JUL-2003.  
XX  
XX 26-DEC-2002; 2002WO-US041582.  
XX  
XX 28-DEC-2001; 2001US-0346460P.  
XX  
XX (ABGE-) ABGENIX INC.  
XX  
XX Gudas J, Bar-Eli M;  
XX  
XX WPI; 2003-577496/54.  
XX  
XX N-PSDB; ADD05390.  
XX

XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
 PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
 PT associated with melanoma, or increasing survival of an animal having a  
 PT metastatic tumor.

XX Claim 1; SEQ ID NO 13; 87pp; English.

XX The invention relates to a novel monoclonal antibody used for inhibiting  
 CC tumor growth in an animal. The tumor inhibition process comprises  
 CC selecting an animal in need of treatment for a tumor, providing a  
 CC monoclonal antibody comprising a heavy chain amino acid, where the  
 CC antibody consists of any one of 10 fully defined sequences of 117-123  
 CC amino acids given in the specification, and where the monoclonal antibody  
 CC binds MUC18, and contacting the tumor with the antibody resulting in  
 CC inhibited proliferation of the cells. The monoclonal antibody has  
 CC cytostatic and can be used in the production of a vaccine. The monoclonal  
 CC antibodies against the MUC18 antigen are useful for diagnosing and  
 CC treating tumors, inhibiting tumor growth (e.g. melanoma, lung tumor or  
 CC tumor metastasis), inhibiting cell invasion associated with melanoma, or  
 CC increasing survival of an animal having a metastatic tumor. This  
 CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
 CC protein of the invention.

XX Sequence 117 AA;

Query Match 90.7%; Score 568; DB 7; Length 117;  
 Best Local Similarity 88.9%; Pred. No. 1.8e-41;  
 Matches 104; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGKLEWIGYIYSGSTY 60  
 Db 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGKLEWIGYIYSGSTY 60

Qy 61 HNPFLSKRITISVDTSKNQFSLKLSVTAADTAVYVCARGDGYRYWGQGLTVTVSS 117  
 Db 61 YNPSLSKRSVTISVDTSKNQFSLKLSVTAADTAVYVCAREGDGFDYWGQGLTVTVSS 117

RESULT 9

ADFO9826  
 ID ADF09826 standard; protein; 117 AA.

AC ADF09826;

XX 12-FEB-2004 (first entry)

XX Human anti-MUC18 monoclonal antibody heavy chain #4.

XX cell proliferation inhibition; MUC18 tumor antigen;  
 KW anti-MUC18 monoclonal antibody; tumor metastasis inhibition; tumor;  
 KW carcinoma; cancer; malignancy; heavy chain; human.

XX Homo sapiens.

XX WO2003057837-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041580.

XX 28-DEC-2001; 2001US-0346414P.

XX (ABGE-) ABGENIX INC.

XX Gudas J;

XX WPI; 2003-598367/56.

XX N-PSDB; ADF09828.

XX Inhibiting cell proliferation associated with expression of MUC18 tumor  
 PT antigen, involves incubating and inhibiting cell by administering anti-  
 PT MUC18 monoclonal antibody.

XX

PS Claim 1; SEQ ID NO 13; 83pp; English.

XX The invention comprises a method for inhibiting cell proliferation  
 CC associated with expression of MUC18 tumor antigen. The method involves  
 CC administering anti-MUC18 monoclonal antibody. The method of the invention  
 CC is useful for inhibiting cell (e.g. melanoma or tumor cell)  
 CC proliferation associated with the expression of MUC18 tumor antigen, the  
 CC method is preferably useful for inhibiting tumor metastasis. The method  
 CC is useful for inhibiting cell proliferation in patients with tumors,  
 CC carcinomas, cancer and other malignancies. The present amino acid  
 CC sequence represents a heavy chain from an MUC18 tumor antigen-specific  
 CC monoclonal antibody.

XX Sequence 117 AA;

Query Match 90.7%; Score 568; DB 7; Length 117;  
 Best Local Similarity 88.9%; Pred. No. 1.8e-41;  
 Matches 104; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGKLEWIGYIYSGSTY 60  
 Db 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGKLEWIGYIYSGSTY 60

Qy 61 HNPFLSKRITISVDTSKNQFSLKLSVTAADTAVYVCARGDGYRYWGQGLTVTVSS 117  
 Db 61 YNPSLSKRSVTISVDTSKNQFSLKLSVTAADTAVYVCAREGDGFDYWGQGLTVTVSS 117

RESULT 10

ADPO3968

ID ADPO3968 standard; protein; 118 AA.

AC ADPO3968;

XX 29-JUL-2004 (first entry)

XX Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 138.

XX monoclonal antibody; carbonic anhydrase IX; CA IX tumor antigen;  
 KW cytostatic; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;  
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; heavy chain variable domain.

XX Unidentified.

XX WO2003048328-A2.

XX 12-JUN-2003.

XX 02-DEC-2002; 2002WO-US038550.

XX 03-DEC-2001; 2001US-0337275P.

XX (ABGE-) ABGENIX INC.

XX Gudas J, Foltz I, Handa M, Gallo M;

XX WPI; 2003-523295/49.

XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX Example 2; SEQ ID NO 138; 89pp; English.

XX The invention relates to a novel isolated monoclonal antibody (mAb)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumor antigen. The antibody of the invention  
 CC demonstrates cytostatic activity and may be useful for treating a tumor,

CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma, cervical intraepithelial squamous and glandular neoplasia, oesophageal CC tumour or breast cancer, possibly via gene therapy. The current sequence CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH CC (heavy chain variable domain) protein of the invention. The protein was CC generated via the introduction of the human CA IX protein into a CC transgenic mouse strain.

XX SQ Sequence 118 AA;  
Query Match 88.1%; Score 552.5; DB 7; Length 118;  
Best Local Similarity 89.0%; Pred. No. 4e-40; 5; Indels 1; Gaps 1;  
Matches 105; Conservative 7; Mismatches 5;  
QY 1 QVQLQSGPLGPKVPSQTLSLTCTVSGGSISSGTYHMSWIRQHPGKLEWIGYIYSGSTY 60  
Db 1 QVQLQSGPLGPKVPSQTLSLTCTVSGGSISSGTYHMSWIRQHPGKLEWIGYIYSGSTY 60  
QY 61 HNPSTLSKSRITISVDTSKQFSLKLSVTAADTAIVYCAR-GGDGYRWGGTLTVTSS 117  
Db 61 YNPSTLSKSRITISVDTSKQFSLKLSVTAADTAIVYCAR-YGSGDYWGQGTLLTVTSS 118

RESULT 11  
ADP03870  
ID ADP03870 standard; protein; 123 AA.  
XX AC ADP03870;  
XX DT 29-JUL-2004 (first entry)  
XX DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 10.  
XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
KW cytotatic; colorectal neoplasm; renal cell carcinoma;  
KW cervical intraepithelial squamous neoplasia;  
KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
KW gene therapy; murine; mouse; human; heavy chain variable domain.  
XX OS Unidentified.  
XX PN WQ2003048328-A2.  
XX PD 12-JUN-2003.  
XX PF 02-DEC-2002; 2002WO-US038550.  
XX PR 03-DEC-2001; 2001US-0337275P.  
XX PA (ABGE-) ABGENIX INC.  
XX PI Gudas J, Foltz I, Handa M, Gallo M;  
XX WPI; 2003-523295/49.  
XX PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

PS Claim 1; SEQ ID NO 10; 89pp; English.  
XX CC The invention relates to a novel isolated monoclonal antibody (mAb)  
CC comprising a heavy chain polypeptide and light chain polypeptide having a  
CC sequence chosen from one of 53 fully defined amino acid sequences given  
CC in the specification, where the antibody specifically binds carbonic  
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
CC demonstrates cytostatic activity and may be useful for treating a tumour,  
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a

CC transgenic mouse strain.  
XX SQ Sequence 123 AA;  
Query Match 88.2%; Score 552; DB 7; Length 123;  
Best Local Similarity 85.4%; Pred. No. 4.6e-40; 5; Indels 6; Gaps 1;  
Matches 105; Conservative 7; Mismatches 5;  
QY 1 QVQLQSGPLGPKVPSQTLSLTCTVSGGSISSGTYHMSWIRQHPGKLEWIGYIYSGSTY 60  
Db 1 QVQLQSGPLGPKVPSQTLSLTCTVSGGSISSGTYHMSWIRQHPGKLEWIGYIYSGSTY 60  
QY 61 HNPSTLSKSRITISVDTSKQFSLKLSVTAADTAIVYCARGGDY-----RWGGQTLTVT 114  
Db 61 YNPSTLSKSRITISVDTSKQFSLKLSVTAADTAIVYCARAGKYGGSYLDYWGQGTLLTVT 120  
QY 115 VSS 117  
Db 121 VSS 123  
RESULT 12  
ADP03974  
ID ADP03974 standard; protein; 120 AA.  
XX AC ADP03974;  
XX DT 29-JUL-2004 (first entry)  
XX DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 144.  
XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
KW cytotatic; colorectal neoplasm; renal cell carcinoma;  
KW cervical intraepithelial squamous neoplasia;  
KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
KW gene therapy; murine; mouse; human; heavy chain variable domain.  
XX OS Unidentified.  
XX PN WQ2003048328-A2.  
XX PD 12-JUN-2003.  
XX PF 02-DEC-2002; 2002WO-US038550.  
XX PR 03-DEC-2001; 2001US-0337275P.  
XX PA (ABGE-) ABGENIX INC.  
XX PI Gudas J, Foltz I, Handa M, Gallo M;  
XX WPI; 2003-523295/49.  
XX PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
XX Example 2; SEQ ID NO 144; 89pp; English.  
XX CC The invention relates to a novel isolated monoclonal antibody (mAb)  
CC comprising a heavy chain polypeptide and light chain polypeptide having a  
CC sequence chosen from one of 53 fully defined amino acid sequences given  
CC in the specification, where the antibody specifically binds carbonic  
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
CC demonstrates cytostatic activity and may be useful for treating a tumour,  
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.

SQ Sequence 120 AA;

Query Match 87.8%; Score 549.5; DB 7; Length 120;  
Best Local Similarity 86.1%; Pred. No. 7.3e-40;  
Matches 105; Conservative 8; Mismatches 2; Indels 7; Gaps 2;

Qy 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60  
Qy 61 HNPFLKSRITISVDTSKNQFSLKLSVTAADTAIVYICARGDGVY-----WGQGLTVTV 115  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 YNPSLKSRTISVDTSKNQFSLKLSVTAADTAIVYICAR--DGYNYWYFDLMWGRGLTVTV 118  
Qy 116 SS 117  
|||  
Db 119 SS 120

RESULT 13

ADP03873  
ID ADP03873 standard; protein; 120 AA.

XX AC ADP03873;

XX DT 29-JUL-2004 (first entry)

XX DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 13.

XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
XX KW cytotatic; colorectal neoplasm; renal cell carcinoma;  
XX KW cervical intraepithelial squamous neoplasia;  
XX KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
XX KW gene therapy; murine; mouse; human; heavy chain variable domain.

XX OS Unidentified.

XX PN WO2003048328-A2.

XX PD 12-JUN-2003.

XX PF 02-DEC-2002; 2002WO-US038550.

XX PR 03-DEC-2001; 2001US-0337275P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J, Foltz I, Handa M, Gallo M;

XX DR WPI; 2003-523295/49.

XX PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
XX PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
XX PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX PS Claim 1; SEQ ID NO 13; 89pp; English.

XX CC The invention relates to a novel isolated monoclonal antibody (mAb)  
XX CC comprising a heavy chain polypeptide and light chain polypeptide having a  
XX CC sequence chosen from one of 53 fully defined amino acid sequences given  
XX CC in the specification, where the antibody specifically binds carbonic  
XX CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
XX CC demonstrates cytostatic activity and may be useful for treating a tumour,  
XX CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
XX CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
XX CC tumour or breast cancer, possibly via gene therapy. The current sequence  
XX CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
XX CC (heavy chain variable domain) protein of the invention. The protein was  
XX CC generated via the introduction of the human CA IX protein into a  
XX CC transgenic mouse strain.

XX SQ Sequence 120 AA;

Query Match 87.5%; Score 548; DB 7; Length 123;  
Best Local Similarity 85.4%; Pred. No. 1e-39;

Query Match 87.8%; Score 549.5; DB 7; Length 120;  
Best Local Similarity 86.1%; Pred. No. 7.3e-40;  
Matches 105; Conservative 8; Mismatches 2; Indels 7; Gaps 2;  
Qy 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60  
Qy 61 HNPFLKSRITISVDTSKNQFSLKLSVTAADTAIVYICARGDGVY-----WGQGLTVTV 115  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 YNPSLKSRTISVDTSKNQFSLKLSVTAADTAIVYICAR--DGYNYWYFDLMWGRGLTVTV 118  
Qy 116 SS 117  
|||  
Db 119 SS 120

RESULT 14

ADP03869  
ID ADP03869 standard; protein; 123 AA.

XX AC ADP03869;

XX DT 29-JUL-2004 (first entry)

XX DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 9.

XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
XX KW cytotatic; colorectal neoplasm; renal cell carcinoma;  
XX KW cervical intraepithelial squamous neoplasia;  
XX KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
XX KW gene therapy; murine; mouse; human; heavy chain variable domain.  
XX OS Unidentified.

XX PN WO2003048328-A2.

XX PD 12-JUN-2003.

XX PF 02-DEC-2002; 2002WO-US038550.

XX PR 03-DEC-2001; 2001US-0337275P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J, Foltz I, Handa M, Gallo M;

XX DR WPI; 2003-523295/49.

XX PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
XX PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
XX PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX PS Claim 1; SEQ ID NO 9; 89pp; English.

XX CC The invention relates to a novel isolated monoclonal antibody (mAb)  
XX CC comprising a heavy chain polypeptide and light chain polypeptide having a  
XX CC sequence chosen from one of 53 fully defined amino acid sequences given  
XX CC in the specification, where the antibody specifically binds carbonic  
XX CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
XX CC demonstrates cytostatic activity and may be useful for treating a tumour,  
XX CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
XX CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
XX CC tumour or breast cancer, possibly via gene therapy. The current sequence  
XX CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
XX CC (heavy chain variable domain) protein of the invention. The protein was  
XX CC generated via the introduction of the human CA IX protein into a  
XX CC transgenic mouse strain.

XX SQ Sequence 123 AA;

Job time : 73.1353 secs

Matches 105; Conservative 6; Mismatches 6; Indels 6; Gaps 1;

QY 1 QVLEQSGPGLVXPSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 QVLEQSGPGLVXPSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 HNFSLKSRITISVDTSKNQFSLKLSVTAADTAVYVCARGDGY-----RYWGQGTLLVT 114  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 YNPSLSRVTISIDTSKNQFSLKLSVTAADTAVYVCARGDGY-----RYWGQGTLLVT 120  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 115 VSS 117  
|||  
Db 121 VSS 123  
|||

RESULT 15  
AAB62775  
ID AAB62775 standard; protein; 120 AA.  
XX  
AC AAB62775;  
XX  
DT 03-APR-2001 (first entry)  
XX  
DE Human HIV-1 monoclonal antibody SEQ ID NO: 74.  
XX  
KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;  
KW envelope glycoprotein; gp120; diagnosis.  
XX  
OS Homo sapiens.  
XX  
PN WO200100678-A1.  
XX  
PD 04-JAN-2001.  
XX  
PF 23-JUN-2000; 2000WO-US017327.  
XX  
PR 30-JUN-1999; 99US-0141701P.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Watkins BA, Reitz MS;  
XX  
DR WPI; 2001-112438/12.  
DR N-PSDB; AAF29076.  
XX  
PT Novel human monoclonal antibody immunoreactive with human  
PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1  
PT in biological sample and providing passive immunotherapy to HIV-1  
PT infected mammal.  
XX  
PS Claim 1; Page 69; 81pp; English.  
XX  
CC The present invention provides the protein and coding sequences for the  
CC variable regions of human monoclonal antibodies which are immunoreactive  
CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.  
CC These can be used in diagnosis and therapy of HIV-1 infection  
XX  
SQ Sequence 120 AA;

Query Match 86.6%; Score 542; DB 4; Length 120;  
Best Local Similarity 86.6%; Pred. No. 3.3e-39;  
Matches 103; Conservative 9; Mismatches 5; Indels 2; Gaps 1;

QY 1 QVLEQSGPGLVXPSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 2 EVQLESGPGLVXPSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 61  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 HNFSLKSRITISVDTSKNQFSLKLSVTAADTAVYVCARG--GDGYRYWGQGTLLVTSS 117  
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Db 62 YNPSLSRVTISVDTSKNQFSLKLSVTAADTAVYVCARGVVVDWFDPMGQGTLLVTSS 120  
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Search completed: November 9, 2005, 12:55:31



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:29:55 ; Search time 18.1805 Seconds  
(without alignments)  
480.403 Million cell updates/sec

Title: US-10-660-357A-33

Perfect score: 626

Sequence: 1 QVQLQSGPGGLVPSFETLSL.....ARGGDGYRWGQGLTVTS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCFUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	530	84.7	119	3	US-09-025-769B-39
2	530	84.7	119	3	US-09-025-769B-65
3	530	84.7	119	4	US-09-490-070A-39
4	530	84.7	119	4	US-09-490-070A-65
5	530	84.7	119	4	US-09-490-153-39
6	530	84.7	119	4	US-09-490-153-65
7	530	84.7	119	4	US-09-490-324-39
8	530	84.7	119	4	US-09-490-324-65
9	520.5	83.1	122	1	US-08-360-125-11
10	520.5	83.1	122	2	US-08-450-578-11
11	520.5	83.1	122	2	US-09-017-628-11
12	520.5	83.1	122	2	US-09-014-880-11
13	520.5	83.1	122	4	US-08-450-363-11
14	520.5	83.1	122	4	US-09-467-903-11
15	519.5	83.0	473	3	US-09-049-672A-4
16	517	82.6	119	1	US-08-360-125-5
17	517	82.6	119	2	US-08-450-578-5
18	517	82.6	119	2	US-09-017-628-5
19	517	82.6	119	2	US-09-014-880-5
20	517	82.6	119	4	US-08-450-363-5
21	517	82.6	119	4	US-09-467-903-5
22	513.5	82.0	487	4	US-09-800-729-145
23	511.5	81.7	118	3	US-09-025-769B-25
24	511.5	81.7	118	4	US-09-490-070A-25
25	511.5	81.7	118	4	US-09-490-153-25
26	511.5	81.7	118	4	US-09-490-324-25
27	503	80.4	117	4	US-09-720-493-2

Sequence 79, Appl  
Sequence 77, Appl  
Sequence 20, Appl  
Sequence 7, Appl  
Sequence 86, Appl  
Sequence 116, App  
Sequence 2, Appl  
Sequence 142, App  
Sequence 3, Appl  
Sequence 10, Appl  
Sequence 837, App  
Sequence 75, Appl  
Sequence 75, Appl  
Sequence 123, App  
Sequence 47, Appl  
Sequence 888, App  
Sequence 140, App  
Sequence 14, Appl

#### ALIGNMENTS

RESULT 1  
US-09-025-769B-39  
; Sequence 39, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckhuhn, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-025-769B-39

Query Match 84.7%; Score 530; DB 3; Length 119;  
Best Local Similarity 86.8%; Pred. No. 3.3e-45;  
Matches 105; Conservative 7; Mismatches 3; Indels 6; Gaps 3;

Qy		60
1 QVQLFESGSGPLVKPSETLSLTCTVSGGSISSGTTHWSWIRQHPRGLEWIGYIYYSGSTY		60
:	:	
:	:	
:	:	
Db	1 QVQLFESGSGPLVKPSETLSLTCTVSGGSISS--YVWSWIRQPCKGLEWIGYIYYSGSTN	58
Qy	61 HNPSLKSRITISVDTSKNQFSLKLSSVTAAADTAIVYCAR--GGDGY---RYWGQGLTVTYS	116
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:	:	
Db	59 YNP SLKSRVITISVDTSKNQFSLKLSSVTAAADTAIVYCARWGGDGDFYAMDYWGQGLTVTYS	118
Qy	117 S 117	
Db	119 S 119	

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RESULT 2
US-09-025-769B-65
; Sequence 65, Application US/09025769B
; Patent No. 630064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-65

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119 S 119

RESULT 3  
US-09-490-070A-39  
; Sequence 39, Application US/09490070A  
; Patent No. 6696248  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; Pack, Peter  
; Ilag, Vic  
; Ge, Liming  
; Moroney, Simon  
; Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Colin G. Sandercock, Esq. c/o Heller Ehrman  
; White & McAuliffe  
; STREET: 1666 K Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/490,070A  
; FILING DATE: 24-Jan-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Colin G. Sandercock, Esq.  
; REGISTRATION NUMBER: 31,298  
; REFERENCE/DOCKET NUMBER: 37629-0005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 912-2000  
; TELEFAX: (202) 912-2020  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
; US-09-490-070A-39

RESULT 4  
US-09-490-070A-65  
; Sequence 65, Ap

Patent No. 6696248  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
STREET: 1666 K Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,070A  
FILING DATE: 24-Jan-2000  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Colin G. Sandercock, Esq.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37629-0005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 912-2000  
TELEFAX: (202) 912-2020  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 65:  
US-09-490-070A-65  
Query Match 84.7%; Score 530; DB 4; Length 119;  
Best Local Similarity 86.8%; Pred. No. 3.3e-45;  
Matches 105; Conservative 7; Mismatches 3; Indels 6; Gaps 3;  
Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISSTGYHWSWIRQHPGKGLWIGIYVSGSTY 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISSTGYHWSWIRQHPGKGLWIGIYVSGSTN 58  
Qy 61 HNPSLKSRITISVDTSKNQFSLKLSVTAADTAVYYCAR-GGDGY---RYWGQGLTVTVS 116  
Db 59 YNPFLKSRVITISVDTSKNQFSLKLSVTAADTAVYYCARWGDDGFYAMDYWGQGLTVTVS 118  
Qy 117 S 117  
Db 119 S 119  
RESULT 5  
US-09-490-153-39  
Sequence 39, Application US/09490153  
Patent No. 6706484  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,153  
FILING DATE: 24-Jan-2000  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: <unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-490-153-39  
Query Match 84.7%; Score 530; DB 4; Length 119;  
Best Local Similarity 86.8%; Pred. No. 3.3e-45;  
Matches 105; Conservative 7; Mismatches 3; Indels 6; Gaps 3;  
Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISSTGYHWSWIRQHPGKGLWIGIYVSGSTY 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISSTGYHWSWIRQHPGKGLWIGIYVSGSTN 58  
Qy 61 HNPFLKSRITISVDTSKNQFSLKLSVTAADTAVYYCAR-GGDGY---RYWGQGLTVTVS 116  
Db 59 YNPFLKSRVITISVDTSKNQFSLKLSVTAADTAVYYCARWGDDGFYAMDYWGQGLTVTVS 118  
Qy 117 S 117  
Db 119 S 119  
RESULT 6  
US-09-490-153-65  
Sequence 65, Application US/09490153  
Patent No. 6706484  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York

Patent No. 6696248  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,153  
FILING DATE: 24-Jan-2000  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: <unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-490-153-39  
Query Match 84.7%; Score 530; DB 4; Length 119;  
Best Local Similarity 86.8%; Pred. No. 3.3e-45;  
Matches 105; Conservative 7; Mismatches 3; Indels 6; Gaps 3;  
Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISSTGYHWSWIRQHPGKGLWIGIYVSGSTY 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISSTGYHWSWIRQHPGKGLWIGIYVSGSTN 58  
Qy 61 HNPFLKSRITISVDTSKNQFSLKLSVTAADTAVYYCAR-GGDGY---RYWGQGLTVTVS 116  
Db 59 YNPFLKSRVITISVDTSKNQFSLKLSVTAADTAVYYCARWGDDGFYAMDYWGQGLTVTVS 118  
Qy 117 S 117  
Db 119 S 119  
RESULT 6  
US-09-490-153-65  
Sequence 65, Application US/09490153  
Patent No. 6706484  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York



FILING DATE: 18-FEB-1998  
 APPLICATION NUMBER: EP 35 11 3021.0  
 FILING DATE: 18-AUG-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: James F. Haley, Jr., Esq.  
 REGISTRATION NUMBER: 27,794  
 REFERENCE/DOCKET NUMBER: MORPHO/5  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 596-9000  
 TELEFAX: (212) 596-9090  
 INFORMATION FOR SEQ ID NO: 65:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 119 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 65:  
 US-09-490-324-65

Query Match	84.7%;	Score 530;	DB 4;	Length 119;
Best Local Similarity	86.8%;	Pred. No. 3.3e-45;		
Matches 105;	Conservative 7;	Mismatches 3;	Indels 6;	Gaps 3;
QY	1	QVQLFQSGPGLVKPSETLSLTCTVSGGISISGTYHHSWIRQPGKLEWIGIYYSGSTY	60	
		:::		
Db	1	QVQLDSEPGIIVKPSSETLSLTCTVSGGIS--YYWSWIRQPGKLEWIGIYYSGSTN	58	
		:::		
QY	61	HNPSLKSRITTVISVDTSKNQPSKLKLSVTAADTAVVYCAR--GGDGY--RYWGQGLTVTVS	116	
		:::		
Db	59	YNPSLKSRVTVISVDTSKNQPSKLKLSVTAADTAVVYCARWGDDGFYMDWYQGGLTVTVS	118	
		:::		
QY	117	S 117		
		↑		
Db	119	S 119		

RESULT 9  
 US-08-360-125-11  
 ; Sequence 11, Application US/08360125  
 ; Patent No. 5767246  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Saiko HOSOKAWA  
 ; APPLICANT: Toshiaki TAGAWA  
 ; APPLICANT: Yoko HIRAKAWA  
 ; APPLICANT: NO. 5767246ihiko ITO  
 ; APPLICANT: Kazuhiro NAGAIKE  
 ; TITLE OF INVENTION: Human Monoclonal Antibody  
 ; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
 ; TITLE OF INVENTION: Cell Membrane  
 ; NUMBER OF SEQUENCES: 42  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Wenderoth, Lind & Ponack  
 ; STREET: 805 Fifteenth Street, N.W., #700  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: MS-DOS  
 ; SOFTWARE: Wordperfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/360,125  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/905,534  
 ; FILING DATE: June 29, 1992  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,347  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human antibody 1-3-1  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-360-125-11

Query Match	83.1%	Score	520.5;	DB 1;	Length	122;	
Best Local Similarity	82.0%;	Pred. No.	2.9e-44;				
Matches 101; Conservative	8;	Mismatches	8;	Indels	5;	Gaps	2;
Qy	1	OVLQGGGCLVKPSETLSLCTCVSGSISSTGYHNSWIRQHPCRGLEWIGYIYSGSTY	60				
		: ::	:	:	:	:	
Dd	1	QLQLQGSPGLVKPSETLSLCTCVSGSISSSSYMGWIRQPCKGLEWIGYIYSGSTY	60				
		: ::	:	:	:	:	
Qy	61	HNPFLSKRITISVDTSKNQFSLKSSVTADTAVVYCARGG-DGYRY----	WGOGTLVTV 115				
		: ::	:	:	:	:	
Dd	61	YNPFLSKRITISVDTSKNQFSLKSSVTADTAVVYCARGSYGGYYCMVMWGQGTIVTV	120				
		: ::	:	:	:	:	
Qy	116	SS 117					
Dd	121	SS 122					

RESULT 10  
US-08-450-578-11  
; Sequence 11, Application US/08450578  
; Patent No. 5837845



## RESULT 12

US-09-014-880-11  
; Sequence 11, Application US/09014880  
; Patent No. 5990297  
; GENERAL INFORMATION:  
; APPLICANT: Saiko HOSOKAWA et al.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY  
; TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
; STREET: 2033 K Street, N.W., #800  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/014,880  
; FILING DATE: January 28, 1998  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/450,578  
; FILING DATE: May 25, 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/360,125  
; FILING DATE: December 20, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/905,534  
; FILING DATE: June 29, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-721-8200  
; TELEFAX: 202-721-8250  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 122 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; CELL TYPE: Hybridoma producing human antibody 1-3-1  
US-09-014-880-11

Query Match 83.1%; Score 520.5; DB 2; Length 122;  
Best Local Similarity 82.8%; Pred. No. 2.9e-44;  
Matches 101; Conservative 8; Mismatches 8; Indels 5; Gaps 2;  
Qy 1 QVLEQSGPLGVKPSLTLCTVSGGSISSTGTHWSWIRQHPGRGLEWIGYIYSGSTY 60  
Db 1 QLQLQESGPGVLKPSLTLCTVSGGSISSTGTHWSWIRQHPGRGLEWIGYIYSGSTY 60  
Qy 61 HNPGLKSRITTSVDTSKNQPSLKVSVTAADTAVVYCARGG-DGYRY---WGQGLTAVTV 115  
Db 61 YNPGLKSRITTSVDTSKNQPSLKVSVTAADTAVVYCARGSYGGYGMVWQGGTAVTV 120  
Qy 116 SS 117  
Db 121 SS 122

## RESULT 13

US-08-450-363-11

; Sequence 11, Application US/08450363  
; Patent No. 6436434  
; GENERAL INFORMATION:  
; APPLICANT: Saiko HOSOKAWA  
; APPLICANT: Yoshiaki TAGAWA  
; APPLICANT: Yoko HIRAKAWA  
; APPLICANT: No. 6436434iiko ITO  
; APPLICANT: Kazuhiko NAGAIKE  
; TITLE OF INVENTION: Human Monoclonal Antibody  
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/450,363  
; FILING DATE: May 25, 1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/360,125  
; FILING DATE: December 20, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/905,534  
; FILING DATE: June 29, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 122 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL:  
; ANTI-SENSE:  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM:  
; STRAIN:  
; INDIVIDUAL ISOLATE:  
; DEVELOPMENTAL STAGE:  
; HAPLOTYPE:  
; TISSUE TYPE:  
; CELL TYPE: Hybridoma producing human antibody 1-3-1  
; CELL LINE:  
; ORGANELLE:  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE:  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT:  
; MAP POSITION:  
; UNITS:  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:

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;
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
;   AUTHORS:
;   TITLE:
;   JOURNAL:
;   VOLUME:
;   ISSUE:
;   PAGES:
;   DATE:
;   DOCUMENT NUMBER:
;   FILING DATE:
;   PUBLICATION DATE:
;   RELEVANT RESIDUES IN SEQ ID NO:
;
US-08-450-363-11
;
Query Match      83.1%; Score 520.5; DB 4; Length 122;
Best Local Similarity 82.8%; Pred. No. 2.9e-44;
Matches 101; Conservative 8; Mismatches 8; Indels 5; Gaps 2;

Qy 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60
Db 1 QLOLQESGPGLVKVPSETLSLTCTVSGGSISSSYWGWIRQPPKGLEWIGSYIYSGSTY 60
Qy 61 HNPGLSKSRITISVDTSKNQFSLKLSVTAADTAVYVCARGG-DGYRY----WGQGTLTVT 115
Db 61 YNPGLSKSRVTISVDTSKNQFSLKLSVTAADTAVYVCARGSGYGGYYGMDVMWQGTTLTV 120
Qy 116 SS 117
Db 121 SS 122

RESULT 14
US-09-467-903-11
; Sequence 11, Application US/09467903
; Patent No. 6787153
; GENERAL INFORMATION:
;   APPLICANT: Saiko HOSOKAWA
;               Yoshiaki TAGAWA
;               Yoko HIRAKAWA
;               No. 6787153ihiko ITO
;               Kazuhito NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
;                   Specifically Binding to Surface Antigen of Cancer
;                   Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Wenderoth, Lind & Ponack
;   STREET: 2033 K Street, N.W., #800
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: U.S.A.
;   ZIP: 20006
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: MS-DOS
;   SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/467,903
;   FILING DATE: 21-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/450,363
;   FILING DATE: May 25, 1995
;   APPLICATION NUMBER: 08/360,125
;   FILING DATE: December 20, 1994
;   APPLICATION NUMBER: 07/905,534
;   FILING DATE: June 29, 1992
;   APPLICATION NUMBER: JP158859/1991
;   FILING DATE: June 28, 1991
;   APPLICATION NUMBER: JP158860/1991
;   FILING DATE: June 28, 1991
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;
; APPLICATION NUMBER: JP158861/1991
; FILING DATE: June 28, 1991
; ATTORNEY/AGENT INFORMATION:
;   NAME: Warren M. Cheek Jr.
;   REGISTRATION NUMBER: 33,367
;   REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 202-721-8200
;   TELEFAX: <Unknown>
;   TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 122 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: <Unknown>
; ANTI-SENSE: <Unknown>
; ORIGINAL SOURCE:
;   ORGANISM: <Unknown>
;   STRAIN: <Unknown>
;   INDIVIDUAL ISOLATE: <Unknown>
;   DEVELOPMENTAL STAGE: <Unknown>
;   HAPLOTYPE: <Unknown>
; TISSUE TYPE: <Unknown>
; CELL TYPE: Hybridoma producing human antibody 1-3-1
; ORGANELLE: <Unknown>
; IMMEDIATE SOURCE:
;   LIBRARY: <Unknown>
;   CLONE: <Unknown>
; POSITION IN GENOME:
;   CHROMOSOME/SEGMENT: <Unknown>
;   MAP POSITION: <Unknown>
;   UNITS: <Unknown>
; FEATURE:
;   NAME/KEY:
;   LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
;   AUTHORS:
;   TITLE:
;   JOURNAL:
;   VOLUME:
;   ISSUE:
;   PAGES:
;   DATE:
;   DOCUMENT NUMBER:
;   FILING DATE:
;   PUBLICATION DATE:
;   RELEVANT RESIDUES IN SEQ ID NO:
;   SEQUENCE DESCRIPTION: SEQ ID NO: 11:
;
US-09-467-903-11
;
Query Match      83.1%; Score 520.5; DB 4; Length 122;
Best Local Similarity 82.8%; Pred. No. 2.9e-44;
Matches 101; Conservative 8; Mismatches 8; Indels 5; Gaps 2;

Qy 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60
Db 1 QLOLQESGPGLVKVPSETLSLTCTVSGGSISSSYWGWIRQPPKGLEWIGSYIYSGSTY 60
Qy 61 HNPGLSKSRITISVDTSKNQFSLKLSVTAADTAVYVCARGG-DGYRY----WGQGTLTVT 115
Db 61 YNPGLSKSRVTISVDTSKNQFSLKLSVTAADTAVYVCARGSGYGGYYGMDVMWQGTTLTV 120
Qy 116 SS 117
Db 121 SS 122
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## RESULT 15

US-09-049-672A-4  
 ; Sequence 4, Application US/09049672A  
 ; Patent No. 6135941  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hillman, Jennifer L.  
 ; APPLICANT: Lal, Preeti  
 ; APPLICANT: Tang, Y. Tom  
 ; APPLICANT: Yue, Henry  
 ; APPLICANT: Au-Young, Janice  
 ; APPLICANT: Corley, Neil C.  
 ; APPLICANT: Guegler, Karl J.  
 ; APPLICANT: Baughn, Marian R.  
 ; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
 ; NUMBER OF SEQUENCES: 28  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/049,672A  
 ; FILING DATE: HERewith  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Cerrone, Michael C.  
 ; REGISTRATION NUMBER: 39,132  
 ; REFERENCE/DOCKET NUMBER: PF-0497 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650-855-0555  
 ; TELEFAX: 650-845-4166  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 473 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: PANCTUT01  
 ; CLONE: 1513264  
 ; US-09-049-672A-4

Query Match 83.0%; Score 519.5; DB 3; Length 473;  
 Best Local Similarity 81.5%; Pred. No. 1.9e-43;  
 Matches 101; Conservative 7; Mismatches 9; Indels 7; Gaps 1;  
 Qy 1 QVLEQSGGLVXPSETLSLTCTVSGSISGGTYHWSWIRQHPGRGLEWIGYIYSGSY 60  
 Db ||||:|||||||||||||||:|||||:|||||:|||||:|||||:|||||:|||||  
 20 QVQLQSGGLVXPSETLSLTCAVSGSITSGGYYSWIRQHPGRGLEWIGYIYSGSTL 79  
 Qy ||||:|||||||||||||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db ||||:|||||||||||||||:|||||:|||||:|||||:|||||:|||||:|||||  
 61 HNPFLSKSRITISVDTSKNQPSLKLSSVTAADTAIVYICAR-----GGDGYRYWGQGLV 113  
 Qy ||||:|||||||||||||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db ||||:|||||||||||||||:|||||:|||||:|||||:|||||:|||||:|||||  
 80 YNPFLSKSRITISVDTSKNQPSLKLSSVTAADTAIVYICARDDVGLRGNGYGMVWGQGLV 139  
 Qy ||||:|||||||||||||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db ||||:|||||||||||||||:|||||:|||||:|||||:|||||:|||||:|||||  
 114 TVSS 117  
 Qy ||||  
 Db ||||  
 140 TVSS 143  
 Qy ||||  
 Db ||||

Search completed: November 9, 2005, 11:46:41  
 Job time : 18.1805 secs

RECEIVED  
JAN 20 1962

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:40:37 ; Search time 65 Seconds  
(without alignments) 753.137 Million cell updates

**Title:** US-10-660-357A-33

Perfect score:

Sequence: 1 QVQLEQSGPGLVKPSETLSL.....ARGGDGYRYWGQGLTVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%

POST-PROCESSING: MINIMUM MATCH 0%  
MAXIMUM MATCH 100%

Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep
- 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep
- 18: /cgn2\_6/ptodata/1/pubpaa/US10F\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep
- 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
- 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query			Description	
	Score	Match	Length	ID	
1	626	100.0	117	14	US-10-330-613-33
2	626	100.0	117	14	US-10-330-530-33
3	626	100.0	117	16	US-10-660-357-33
4	604	96.5	117	14	US-10-330-613-5
5	604	96.5	117	14	US-10-330-530-5
6	604	96.5	117	16	US-10-660-357-5
7	568	90.7	117	14	US-10-330-613-13
8	568	90.7	117	14	US-10-330-530-13
9	568	90.7	117	16	US-10-660-357-13
10	552.5	88.3	118	15	US-10-309-762-138
11	552	88.2	123	15	US-10-309-762-10
					Sequence 33, Appl
					Sequence 33, Appl
					Sequence 33, Appl
					Sequence 5, Appl
					Sequence 5, Appl
					Sequence 13, Appl
					Sequence 13, Appl
					Sequence 13, Appl
					Sequence 138, Appl
					Sequence 10, Appl

## ALIGNMENTS

```

RESULT 1
US-10-330-613-33
; Sequence 33, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST TH
; FILE REFERENCE: AGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-33

```

Query Match	100.0%;	Score 626;	DB 14;	Length 117;
Best Local Similarity	100.0%;	Pred. No. 6.4e-48;		
Matches 117;	Conservative	0;	Mismatches 0;	Indels 0;
				Gaps 0;

Qy	1	QVQLFQSGPGLVKPSETLSLCTCTSGGSISSGTYHMSWIROHPGRGLEWIGVYYSGSY	60
Db	1	QVQLFQSGPGLVKPSETLSLCTCTSGGSISSGTYHMSWIROHPGRGLEWIGVYYSGSY	60
Qy	61	HNPSLKSRTITISVDTSKQFSLKSSVTAADTAVYFCARGDGYRYWGQGLTVTVSS	117
Db	61	HNPSLKSRTITISVDTSKQFSLKSSVTAADTAVYFCARGDGYRYWGQGLTVTVSS	117

## RESULT 2

```
US-10-330-530-33
; Sequence 33, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-33

Query Match      100.0%; Score 626; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.4e-48;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60
DB 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60

QY 61 HNPSLKSRITISVDTSKNQFSLKLSVTAADTAVYVCARGDGYRYWGQGLTVTVSS 117
DB 61 HNPSLKSRITISVDTSKNQFSLKLSVTAADTAVYVCARGDGYRYWGQGLTVTVSS 117

RESULT 3
US-10-660-357-33
; Sequence 33, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-33

Query Match      100.0%; Score 626; DB 16; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.4e-48;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60
DB 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60

QY 61 HNPSLKSRITISVDTSKNQFSLKLSVTAADTAVYVCARGDGYRYWGQGLTVTVSS 117
DB 61 HNPSLKSRITISVDTSKNQFSLKLSVTAADTAVYVCARGDGYRYWGQGLTVTVSS 117

RESULT 4
US-10-330-613-5
; Sequence 5, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-5

Query Match      96.5%; Score 604; DB 14; Length 117;
Best Local Similarity 94.0%; Pred. No. 5.8e-46;
Matches 110; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60
DB 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60

QY 61 HNPSLKSRITISVDTSKNQFSLKLSVTAADTAVYVCARGDGYRYWGQGLTVTVSS 117
DB 61 HNPSLKSRITISVDTSKNQFSLKLSVTAADTAVYVCARGDGYRYWGQGLTVTVSS 117

RESULT 5
US-10-330-530-5
; Sequence 5, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-5

Query Match      96.5%; Score 604; DB 14; Length 117;
Best Local Similarity 94.0%; Pred. No. 5.8e-46;
Matches 110; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60
DB 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60

QY 61 HNPSLKSRITISVDTSKNQFSLKLSVTAADTAVYVCARGDGYRYWGQGLTVTVSS 117
DB 61 HNPSLKSRITISVDTSKNQFSLKLSVTAADTAVYVCARGDGYRYWGQGLTVTVSS 117

RESULT 6
US-10-660-357-5
; Sequence 5, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-5

Query Match      100.0%; Score 626; DB 16; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.4e-48;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60
DB 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60

QY 61 HNPSLKSRITISVDTSKNQFSLKLSVTAADTAVYVCARGDGYRYWGQGLTVTVSS 117
DB 61 HNPSLKSRITISVDTSKNQFSLKLSVTAADTAVYVCARGDGYRYWGQGLTVTVSS 117
```

; PRIOR FILING DATE: 2002-12-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-660-357-5

Query Match 96.5%; Score 604; DB 16; Length 117;  
Best Local Similarity 94.0%; Pred. No. 5, 8e-46;  
Matches 110; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKLEWIGYIYSGSTY 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKLEWIGYIYSGSTY 60  
Qy 61 HNPSLKSRITISVDTSKNQFSLKSSVTAADTAVYYCARGDGYRWGQGLTVTVSS 117  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYRWGQGLTVTVSS 117

## RESULT 7

US-10-330-613-13  
; Sequence 13, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-13

Query Match 90.7%; Score 568; DB 14; Length 117;  
Best Local Similarity 88.9%; Pred. No. 9e-43;  
Matches 104; Conservative 10; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKLEWIGYIYSGSTY 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKLEWIGYIYSGSTY 60  
Qy 61 HNPSLKSRITISVDTSKNQFSLKSSVTAADTAVYYCARGDGYRWGQGLTVTVSS 117  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYRWGQGLTVTVSS 117

## RESULT 8

US-10-330-530-13  
; Sequence 13, Application US/10330530  
; Publication No. US20030152514A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES  
; FILE REFERENCE: ABGENIX.031A  
; CURRENT APPLICATION NUMBER: US/10/330,530  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: US 60/346414  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo Sapiens

## US-10-330-530-13

Query Match 90.7%; Score 568; DB 14; Length 117;  
Best Local Similarity 88.9%; Pred. No. 9e-43; Indels 0; Gaps 0;  
Matches 104; Conservative 10; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKLEWIGYIYSGSTY 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKLEWIGYIYSGSTY 60  
Qy 61 HNPSLKSRITISVDTSKNQFSLKSSVTAADTAVYYCARGDGYRWGQGLTVTVSS 117  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYRWGQGLTVTVSS 117

## RESULT 9

US-10-660-357-13  
; Sequence 13, Application US/10660357  
; Publication No. US20040115205A1  
; GENERAL INFORMATION:  
; APPLICANT: Bar-Eli, Menashe  
; APPLICANT: Green, Larry L.  
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18  
; TITLE OF INVENTION: ANTIGEN  
; FILE REFERENCE: ABGENIX.030C1  
; CURRENT APPLICATION NUMBER: US/10/660,357  
; CURRENT FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 10/330,580  
; PRIOR FILING DATE: 2002-12-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-660-357-13

Query Match 90.7%; Score 568; DB 16; Length 117;  
Best Local Similarity 88.9%; Pred. No. 9e-43; Indels 0; Gaps 0;  
Matches 104; Conservative 10; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKLEWIGYIYSGSTY 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHMSWIRQHPGKLEWIGYIYSGSTY 60  
Qy 61 HNPSLKSRITISVDTSKNQFSLKSSVTAADTAVYYCARGDGYRWGQGLTVTVSS 117  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 YNPSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARGDGYRWGQGLTVTVSS 117

## RESULT 10

US-10-309-762-138  
; Sequence 138, Application US/10309762  
; Publication No. US20040018198A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; APPLICANT: Foltz, Ian  
; APPLICANT: Handa, Masahisa  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
; FILE REFERENCE: ABGENIX.027A  
; CURRENT APPLICATION NUMBER: US/10/309,762  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/337275  
; PRIOR FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 138  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-309-762-138

```

Query Match      88.3%; Score 552.5; DB 15; Length 118;
Best Local Similarity 89.0%; Pred. No. 2.1e-41;
Matches 105; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

QY 1 QVQLQSGPGLVKPSETLSLTCTVSGGISGGYHWSWIRQHPGRGLEWIGYIYSGSTY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLQSGPGLVKPSETLSLTCTVSGGISGGYHWSWIRQHPGRGLEWIGYIYSGSTY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 HNPSLKSRITISVDTSKNQFSLKSSVTAADTAVYYCAR--GGDGYRYWGQGLTLTVSS 117
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 YNPFLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARYGSGSDYWGQGLTLTVSS 118
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
US-10-309-762-10
; Sequence 10, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-10

Query Match      88.2%; Score 552; DB 15; Length 123;
Best Local Similarity 85.4%; Pred. No. 2.5e-41;
Matches 105; Conservative 7; Mismatches 5; Indels 6; Gaps 1;

QY 1 QVQLQSGPGLVKPSETLSLTCTVSGGISGGYHWSWIRQHPGRGLEWIGYIYSGSTY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLQSGPGLVKPSETLSLTCTVSGGISGGYHWSWIRQHPGRGLEWIGYIYSGSTY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 HNPFLKSRITISVDTSKNQFSLKSSVTAADTAVYYCARGGDGY-----RYWGQGLTVT 114
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 YNPFLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARAGKYGSGSYLDYWGQGLTVT 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 115 VSS 117
   |||
Db 121 VSS 123
   |||

RESULT 12
US-10-309-762-13
; Sequence 13, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 13
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-13

Query Match      87.8%; Score 549.5; DB 15; Length 120;
Best Local Similarity 86.1%; Pred. No. 4e-41;
Matches 105; Conservative 8; Mismatches 2; Indels 7; Gaps 2;

QY 1 QVQLQSGPGLVKPSETLSLTCTVSGGISGGYHWSWIRQHPGRGLEWIGYIYSGSTY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLQSGPGLVKPSETLSLTCTVSGGISGGYHWSWIRQHPGRGLEWIGYIYSGSTY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 HNPFLKSRITISVDTSKNQFSLKSSVTAADTAVYYCARGGDGYR-----WGQGLTVTV 115
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 YNPFLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCAR--DGNYWYFDMWGRGLTVTV 118
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 116 SS 117
   ||
Db 119 SS 120
   ||

RESULT 13
US-10-309-762-144
; Sequence 144, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-144

Query Match      87.8%; Score 549.5; DB 15; Length 120;
Best Local Similarity 86.1%; Pred. No. 4e-41;
Matches 105; Conservative 8; Mismatches 2; Indels 7; Gaps 2;

QY 1 QVQLQSGPGLVKPSETLSLTCTVSGGISGGYHWSWIRQHPGRGLEWIGYIYSGSTY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLQSGPGLVKPSETLSLTCTVSGGISGGYHWSWIRQHPGRGLEWIGYIYSGSTY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 HNPFLKSRITISVDTSKNQFSLKSSVTAADTAVYYCARGGDGYR-----WGQGLTVTV 115
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 YNPFLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCAR--DGNYWYFDMWGRGLTVTV 118
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 116 SS 117
   ||
Db 119 SS 120
   ||

RESULT 14
US-10-309-762-9
; Sequence 9, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael

```

; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN  
; FILE REFERENCE: ARGENIX.027A  
; CURRENT APPLICATION NUMBER: US/10/309,762  
; PRIOR FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/337275  
; PRIOR FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-309-762-9

Query Match 87.5%; Score 548; DB 15; Length 123;  
Best Local Similarity 85.4%; Pred. No. 5.6e-41;  
Matches 105; Conservative 6; Mismatches 6; Indels 6; Gaps 1;  
  
Qy 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGYHNSWIRQHPGRGLEWIGYIYSGSTY 60  
Db 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGYHNSWIRQHPGRGLEWIGYIYSGSTY 60  
  
Qy 61 HNPFLKSRITISVDTSKNQFSLKLSVTAADTAVYICARGGQY-----RYWGQGTTLV 114  
Db 61 YNPFLKSRITISVDTSKNQFSLKLSVTAADTAVYICARGGQY-----RYWGQGTTLV 120  
  
Qy 115 VSS 117  
Db 121 VSS 123

RESULT 15  
US-10-805-177-53  
; Sequence 53, Application US/10805177  
; Publication No. US2005008449A1  
; GENERAL INFORMATION:  
; APPLICANT: Landes, Gregory M.  
; APPLICANT: Chen, Francine  
; APPLICANT: Bezabeh, Binyam  
; APPLICANT: Foltz, Ian  
; APPLICANT: Tse, Kam Fai  
; APPLICANT: Jeffers, Michael  
; APPLICANT: Mesri, Mehdi  
; APPLICANT: Starling, Gary  
; APPLICANT: Mezes, Peter  
; APPLICANT: Khramtsov, Nikolai  
; TITLE OF INVENTION: ANTIBODIES AGAINST T CELL IMMUNOGLOBULIN  
; FILE REFERENCE: AEXCUR.006A  
; CURRENT APPLICATION NUMBER: US/10/805,177  
; PRIOR FILING DATE: 2004-03-19  
; PRIOR APPLICATION NUMBER: 60/456,652  
; PRIOR FILING DATE: 2003-03-19  
; NUMBER OF SEQ ID NOS: 141  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 53  
; LENGTH: 125  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-805-177-53

Query Match 87.3%; Score 546.5; DB 17; Length 125;  
Best Local Similarity 83.1%; Pred. No. 7.7e-41;  
Matches 103; Conservative 9; Mismatches 5; Indels 7; Gaps 1;  
  
Qy 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGYHNSWIRQHPGRGLEWIGYIYSGSTY 60  
Db 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGYHNSWIRQHPGRGLEWIGYIYSGSTY 60  
  
Qy 61 HNPFLKSRITISVDTSKNQFSLKLSVTAADTAVYICARGG-----DGYRWGQGTTLV 113  
Db 61 YNPFLKSRITISVDTSKNQFSLKLSVTAADTAVYICARNNNNNSSWYNNFDYWGQGTTLV 120

Qy 114 TVSS 117  
Db 121 TVSS 124  
  
Search completed: November 9, 2005, 12:43:03  
Job time : 66 secs

(CLASS) XAT/EC/10/11/11



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 12:25:58 ; Search time 12.609 Seconds  
(without alignments)  
892.802 Million cell updates/sec

Title: US-10-660-357A-33

Perfect score: 626

Sequence: 1 QVQLQESGPGLVKPSSTLSL.....ARGGDGYRWGQGLTVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	523	83.5	147	2 S13519	Ig heavy chain V r
2	514	82.1	140	2 I37782	Ig variable region
3	510	81.5	116	2 S37456	Ig mu chain - huma
4	510	81.5	130	2 S31690	Ig heavy chain V r
5	507	81.0	135	2 S78051	Ig heavy chain pre
6	503	80.4	121	2 S44113	Ig heavy chain V r
7	498	79.6	155	2 S31511	Ig heavy chain - h
8	496	79.2	155	2 S31512	Ig heavy chain - h
9	493.5	78.8	139	2 S31586	Ig heavy chain V r
10	493	78.8	99	2 S26801	Ig heavy chain V r
11	492.5	78.7	130	2 S30534	Ig heavy chain V r
12	488	78.0	128	2 S31514	Ig heavy chain - h
13	484	77.3	99	2 S26802	Ig heavy chain V r
14	484	77.3	99	2 S26803	Ig heavy chain V r
15	480.5	76.8	129	2 S44114	Ig heavy chain V r
16	479	76.5	118	2 A26340	Ig heavy chain pre
17	479	76.5	123	2 S30530	Ig heavy chain V r
18	476	76.0	146	2 S09711	Ig heavy chain V r
19	474.5	75.8	122	2 S69912	Ig V-D-J region (N
20	474.5	75.8	137	2 S31676	Ig heavy chain V r
21	474	75.7	146	2 S09710	Ig heavy chain V r
22	472	75.4	140	2 A49045	Ig heavy chain V r
23	470	75.1	139	2 S31696	Ig heavy chain V r
24	468	74.8	105	2 S44125	Ig lambda chain V
25	467.5	74.7	140	2 S78052	Ig heavy chain pre
26	467	74.6	99	2 S12418	Ig heavy chain V r
27	464.5	74.2	110	2 S44110	Ig heavy chain V-D
28	464.5	74.2	145	2 S78055	Ig heavy chain pre
29	464	74.1	135	2 S31604	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S13519

Ig heavy chain V region precursor - human

C;Species: Homo sapiens (man)

C;Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C;Accession: S13519

R;Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.

Nucleic Acids Res. 19, 673, 1991

A;Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked A;Reference number: S13519; MUID:91187691; PMID:2011536

A;Accession: S13519

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-147 <MOR>

A;Cross-references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

P;41-125/Domain: immunoglobulin homology <IMM>

Query Match 83.5%; Score 523; DB 2; Length 147;

Best Local Similarity 82.8%; Pred. No. 4.2e-39;

Matches 100; Conservative 10; Mismatches 7; Indels 4; Gaps 1;

QY 1 QVQLQESGPGLVKPSSTLSLCTCTVSGSSISGQYHWSWIRQHPGRGLEWIGYIYSGSTY 60

Db 27 QQLQESGPGLVKPSSTLSLCTCTVSGSSISGQYHWSWIRQHPGRGLEWIGYIYSGSTY 86

QY 61 HNPSLKSRITISVDTSKNQFSLKLSSTVAADTAATVAVYICARG----GDGYRWGQGLTVTVS 116

Db 87 YNPFLKSRITISVDTSKNQFSLKLSSTVAADTAATVAVYICARPLLWFGLFDYWGQGLTVTVS 146

QY 117 S 117

Db 147 S 147

RESULT 2

I37782

Ig variable region (VDJ) (clone T23-9) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999

C;Accession: I37782; S25476

R;Demaison, C.; Chastagner, P.; There, J.; Zouali, M.

Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994

A;Title: Somatic diversification in the heavy chain variable region genes expressed by A;Reference number: A36876; MUID:94119917; PMID:8290556

A;Accession: I37782

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-140 <RES>

A;Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA448104.1; PID:g33583

C;Superfamily: immunoglobulin V region; immunoglobulin homology



A;Cross-references: EMBL:Z31389; NID:G472967; PIDN:CAA83264.1; PID:G940524  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 503; DB 2; Length 121;  
Best Local Similarity 79.3%; Pred. No. 1.9e-37;  
Matches 96; Conservative 9; Mismatches 12; Indels 4; Gaps 1;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 HNPFLSKSRITISVDTSKNQFSLKSSVTAADTAVYYCARGDGY----RYWGQGTLLTVTS 116  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 YNPFLSKSRVITISVDTSKNQFSLKSSVTAADTAVYYCARGDGYSSDYFWSQGTLLTVTS 120  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 117 S 117  
|

Db 121 S 121

## RESULT 7

S31511  
Ig heavy chain - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S31511  
R;Chastagner, P.; Denaison, C.; Theze, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto  
A;Reference number: S31509  
A;Accession: S31511  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-155 <CHA>  
A;Cross-references: EMBL:X69866; NID:G33094; PIDN:CAA49500.1; PID:G33095  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;47-129/Domain: immunoglobulin homology <IMM>

Query Match 79.6%; Score 498; DB 2; Length 155;  
Best Local Similarity 78.4%; Pred. No. 6.9e-37;  
Matches 98; Conservative 8; Mismatches 9; Indels 10; Gaps 2;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 33 QVQLQESGPGLVKPSSETLSLTCTVSGGSISS--YYWSWIRQPPGKLEWIGYIYTGSA 90  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 HNPFLSKSRITISVDTSKNQFSLKSSVTAADTAVYYCARGD-----GYRWGQGTLL 112  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 91 YNPFLSKSRVITISVDTSKNQFSLKSSVTAADTAVYYCARGGSISSWYDYGMVWGQGT 150  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 113 VTVSS 117  
|||

Db 151 VTVSS 155  
|||

## RESULT 8

S31512  
Ig heavy chain - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S31512  
R;Chastagner, P.; Denaison, C.; Theze, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto  
A;Reference number: S31509  
A;Accession: S31512  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-155 <CHA>  
A;Cross-references: EMBL:X69860; NID:G33082; PIDN:CAA49494.1; PID:G33083

C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;47-129/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 496; DB 2; Length 155;  
Best Local Similarity 77.6%; Pred. No. 1e-36;  
Matches 97; Conservative 9; Mismatches 9; Indels 10; Gaps 2;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 33 QVQLQESGPGLVKPSSETLSLTCTVSGGSISS--YYWSWIRQPPGKLEWIGYIYTGSA 90  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 HNPFLSKSRITISVDTSKNQFSLKSSVTAADTAVYYCARGD-----GYRWGQGTLL 112  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 91 YNPFLSKSRVITISVDTSKNQFSLKSSVTAADTAVYYCARGGSISSWYDYGMVWGQGT 150  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 113 VTVSS 117  
|||

Db 151 VTVSS 155  
|||

## RESULT 9

S31586  
Ig heavy chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S31586  
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.  
submitted to the EMBL Data Library, June 1992  
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A;Reference number: S31585  
A;Accession: S31586  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-139 <CUI>  
A;Cross-references: EMBL:Z14196; NID:G30978; PIDN:CAA78565.1; PID:G30979  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 78.8%; Score 493.5; DB 2; Length 139;  
Best Local Similarity 81.1%; Pred. No. 1.5e-36;  
Matches 99; Conservative 8; Mismatches 8; Indels 7; Gaps 2;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISS--YYWSWIRQPPGKLEWIGRIYTGSTN 77  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 HNPFLSKSRITISVDTSKNQFSLKSSVTAADTAVYYCARGDGYR-----YWGQGTLLTV 115  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 78 YNPFLSKSRVITISVDTSKNQFSLKSSVTAADTAVYYCARGGLGIRGAFDIWGQGTWTV 137  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 116 SS 117  
||

Db 138 SS 139  
||

## RESULT 10

S26801  
Ig heavy chain V region (DP-65) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 25-Oct-1996 #text\_change 20-Jun-2000  
C;Accession: S26801; S26900  
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.  
Eur. J. Immunol. 22, 1075-1082, 1992  
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.  
A;Reference number: S26800; MUID:92201299; PMID:1348029  
A;Accession: S26801  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-99 <WEN>  
A;Cross-references: EMBL:Z14237; NID:G37706; PIDN:CAA78606.1; PID:G1335372  
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A; Title: The repertoire of human germline V(H) sequences reveals about fifty groups of v  
A; Reference number: S26885; MUID:93021117; PMID:1404388  
A; Accession: S26900  
A; Status: preliminary  
A; Molecule type: DNA  
A; Residues: 1-99 <TOM>  
A; Cross-references: EMBL:Z12365; NID:g32948; PIDN:CMA78235.1; PID:g32949  
C; Superfamily: immunoglobulin v region; immunoglobulin homology  
C; Keywords: heterotrimer; immunoglobulin  
F; 15-99/Domain: immunoglobulin homology <IMM>

	Query Match	Best Local Similarity	Score 493;	DB 2;	Length 99;
	Matches	91;	Conservative	7;	Mismatches 1;
					Gaps 0;
Qy	1	OVQLQGSGPLVKEPSETLSLTCTCVSGSISGGYTHNSWIRQHPGRLGLEWIGIYYSGSY	60		
Dd	1	OVQLQGSGPLVKEPSQTLSLTCTCVSGSISGGYTHNSWIRQHPGKLEWIGIYYSGSY	60		
Qy	61	HNFSLSKRITISVDTSKNQFSLKLSSVTAAADTAIVYICAR	99		
Dd	61	YNFSLSKRITISVDTSKNQFSLKLSSVTAAADTAIVYICAR	99		

```

RESULT 11
S30534
IG heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C;Accession: S30534
R;Mariette, X.
submitted to the EMBL Data Library, October 1992
A;Reference number: S30520
A;Accession: S30534
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <MAR>
A;Cross-references: EMBL:Z18320
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMW>

```

```

Qy      108  GQGTFLVTSS 117
      ||||:||||
Db      121  GQGTMTVSS 130

RESULT 12
S31514
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C/Accession: S31514
R/Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A/Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A/Reference number: S31509
A/Accession: S31514
A/Status: preliminary
A/Molecule type: mRNA

```

A;Residues: 1-128 <CHA>						
A;Cross-references: EMBL:X69862; NID:g33086; PIDN:CAA49496.1; PID:g33087						
C;Superfamily: immunoglobulin V region; immunoglobulin homology						
C;Keywords: heterotetramer; immunoglobulin						
P;22-106/Domain: immunoglobulin homology <IMM>						
Query Match	78.0%	Score 488	DB 2:	Length 128;		
Best Local Similarity	76.0%	Pred. No. 4.3e-36;				
Matches 92;	Conservative 14;	Mismatches 11;	Indels 4;	Gaps 1		
Qy	1	QVQLQESGPGLVKRPSETLSLTCTVSGGSISGGTYHMSWIRQHPGRGLEWIGYIYSGSTY	60			
		:     :     :     :     :     :     :     :     :     :				
Db	8	QVQLQESGPGLVKRPSETLSLTCTVSGGSISGGTYHMSWIRQHPGRGLEWIAHIYFSGSTY	67			
		:     :     :     :     :     :     :     :     :				
Qy	61	HNPSLKRITISVDTSKNQPSLKLSVTPADTAVYYCARGSGDGYR.---WGQGTLTVTS	116			
		:     :     :     :     :     :     :     :     :				
Db	68	YNPFLKSRVLIISVDTSNQLSLRITSVTPADTAVYYCARIGYFGDFPMWGQGTLTVTS	127			
		:     :     :     :     :     :     :     :     :				
Qy	117	S 117				
Db	128	S 128				

RESULT 13  
S26802  
Ig heavy chain V region - human  
C/Species: Homo sapiens (man)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
C/Accession: S26802  
R/Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.  
Eur. J. Immunol. 22, 1075-1082, 1992  
A/Title: Polymorphism of human immunoglobulin V(H) 4 germ-line genes.  
A/Reference number: S26800; MUID:92201299; PMID:1348029  
A/Accession: S26802  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-99 <WEN>  
A/Cross-references: EMBL:Z14239; NID:g37708; PID:g1335373  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:15-99/Domain: immunoglobulin homology <IMM>

RESULT 14  
S26803  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S26803  
R:Wang, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.  
Eur J Immunol. 22, 1075-1082, 1992  
A:Title. Polymorphism of human immunoglobulin V(H)4 germ-line genes.  
A:Reference number: S26800; MUID:92201299; PMID:1348029  
A:Accession: S26803  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-99 <WEN>  
A:Cross-references: EMBL:Z14238; NID:G37710; PID:gr1335374  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 77.3%; Score 484; DB 2; Length 99;  
Best Local Similarity 90.9%; Pred. No. 7.4e-36;  
Matches 90; Conservative 7; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60  
Db 1 QVQLQESGPGLVKPSQTLSTLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60  
  
Qy 61 HNPFLSKRITISVDTSKNQFSLKLSSTVAADTAVYYCAR 99  
Db 61 YNPFLSKSRVTISVDTSKNQFSLKLSSTVAADTAVYYCAR 99

## RESULT 15

S44114  
Ig heavy chain V region - human  
C/Species: Homo sapiens (man)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
C/Accession: S44114  
R/Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
submitted to the EMBL Data Library, March 1994  
A/Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable  
A/Reference number: S44105  
A/Accession: S44114  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-129 <HAW>  
A/Cross-references: EMBL:Z31579, NID:9472968; PIDN:CAA83451.1; PID:9940525  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.8%; Score 480.5; DB 2; Length 129;  
Best Local Similarity 76.0%; Pred. No. 2e-35;  
Matches 95; Conservative 11; Mismatches 10; Indels 9; Gaps 3;  
  
Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYSGSTY 60  
Db 1 QVQLQESGPGLVKPSGTLSTLCAVSGGSISSNNW-WSWVRQPPGKGLEWIGEIVHSGSTN 59  
  
Qy 61 HNPFLSKRITISVDTSKNQFSLKLSSTVAADTAVYYCAR-----GGDG-YRYWGQGTLL 112  
Db 60 YNPFKSRVTISADTSKNQFSLKYSVTAADTAVYYCARRNYDFWGGGDFDYWGQGTLL 119  
  
Qy 113 VTVSS 117  
Db 120 VTVSS 124

Search completed: November 9, 2005, 13:08:05  
Job time : 13.609 secs

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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:46:52 ; Search time 60.406 Seconds  
(without alignments)  
991.843 Million cell updates/sec

Title: US-10-660-357A-33

Perfect score: 626

Sequence: 1 QVQLQESGPGLVKPSSETLSL.....ARGGDGYRYMGQGLTVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	533	85.1	476	2 Q6GMX1	Q6gm1 homo sapien
2	508.5	81.2	478	2 Q72379	Q72379 homo sapien
3	487.5	77.9	465	2 Q6GMX6	Q6gm6 homo sapien
4	487	77.8	119	2 Q9UL73	Q9ul73 homo sapien
5	484.5	77.4	477	2 Q6GMX7	Q6gm7 homo sapien
6	476.5	76.1	150	2 Q5973	Q5973 homo sapien
7	475.5	76.0	496	2 Q96KX8	Q96kx8 homo sapien
8	474.5	75.8	620	2 Q96EY0	Q96ey0 homo sapien
9	473.5	75.6	576	2 Q6P4I8	Q6p4i8 homo sapien
10	472.5	75.5	130	2 Q812D7	Q812d7 homo sapien
11	466	74.4	492	2 Q72374	Q72374 homo sapien
12	462	73.8	139	2 Q86SX2	Q86sx2 homo sapien
13	440	70.3	129	1 HV2F HUMAN	P01824 homo sapien
14	436	69.6	478	2 Q6NYH3	Q6nyh3 homo sapien
15	431	68.8	595	2 Q8WUX4	Q8wux4 homo sapien
16	431	68.8	597	2 Q6GMX5	Q6gm5 homo sapien
17	431	68.8	597	2 Q9BU10	Q9bu10 homo sapien
18	431	68.8	625	2 Q96AA6	Q96aa6 homo sapien
19	428.5	68.5	146	1 HV2I HUMAN	P06331 homo sapien
20	425	67.9	597	2 Q9BQ88	Q9bqb8 homo sapien
21	417.5	66.7	136	2 Q6LBQ5	Q6lbq5 mus musculus
22	411	65.7	479	2 Q99M22	Q99m22 mus musculus
23	410.5	65.6	473	2 Q8TC63	Q8tc63 homo sapien
24	409	65.3	117	1 HV2G HUMAN	P01825 homo sapien
25	408.5	65.3	122	2 Q9UL75	Q9ul75 homo sapien
26	398	63.6	116	2 Q723Y6	Q723y6 homo sapien
27	397	63.4	137	1 HV46 MOUSE	P01822 mus musculus
28	396	63.3	262	2 Q65ZT1	Q65zt1 mus musculus
29	393	62.8	476	2 Q6MZK7	Q6mzk7 mus musculus
30	390	62.3	113	1 HV47 MOUSE	P01823 mus musculus
31	372	59.4	117	1 HV62 MOUSE	P18533 mus musculus

32	367.5	58.7	116	1 HV61 MOUSE	P18532 mus musculus
33	366.5	58.5	116	1 HV60 MOUSE	P18531 mus musculus
34	342	54.6	121	2 Q9UL56	Q9ul56 homo sapien
35	339.5	54.2	118	2 Q811U5	Q811u5 mus musculus
36	337.5	53.9	482	2 Q91X92	Q91x92 mus musculus
37	336	53.7	144	1 HV43 MOUSE	P01819 mus musculus
38	335.5	53.6	135	1 HV02 XENLA	P20957 xenopus lae
39	330.5	52.8	121	2 Q99NG4	Q99ng4 mus musculus
40	327	52.2	118	2 Q9UL74	Q9ul74 homo sapien
41	320	51.1	466	2 Q6IN78	Q6in78 homo sapien
42	317	50.6	119	1 HV2C HUMAN	P01816 homo sapien
43	316.5	50.6	606	2 Q6GMV2	Q6gm2 homo sapien
44	314	50.2	116	2 Q9UL93	Q9ul93 homo sapien
45	313.5	50.1	147	2 Q9Y509	Q9y509 homo sapien

#### ALIGNMENTS

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RESULT 1
Q6GMX1 PRELIMINARY; PRT; 476 AA.
AC Q6GMX1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
EMBL; BC073773; AAH73773.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00407; Ig; 4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RN NCBI\_TaxID=9606;  
[1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
DR EMBL; AF035041; AAD56277.1; -  
DR PIR; PH0876; PH0876.  
DR S12416; S12416.  
DR HSSP; P01820; 1G7J.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON TER 1  
FT NON TER 119  
SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;  
  
Query Match 77.8%; Score 487; DB 2; Length 119;  
Best Local Similarity 79.3%; Pred. No. 3.2e-41;  
Matches 96; Conservative 10; Mismatches 9; Indels 6; Gaps 2;  
  
Qy 1 QVLEQSGPGLVKPSETLSLTCTVSGSGISGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60  
Db 1 QVLEQSGPGLVKPSETLSLTCTVSGSGISGTYHMSWIRQHPGRGLEWIGYIYSGSTN 58  
  
Qy 61 HNPGLSKRITISVDTSKNQFSLKSLSVTAADTAVYCAR-----GGDGYRYWGQGLTVTVS 116  
Db 59 YTPSLKSRVTSVDRSKNQFSLKSLTSLTAADTAVYFCARLSNWPYFYDYGQGLTVTVS 118  
  
Qy 117 S 117  
Db 119 S 119  
  
RESULT 5  
Q6GMX7 PRELIMINARY; PRT; 477 AA.  
AC Q6GMX7;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RP SEQUENCE FROM N.A.  
TX TISSUE=Primary B-Cells;  
RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;  
RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;  
RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;  
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Haie H.;  
RA Datchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;  
RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;  
RA Brownstein M.J.; Uedin T.B.; Toshiyuki S.; Carninci P.; Prange C.;  
RA Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullany S.J.;  
RA Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;  
RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;  
RA Villalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;  
RA Fahey J.; Helton E.; Kettman M.; Madan A.; Rodriguez S.; Sanchez A.;  
RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;  
RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;  
RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.;  
RA Krzywinski M.I.; Skalska U.; Smallos D.E.; Schnerch A.; Schein J.E.;  
RA Jones S.J.; Marra M.A.

RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073765; AAH73765.1; -  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 2.  
DR SMART; SM00407; IGV; 3.  
DR SMART; SM00409; IGV; 4.  
DR SMART; SM00407; IGV; 3.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
DR PROSITE; PS00290; IG\_MHC; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CFF85 CRC64;  
  
Query Match 77.4%; Score 484.5; DB 2; Length 477;  
Best Local Similarity 78.3%; Pred. No. 2.5e-40;  
Matches 94; Conservative 12; Mismatches 9; Indels 5; Gaps 2;  
  
Qy 1 QVLEQSGPGLVKPSETLSLTCTVSGSGISGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60  
Db 20 QVLEQSGPGLVKPSETLSLTCTVSGSGISGTYHMSWIRQHPGRGLEWIGYIYSGSTT 77  
  
Qy 61 HNPGLSKRITISVDTSKNQFSLKSLSVTAADTAVYCARGD---GYRYWGQGLTVTVSS 117  
Db 78 YNPGLSKRITISVDTSKNQFSLKSLSVTAADTAVYCARGD---GYRYWGQGLTVTVSS 137  
  
RESULT 6  
O95973 PRELIMINARY; PRT; 150 AA.  
AC O95973;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE VH4 heavy chain variable region precursor (Fragment).  
GN Name=IGH;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RP SEQUENCE FROM N.A.  
TX TISSUE=Primary B-Cells;  
RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;  
RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;  
RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;  
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Haie H.;  
RA Datchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;  
RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;  
RA Brownstein M.J.; Uedin T.B.; Toshiyuki S.; Carninci P.; Prange C.;  
RA Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullany S.J.;  
RA Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;  
RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;  
RA Villalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;  
RA Fahey J.; Helton E.; Kettman M.; Madan A.; Rodriguez S.; Sanchez A.;  
RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;  
RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;  
RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.;  
RA Krzywinski M.I.; Skalska U.; Smallos D.E.; Schnerch A.; Schein J.E.;  
RA Jones S.J.; Marra M.A.



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Oy 116 SS 117
Db 145 SS 146

RESULT 9
Q6P418 PRELIMINARY; PRT; 576 AA.
AC Q6P418;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGH protein.
GN Name=IGH;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063384; AAH63384.1; -
DR HSSP; P01820; 1A7N.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; Igcl; 3.
DR SMART; SM00407; Igcl; 3.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 576 AA; 63363 MW; PFB97C949D720F1E CRC64;

Query Match 75.6%; Score 473.5; DB 2; Length 576;
Best Local Similarity 78.5%; Pred. No. 4e-39;
Matches 95; Conservative 8; Mismatches 13; Indels 5; Gaps 2;

Oy 1 QVQLQSGPGLVKPSETLSLTCTVSGGISGTYHWSWIRQHPGRGLEWIGYISGSTY 60
Db 27 QVQLQSGPGLVKPSETLSLTCTVSGGISGTYHWSWIRQHPGRGLEWIGYISGSTN 85
Oy 61 HNPFLSKRITISVDTSKNQFSLKLSVTAADTAIVYCA-----WGQGLTVTVS 116

RESULT 10
Q81ZD7 PRELIMINARY; PRT; 130 AA.
AC Q81ZD7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 26, Last annotation update)
DE Anti-thyroglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jang Y.-J., Chung J., Park J.-Y.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY145445; AAN64329.1; -
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 130
SQ SEQUENCE 130 AA; 13901 MW; 036131FC6EC1551E CRC64;

Query Match 75.5%; Score 472.5; DB 2; Length 130;
Best Local Similarity 73.1%; Pred. No. 1e-39;
Matches 95; Conservative 11; Mismatches 11; Indels 13; Gaps 3;

Oy 1 QVQLQSGPGLVKPSETLSLTCTVSGGISGTYHWSWIRQHPGRGLEWIGYISGSTY 59
Db 1 QVQLQSGPGLVKPSETLSLTCTVSGGISGTYHWSWIRQHPGRGLEWIGYISGSTY 60
Oy 60 ----YHNPFLSKRITISVDTSKNQFSLKLSVTAADTAIVYCA-----RGDGY---RYW 107
Db 61 SGSPYVAPSLRSRVLSVDTSKNQLSLRLSSVTAADTAIVYCA-----RGDGY---RYW 107
Oy 108 GQGLTVTVSS 117
Db 121 GQGLTVTVSS 130

RESULT 11
Q72374 PRELIMINARY; PRT; 492 AA.
AC Q72374;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686C02218 (Fragment).
GN Name=DKFZp686C02218;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wienann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538077; CAD98001.1; -
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; Ig-like.
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DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 492 AA; 53776 MW; 1E7A1576F0CA74B CRC64;

Query Match 74.4%; Score 466; DB 2; Length 492;
Best Local Similarity 72.7%; Pred. No. 1.9e-38;
Matches 88; Conservative 16; Mismatches 13; Indels 4; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60
Db 32 QLQQLQESGPGLVKPSSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGSIYYNENTY 91

QY 61 HNPSLKSRITISVDTSKNQFSLKLSVTAADTAVYICARGDGG----YRWGQGLTVTVS 116
Db 92 YSPSLKSLRITFVDTSKNHFSLRLTSVTAADTAVYICVRHVEGPGYGNFDPWGQGLTVTVS 151

QY 117 S 117
Db 152 S 152

RESULT 12
Q86SX2 PRELIMINARY; PRT; 139 AA.
AC Q86SX2
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Full-length cDNA clone CSODL004YM19 of B cells (Ramos cell line) of
DE Homo sapiens (human) (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Li W.B., Gruber C., Jessee J., Polayes D.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX248300; CAD62627.1; -.
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;

Query Match 73.8%; Score 462; DB 2; Length 139;
Best Local Similarity 89.9%; Pred. No. 1.2e-38;
Matches 89; Conservative 6; Mismatches 2; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60
Db 33 QVQLQESGPGLVKPSSETLSLTCTVSGGSISS--YYMSWIRQHPGRGLEWIGYIYSGSTN 90

QY 61 HNPSLKSRITISVDTSKNQFSLKLSVTAADTAVYICAR 99
Db 91 YNPSLKSRVITISVDTSKNQFSLKLSVTAADTAVYICAR 129
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RESULT 13
HV2F_HUMAN STANDARD; PRT; 129 AA.
ID HV2F_HUMAN
AC P01824;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-II region WAH.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1[1]
RP SEQUENCE.
RX MEDLINE=8222235; PubMed=6806818;
RA Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;
RT "Complete amino acid sequence of the delta heavy chain of human
immunoglobulin D.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
CC -!- MISCELLANEOUS: This chain was isolated from an IgD myeloma
protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02099; D2HUWA.
DR HSSP; P01820; 1G7J.
DR GlycoSuiteDB; P01824; -.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 113
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Query Match 70.3%; Score 440; DB 1; Length 129;
Best Local Similarity 64.3%; Pred. No. 1.9e-36;
Matches 83; Conservative 15; Mismatches 19; Indels 12; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSGTYHMSWIRQHPGRGLEWIGYIYSGSTY 60
Db 1 RLQQLQESGPGLVKPSSETLSLTCTVSGGPIRRRTGYMGWIRQHPGRGLEWIGGYIYGSY 60

QY 61 HNPSLKSRITISVDTSKNQFSLKLSVTAADTAVYICARGG-----DGYYWG 108
Db 61 YNPSLKGRVITISVDTSKNQFSLNLRMSAADTAWYICARGNPPPYDYGTSDDGIDVMG 120

QY 109 QGTLVTVSS 117
Db 121 QGTTVHVS 129

RESULT 14
Q6NYH3 PRELIMINARY; PRT; 478 AA.
ID Q6NYH3
AC Q6NYH3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RC Strausberg R.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC066594; AAHG6594.1; -.
DR HSP; P01820; IATN.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 478 AA; 51856 MW; 5F8B98F60F077256 CRC64;

Query Match 69.6%; Score 436; DB 2; Length 478;
Best Local Similarity 70.2%; Pred. No. 1.9e-35;
Matches 85; Conservative 19; Mismatches 11; Indels 6; Gaps 3;

Qy 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGYTHSWIRQHPGRGLEWIGYIYSGSTY 60
Db 20 QVLDQESGPGLVKPSETLSLTCTVSGGSISSGYTHSWIRQHPGRGLEWIGYIYSGSTL 77
Qy 61 HNPSLKSRITISVDTSKNQPSLKLSSVTAADTAIVYICARG-GDGYRY---WGQTLVTVS 116
Db 78 YNPSSLSRVTVMSVDTSKNQPSLKLSSVTAADTAIVYICARGYDGKGRYFDLWGRGVPVTVS 137
Qy 117 S 117
Db 138 S 138

RESULT 15
Q8WUX4 PRELIMINARY; PRT; 595 AA.
AC Q8WUX4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RC Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RC Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019235; AAH19235.2; -.
DR HSP; P01861; IADQ.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 595 AA; 65290 MW; 0D4B50776545714E CRC64;

Query Match 68.8%; Score 431; DB 2; Length 595;
Best Local Similarity 71.9%; Pred. No. 7.9e-35;
Matches 92; Conservative 7; Mismatches 15; Indels 14; Gaps 4;

Qy 1 QVLEQSGPGLVKPSETLSLTCTVSGGSISSGYTHSWIRQHPGRGLEWIGYIYSGSTY 60
Db 27 QVLDQWAGGLKPSSETLSLTCTVSGGSISSGYTHSWIRQHPGRGLEWIGYIYSGSTN 84
Qy 61 HNPSLKSRITISVDTSKNQPSLKLSSVTAADTAIVYICAR-----GDGYRY---WGQ 109
Db 85 YNPSSLSRVTVMSVDTSKNQPSLKLSSVTAADTAIVYICARVITRASPPTDG-RYGMQVWQ 143
Qy 110 GTTLVTSS 117
Db 144 GTTLVTSS 151

Search completed: November 9, 2005, 13:05:51
Job time : 60.406 secs

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(0150) XRAY (1000) 1000

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:43:32 ; Search time 74.6015 Seconds  
(without alignments)  
627.306 Million cell updates/sec

Title: US-10-660-357A-37

Perfect score: 651

Sequence: 1 QVQLQESGPGLVKPSSETLSL.....WLVPDAFDWQGTMTSVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_16Dec04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	651	100.0	121	7 ADC99808	Adc99808 Anti-huma
2	651	100.0	121	7 ADD05412	Add05412 Anti-MUC1
3	651	100.0	121	7 Adf09850	Adf09850 Human ant
4	598	91.9	121	7 ADC99780	Adc99780 Anti-huma
5	598	91.9	121	7 ADD05384	Add05384 Anti-MUC1
6	598	91.9	121	7 Adf09822	Adf09822 Human ant
7	597	91.7	121	7 ADC99772	Adc99772 Anti-huma
8	597	91.7	121	7 ADC99788	Adc99788 Anti-huma
9	597	91.7	121	7 ADD05376	Add05376 Anti-MUC1
10	597	91.7	121	7 ADD05392	Add05392 Anti-MUC1
11	597	91.7	121	7 Adf09814	Adf09814 Human ant
12	597	91.7	121	7 Adf09830	Adf09830 Human ant
13	562.5	86.4	243	8 ADO58076	Ado58076 S9 cell d
14	554	85.1	125	5 Adp03871	Adp03871 Murine-ex
15	547	84.0	121	5 ABg92884	Abg92884 Human imm
16	546	83.9	123	6 ADA89258	Ada89258 Human ant
17	544.5	83.6	121	5 ABB07171	Abb07171 ebvHgm M
18	544.5	83.6	121	8 ADI26658	Adi26658 Human ant
19	543	83.4	125	7 Adp03868	Adp03868 Murine-ex
20	543	83.4	125	7 Adp03876	Adp03876 Murine-ex
21	541.5	83.2	122	7 Adp03885	Adp03885 Murine-ex
22	541.5	83.2	122	7 Adp03889	Adp03889 Murine-ex
23	539	82.8	125	7 Adp03983	Adp03983 Murine-ex
24	539	82.8	446	8 ADK52356	Adk52356 Human ant
25	538.5	82.7	120	2 AAW90287	Aaw90287 Human ant

## ALIGNMENTS

### RESULT 1

ADC99808

ID ADC99808 standard; protein; 121 AA.

XX AC ADC99808;

XX AC (first entry)

DT 01-JAN-2004

DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 37.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
KW cytotostatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
KW lung cancer; human.

XX Homo sapiens.

XX WC2003057838-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

XX Gudas J;

XX WPI; 2003-587113/55.

XX N-PSDB; ADC99810.

XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
PT or condition associated with expression of MUC18 in a patient, e.g.  
PT tumors, cancers, and other malignancies.

PS Claim 1; SEQ ID NO 37; 78pp; English.

XX The invention relates to a novel isolated monoclonal antibody comprising  
CC a heavy or light chain amino acid or a heavy or light chain variable  
CC domain where the antibody binds to MUC18. The monoclonal antibody of the  
CC invention demonstrates cytostatic activity and may be useful for treating  
CC a disease or condition associated with the expression of MUC18 on the  
CC cell surface such as tumours, specifically melanoma, oesophageal,  
CC pancreatic or colorectal tumours, carcinomas, particularly cervical  
CC carcinomas and cervical intraepithelial neoplasia and cancers including  
CC colorectal, breast or lung cancer, as well as other malignancies. The  
CC current sequence is that of the anti-human MUC18 monoclonal antibody

CC heavy chain protein of the invention.

XX SQ Sequence 121 AA;  
 Query Match 100.0%; Score 651; DB 7; Length 121;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-47;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISTYYWSWIROPKGLWIGIYYTGTNTYN 60  
 Db 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISTYYWSWIROPKGLWIGIYYTGTNTYN 60  
 QY 61 PSLSKRVTVSDTSKNQFSLKLSNVTAAADTAVYYCARDPGQWLVPDAFDIWGGQTMVSYS 120  
 Db 61 PSLSKRVTVSDTSKNQFSLKLSNVTAAADTAVYYCARDPGQWLVPDAFDIWGGQTMVSYS 120  
 QY 121 S 121  
 Db 121 S 121

RESULT 2  
 ADD05412  
 ID ADD05412 standard; protein; 121 AA.  
 XX  
 AC ADD05412;  
 XX  
 DT 01-JAN-2004 (first entry)  
 XX  
 DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 37.  
 XX  
 KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
 KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.  
 XX  
 OS Homo sapiens.

XX WO2003057006-A2.  
 XX 17-JUL-2003.  
 XX 26-DEC-2002; 2002WO-US041582.  
 XX 28-DEC-2001; 2001US-0346460P.  
 XX (ABGE-) ABGENIX INC.  
 XX Gudas J, Bar-Eli M;  
 XX WPI; 2003-577496/54.  
 XX N-PSDB; ADD05414.  
 XX  
 PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
 PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
 PT associated with melanoma, or increasing survival of an animal having a  
 PT metastatic tumor.  
 XX  
 PS Claim 1; SEQ ID NO 37; 87pp; English.

XX The invention relates to a novel monoclonal antibody used for inhibiting  
 CC tumour growth in an animal. The tumour inhibition process comprises  
 CC selecting an animal in need of treatment for a tumour, providing a  
 CC monoclonal antibody comprising a heavy chain amino acid, where the  
 CC antibody consists of any one of 10 fully defined sequences of 117-123  
 CC amino acids given in the specification, and where the monoclonal antibody  
 CC binds MUC18, and contacting the tumour with the antibody resulting in  
 CC inhibited proliferation of the cells. The monoclonal antibody has  
 CC cytostatic and can be used in the production of a vaccine. The monoclonal  
 CC antibodies against the MUC18 antigen are useful for diagnosing and  
 CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or  
 CC tumour metastasis), inhibiting cell invasion associated with melanoma, or  
 CC increasing survival of an animal having a metastatic tumour. This  
 CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
 CC protein of the invention.

XX SQ Sequence 121 AA;  
 Query Match 100.0%; Score 651; DB 7; Length 121;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-47;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISTYYWSWIROPKGLWIGIYYTGTNTYN 60  
 Db 1 QVQLQSGPGLVKPSETLSLTCTVSGGSISTYYWSWIROPKGLWIGIYYTGTNTYN 60  
 QY 61 PSLSKRVTVSDTSKNQFSLKLSNVTAAADTAVYYCARDPGQWLVPDAFDIWGGQTMVSYS 120  
 Db 61 PSLSKRVTVSDTSKNQFSLKLSNVTAAADTAVYYCARDPGQWLVPDAFDIWGGQTMVSYS 120  
 QY 121 S 121  
 Db 121 S 121

RESULT 3  
 ADF09850  
 ID ADF09850 standard; protein; 121 AA.  
 XX  
 AC ADF09850;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human anti-MUC18 monoclonal antibody heavy chain #10.  
 XX  
 KW cell proliferation inhibition; MUC18 tumour antigen;  
 KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
 KW carcinoma; cancer; malignancy; heavy chain; human.  
 XX  
 OS Homo sapiens.

XX WO2003057837-A2.  
 XX 17-JUL-2003.  
 XX 26-DEC-2002; 2002WO-US041580.  
 XX 28-DEC-2001; 2001US-0346414P.  
 XX (ABGE-) ABGENIX INC.  
 XX Gudas J;  
 XX WPI; 2003-598367/56.  
 XX N-PSDB; ADF09852.  
 XX  
 PT Inhibiting cell proliferation associated with expression of MUC18 tumour  
 PT antigen, involves incubating and inhibiting cell by administering anti-  
 PT MUC18 monoclonal antibody.  
 XX  
 PS Claim 1; SEQ ID NO 37; 83pp; English.

XX The invention comprises a method for inhibiting cell proliferation  
 CC associated with expression of MUC18 tumour antigen. The method involves  
 CC administering anti-MUC18 monoclonal antibody. The method of the invention  
 CC is useful for inhibiting cell (e.g. melanoma or tumour cell)  
 CC proliferation associated with the expression of MUC18 tumour antigen, the  
 CC method is preferably useful for inhibiting tumour metastasis. The method  
 CC is useful for inhibiting cell proliferation in patients with tumours,  
 CC carcinomas, cancer and other malignancies. The present amino acid  
 CC sequence represents a heavy chain from an MUC18 tumour antigen-specific  
 CC monoclonal antibody.

XX SQ Sequence 121 AA;  
 Query Match 100.0%; Score 651; DB 7; Length 121;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-47;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy	1	QVQLQESGRLVKKPSETISLTCTVSGGSI	STVYHSWIRPPGKGLEWIGVYYTGTNTYN	60
Db	1	QVQLQESGRLVKKPSETISLTCTVSGGSI	STVYHSWIRPPGKGLEWIGVYYTGTNTYN	60
Qy	61	PSLKSRTVTVSDTSKNQFSLKLN	SVTAADTAVYTCARDPGQWLVPDAFDIWGQGTVMVSVS	120
Db	61	PSLKSRTVTVSDTSKNQFSLKLN	SVTAADTAVYTCARDPGQWLVPDAFDIWGQGTVMVSVS	120
Qy	121	S	121	
Db	121	S	121	

Qy	61	PSLSRVTVSDTSKNQFSLKINSVTAADTAVYYCARDPFGQWLVPDAFDIWGGGTWVS	120
Dδ	61	PSLSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGQWLDPDAFDIWGGGTWVS	120
Qy	121	S 121	
Dδ	121	S 121	

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XX
SQ      Sequence 121 AA;
          91.9%; Score 598; DB 7; Length 121;
Query Match
Best Local Similarity 90.9%; Pred. No. 7.9e-43;
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY      1 QVQLQSGGPGLVKPSSETLSLTCTVSGGISISTYVMSWIRPPGKLEWIGIYYVTGNTYIN 60
Db       1 QVQLQSGGPGLVKPSSETLSLTCTVSGGISISYVMSWIRPPGKLEWIGIYYVTGNTYIN 60

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QY 61 PSLKSRVTISVDTSKNQFSLKLSNVTAADTAVYYCARDPQGLVLPDAFDIWGGQTMVSVS 120
DB 61 PSLKSRVTISVDTSKNQFSLKLSNVTAADTAVYYCARDPQGLVLPDAFDIWGGQTMVSVS 120
QY 121 S 121
DB 121 S 121

RESULT 6
ADF09822
ID ADF09822 standard; protein; 121 AA.
XX
AC ADF09822;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human anti-MUC18 monoclonal antibody heavy chain #3.
XX
KW cell proliferation inhibition; MUC18 tumour antigen;
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
KW carcinoma; cancer; malignancy; heavy chain; human.
XX
OS Homo sapiens.
XX
PN WO2003057837-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041580.
XX
PR 28-DEC-2001; 2001US-0346414P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
DR WPI; 2003-598367/56.
DR N-PSDB; ADF09824.
XX
PT Inhibiting cell proliferation associated with expression of MUC18 tumor
PT antigen, involves incubating and inhibiting cell by administering anti-
PT MUC18 monoclonal antibody.
XX
PS Claim 1; SEQ ID NO 9; 83pp; English.
XX
CC The invention comprises a method for inhibiting cell proliferation
CC associated with expression of MUC18 tumour antigen. The method involves
CC administering anti-MUC18 monoclonal antibody. The method of the invention
CC is useful for inhibiting cell (e.g. melanoma or tumour cell)
CC proliferation associated with the expression of MUC18 tumour antigen, the
CC method is preferably useful for inhibiting tumour metastasis. The method
CC is useful for inhibiting cell proliferation in patients with tumours,
CC carcinomas, cancer and other malignancies. The present amino acid
CC sequence represents a heavy chain from an MUC18 tumour antigen-specific
CC monoclonal antibody.
XX
SQ Sequence 121 AA;
Query Match 91.9%; Score 598; DB 7; Length 121;
Best Local Similarity 90.9%; Pred. No. 7.9e-43;
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIITYYWSWIRQPPGKLEWIGYIYYTGTNYN 60
DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIITYYWSWIRQPPGKLEWIGYIYYTGTNYN 60
QY 61 PSLKSRVTISVDTSKNQFSLKLSNVTAADTAVYYCARDPQGLVLPDAFDIWGGQTMVSVS 120
DB 61 PSLKSRVTISVDTSKNQFSLKLSNVTAADTAVYYCARDPQGLVLPDAFDIWGGQTMVSVS 120
QY 121 S 121
DB 121 S 121

RESULT 7
ADC99772
ID ADC99772 standard; protein; 121 AA.
XX
AC ADC99772;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 1.
XX
KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
KW lung cancer; human.
XX
OS Homo sapiens.
XX
PN WO2003057838-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041581.
XX
PR 28-DEC-2001; 2001US-0346299P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
DR WPI; 2003-587113/55.
DR N-PSDB; ADC99774.
XX
PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease
PT or condition associated with expression of MUC18 in a patient, e.g.
PT tumors, cancers, and other malignancies.
XX
PS Claim 1; SEQ ID NO 1; 78pp; English.
XX
CC The invention relates to a novel isolated monoclonal antibody comprising
CC a heavy or light chain amino acid or a heavy or light chain variable
CC domain where the antibody binds to MUC18. The monoclonal antibody of the
CC invention demonstrates cytostatic activity and may be useful for treating
CC a disease or condition associated with the expression of MUC18 on the
CC cell surface such as tumours, specifically melanoma, oesophageal,
CC pancreatic or colorectal tumours, carcinomas, particularly cervical
CC carcinomas and cervical intraepithelial neoplasia and cancers including
CC colorectal, breast or lung cancer, as well as other malignancies. The
CC current sequence is that of the anti-human MUC18 monoclonal antibody
CC heavy chain protein of the invention.
XX
SQ Sequence 121 AA;
Query Match 91.7%; Score 597; DB 7; Length 121;
Best Local Similarity 90.9%; Pred. No. 9.6e-43;
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIITYYWSWIRQPPGKLEWIGYIYYTGTNYN 60
DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIITYYWSWIRQPPGKLEWIGYIYYTGTNYN 60
QY 61 PSLKSRVTISVDTSKNQFSLKLSNVTAADTAVYYCARDPQGLVLPDAFDIWGGQTMVSVS 120
DB 61 PSLKSRVTISVDTSKNQFSLKLSNVTAADTAVYYCARDPQGLVLPDAFDIWGGQTMVSVS 120
QY 121 S 121
DB 121 S 121

RESULT 8

```

ADC99788  
 ID ADC99788 standard; protein; 121 AA.  
 XX AC  
 XX AC ADC99788;  
 XX DT  
 XX DT 01-JAN-2004 (first entry)  
 XX DE  
 XX DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 17.  
 XX KW  
 XX KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
 XX KW cytosolic; melanoma; oesophageal; pancreatic; colorectal tumour;  
 XX KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
 XX KW lung cancer; human.  
 XX OS  
 XX OS Homo sapiens.  
 XX PN  
 XX PN WO2003057838-A2.  
 XX PD  
 XX PD 17-JUL-2003.  
 XX PF  
 XX PF 26-DEC-2002; 2002WO-US041581.  
 XX PR  
 XX PR 28-DEC-2001; 2001US-0346299P.  
 XX PA  
 XX PA (ABGE-) ABGENIX INC.  
 XX PI  
 XX PI Gudas J;  
 XX PI  
 XX PI WPI; 2003-587113/55.  
 XX DR  
 XX DR N-PSDB; ADC99790.  
 XX PS  
 XX PS New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
 XX PT or condition associated with expression of MUC18 in a patient, e.g.  
 XX PT tumors, cancers, and other malignancies.  
 XX PS  
 XX PS Claim 1; SEQ ID NO 17; 78pp; English.  
 XX CC  
 XX CC The invention relates to a novel isolated monoclonal antibody comprising  
 XX CC a heavy or light chain amino acid or a heavy or light chain variable  
 XX CC domain where the antibody binds to MUC18. The monoclonal antibody of the  
 XX CC invention demonstrates cytostatic activity and may be useful for treating  
 XX CC a disease or condition associated with the expression of MUC18 on the  
 XX CC cell surface such as tumours, specifically melanoma, oesophageal,  
 XX CC pancreatic or colorectal tumours, carcinomas, particularly cervical  
 XX CC carcinomas and cervical intraepithelial neoplasia and cancers including  
 XX CC colorectal, breast or lung cancer, as well as other malignancies. The  
 XX CC current sequence is that of the anti-human MUC18 monoclonal antibody  
 XX CC heavy chain protein of the invention.  
 XX SQ

Query Match 91.78; Score 597; DB 7; Length 121;  
 Best Local Similarity 90.9%; Pred. No. 9.6e-43;  
 Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 QVQLQESGPGLVKPESETLSLTCTVSGSGISITYYWSWIRQPPGKGLEWIGYIYYTNTYYN 60  
 Db 1 QVQLQESGPGLVKPESETLSLTCTVSGSGISITYYWSWIRQPPGKGLEWIGYIYYTNTYYN 60  
 Qy 61 PSLSKRVTVSDTSKNQFSLKLNSTAAADTAVYYCARDPQGWLPDADFIDWGQGTWVSVS 120  
 Db 61 PSLSKRVTVSDTSKNQFSLKLNSTAAADTAVYYCARDPQGWLPDADFIDWGQGTWVSVS 120  
 Qy 121 S 121  
 Db 121 S 121

RESULT 9  
 ADD05376  
 ID ADD05376 standard; protein; 121 AA.  
 XX AC  
 XX AC ADD05376;

XX DT  
 XX DT 01-JAN-2004 (first entry)  
 XX DE  
 XX DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID NO 1.  
 XX KW  
 XX KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
 XX KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.  
 XX OS  
 XX OS Homo sapiens.  
 XX PN  
 XX PN WO2003057006-A2.  
 XX PD  
 XX PD 17-JUL-2003.  
 XX PF  
 XX PF 26-DEC-2002; 2002WO-US041582.  
 XX PR  
 XX PR 28-DEC-2001; 2001US-0346460P.  
 XX PA  
 XX PA (ABGE-) ABGENIX INC.  
 XX PI  
 XX PI Gudas J, Bar-Eli M;  
 XX PI  
 XX PI WPI; 2003-577496/54.  
 XX DR  
 XX DR N-PSDB; ADD05378.  
 XX PS  
 XX PS Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
 XX PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
 XX PT associated with melanoma, or increasing survival of an animal having a  
 XX PT metastatic tumor.  
 XX SQ  
 XX SQ Claim 1; SEQ ID NO 1; 87pp; English.  
 XX CC  
 XX CC The invention relates to a novel monoclonal antibody used for inhibiting  
 XX CC tumour growth in an animal. The tumour inhibition process comprises  
 XX CC selecting an animal in need of treatment for a tumour, providing a  
 XX CC monoclonal antibody comprising a heavy chain amino acid, where the  
 XX CC antibody consists of any one of 10 fully defined sequences of 117-123  
 XX CC amino acids given in the specification, and where the monoclonal antibody  
 XX CC binds MUC18, and contacting the tumour with the antibody resulting in  
 XX CC inhibited proliferation of the cells. The monoclonal antibody has  
 XX CC cytostatic and can be used in the production of a vaccine. The monoclonal  
 XX CC antibodies against the MUC18 antigen are useful for diagnosing and  
 XX CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or  
 XX CC tumour metastasis), inhibiting cell invasion associated with melanoma, or  
 XX CC increasing survival of an animal having a metastatic tumour. This  
 XX CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
 XX CC protein of the invention.  
 XX SQ

Query Match 91.7%; Score 597; DB 7; Length 121;  
 Best Local Similarity 90.9%; Pred. No. 9.6e-43;  
 Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 QVQLQESGPGLVKPESETLSLTCTVSGSGISITYYWSWIRQPPGKGLEWIGYIYYTNTYYN 60  
 Db 1 QVQLQESGPGLVKPESETLSLTCTVSGSGISITYYWSWIRQPPGKGLEWIGYIYYTNTYYN 60  
 Qy 61 PSLSKRVTVSDTSKNQFSLKLNSTAAADTAVYYCARDPQGWLPDADFIDWGQGTWVSVS 120  
 Db 61 PSLSKRVTVSDTSKNQFSLKLNSTAAADTAVYYCARDPQGWLPDADFIDWGQGTWVSVS 120  
 Qy 121 S 121  
 Db 121 S 121

RESULT 10  
 ADD05392  
 ID ADD05392 standard; protein; 121 AA.  
 XX AC  
 XX AC ADD05392;



XX OS Homo sapiens.  
 XX PN WO2003057837-A2.  
 XX PD 17-JUL-2003.  
 XX PF 26-DEC-2002; 2002WO-US041580.  
 XX PR 28-DEC-2001; 2001US-0346414P.  
 XX PA (ABGE-) ABGENIX INC.  
 XX PI Gudas J;  
 XX WPI; 2003-598367/56.  
 XX DR N-PSDB; ADF09832.  
 XX PT Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.  
 XX PS Claim 1; SEQ ID NO 17; 83pp; English.  
 XX CC The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a heavy chain from an MUC18 tumour antigen-specific monoclonal antibody.  
 XX SQ Sequence 121 AA;  
 Query Match 91.7%; Score 597; DB 7; Length 121;  
 Best Local Similarity 90.9%; Pred. No. 9.6e-43;  
 Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYTYMSWIRQPPGKLEWIGIYYTGTNYN 60  
 Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYTYMSWIRQPPGKLEWIGIYYTGTNYN 60  
 Qy 61 PSLKSRVTISVDTSKNQFSLKNSVTAADTAVYYCARDPGQWLVPDADFDTWGQGTMTVS 120  
 Db 61 PSLKSRVTISVDTSKNQFSLKNSVTAADTAVYYCARDPGQWLVPDADFDTWGQGTMTVS 120  
 Qy 121 S 121  
 Db 121 S 121  
 RESULT 13  
 ADO58076  
 ID ADO58076 standard; protein; 243 AA.  
 AC ADO58076;  
 XX 12-AUG-2004 (first entry)  
 DE S9 cell derived human scFvVL-VH protein.  
 KW B cell; surface immunoglobulin; Ig; binding site; antigen; human CD28;  
 KW closed system; detection laser-beam; catcher tube;  
 KW electrochemical device; fluorescence activated cell sorter; FACS;  
 KW antibody variable region; human.  
 XX Homo sapiens.  
 OS WO2004044584-A1.  
 PN

PD 27-MAY-2004.  
 XX 12-NOV-2003; 2003WO-EP012664.  
 XX PR 13-NOV-2002; 2002EP-00025335.  
 XX PA (MICR-) MICROMET AG.  
 XX PI Baeuerle P, Hoffmann P, Weinberger S, Kischel R;  
 XX WPI; 2004-449579/42.  
 XX DR N-PSDB; ADO58077.  
 XX PT Identifying a B cell carrying a surface immunoglobulin molecule having a binding site for an antigen of interest, useful for constructing therapeutic antibodies, comprises contacting a sample with the antigen and a receptor.  
 XX PS Claim 22; SEQ ID NO 76; 156pp; English.  
 XX CC The invention relates to a novel method for identifying a B cell carrying a surface immunoglobulin (Ig) molecule having a binding site for an antigen of interest. The method comprises contacting a sample putatively containing the B cell with the antigen of interest and with a receptor specifically binding to the Ig molecule, and assessing the presence of the detectable signal. The invention further comprises: an antibody generated by the method above which is specific for human CD28 or comprising an amino acid(s) sequence(s) given in the specification, and/or are encoded by a nucleic acid sequence(s) also given in the specification; and a device for assessing the presence of a detectable signal defined above, where the device comprises a closed system for the detection laser-beam and a catcher tube, and where the B cell of interest can be collected as a single cell by means of an electrochemical device, which is triggered by an electric signal generated by the fluorescence activated cell sorter (FACS) device, where the electrochemical device moves the nozzle of the steady catcher tube liquid stream for a programmed time over a collecting tube, microtiter plate or other container after a B cell is sorted. The method is useful for identifying a B cell carrying a surface Ig molecule having a binding site for an antigen of interest. The method is also useful for cloning of antibody variable regions from the identified B cells, which may subsequently be employed in the construction of proteins such as antibodies or its fragments or derivatives useful in therapeutic approaches. The method is useful as an alternative to phage display for the gain of antibodies or its fragments. This sequence represents an S2 cell derived human polypeptide of the invention.  
 XX SQ Sequence 243 AA;  
 Query Match 86.4%; Score 562.5; DB 8; Length 243;  
 Best Local Similarity 88.4%; Pred. No. 1.6e-39;  
 Matches 107; Conservative 8; Mismatches 5; Indels 1; Gaps 1;  
 Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYTYMSWIRQPPGKLEWIGIYYTGTNYN 60  
 Db 124 QVQLQESGPGLVKPSSETLSLTCTVSGSISYTYMSWIRQPPGKLEWIGIYYTGTNYN 183  
 Qy 61 PSLKSRVTISVDTSKNQFSLKNSVTAADTAVYYCARDPGQWLVPDADFDTWGQGTMTVS 120  
 Db 184 PSLKSRVTISVDTSKNQFSLKNSVTAADTAVYYCARDPGQWLVPDADFDTWGQGTMTVS 242  
 Qy 121 S 121  
 Db 243 S 243  
 RESULT 14  
 ADP03871  
 ID ADP03871 standard; protein; 125 AA.  
 AC ADP03871;  
 XX 29-JUL-2004 (first entry)  
 DT

XX DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 11.  
 XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KW cytosolic; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;  
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; heavy chain variable domain.  
 XX OS Unidentified.  
 XX WO2003048328-A2.  
 XX PD 12-JUN-2003.  
 XX PF 02-DEC-2002; 2002WO-US038550.  
 XX PR 03-DEC-2001; 2001US-0337275P.  
 XX PA (ABGE-) ABGENIX INC.  
 XX PI Gudas J, Foltz I, Handa M, Gallo M;  
 XX WIPI; 2003-523295/49.  
 XX PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
 XX PS Claim 1; SEQ ID NO 11; 89pp; English.  
 XX CC The invention relates to a novel isolated monoclonal antibody (mAb)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
 CC demonstrates cytostatic activity and may be useful for treating a tumour,  
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumour or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
 CC (heavy chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.  
 XX SQ Sequence 125 AA;  
 Query Match 85.1%; Score 554; DB 7; Length 125;  
 Best Local Similarity 85.6%; Pred. No. 4.1e-39;  
 Matches 107; Conservative 8; Mismatches 6; Indels 4; Gaps 2;  
 QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSIST--YYNSWIRQPPKGLWIGYIYTGNTY 58  
 DB 1 QVQLQESGPGLVKPSQTLSTLTCTVSGSISGGYYSWIRQHPGKGLWIGYIYSGNTY 60  
 QY 59 YNPSLKRVTYVDTSKNQSLKNSVTAADTAVYYCARDPGQWL--PDAFDWGQGTM 116  
 DB 61 YNPSLKRITISVDTSKNQSLKNSVTAADTAVYYCARTYFDLTGYPDAFDWGQGTM 120  
 QY 117 VSVSS 121  
 DB 121 VTVSS 125  
 RESULT 15  
 ABG92884  
 ID ABG92884 standard; protein; 121 AA.  
 AC ABG92884;  
 XX 19-NOV-2002 (first entry)  
 XX Human immunoglobulin variable light domain #1.

XX KW Immunoglobulin; variable heavy chain; variable light chain; human;  
 KW G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;  
 KW immunologic deficiency syndrome; blood protein disorder; nephritis;  
 KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;  
 KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;  
 KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;  
 KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;  
 KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;  
 KW Pneumocystis carni infection; cardiovascular disorder; atherosclerosis;  
 KW Lymphocytopenia.  
 XX OS Homo sapiens.  
 XX WO200264612-A2.  
 XX PD 22-AUG-2002.  
 XX PF 08-FEB-2002; 2002WO-US003634.  
 XX PR 09-FEB-2001; 2001US-00779880.  
 PR 09-FEB-2001; 2001WO-US004153.  
 PR 12-JUN-2001; 2001US-0297257P.  
 PR 08-AUG-2001; 2001US-0310458P.  
 PR 12-OCT-2001; 2001US-0328447P.  
 PR 21-DEC-2001; 2001US-0341725P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX PI Roschke V, Rosen CA, Ruben SM;  
 XX WIPI; 2002-643455/69.  
 XX N-PSDB; ABS68607.  
 XX PT New human G-protein Chemokine Receptor gene (HDGNR10) useful for  
 PT treating, preventing, ameliorating or monitoring diseases or disorders  
 PT associated with aberrant expression of HDGNR10 e.g. cancer.  
 XX Example 55; Fig 4; 562pp; English.  
 XX The invention describes an isolated polynucleotide encoding a first  
 CC antibody at least 95-100% identical to a second antibody consisting of an  
 CC amino acid sequence comprising at least one, two or three CDR regions of  
 CC a variable heavy (VH) or variable light (VL) domain of the antibody  
 CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,  
 CC XF3.6A2, XF3.10B8, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody  
 CC is useful treating, preventing, ameliorating, prognosing or monitoring  
 CC cancers or other diseases or disorders e.g. immunologic deficiency  
 CC syndromes such as blood protein disorders and ataxia telangiectasia,  
 CC inflammation associated disorders such as endotoxin lethality, nephritis  
 CC and inflammatory bowel disease, conditions associated with an increase in  
 CC certain haematopoietic cells such as histiocytosis, defective or aberrant  
 CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,  
 CC an infectious disease, an autoimmune disease such as Addison's disease,  
 CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative  
 CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or  
 CC poxvirus infection, a Pneumocystis carni infection, Kaposi's sarcoma,  
 CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a  
 CC disease or disorder associated with aberrant expression of novel human G-  
 CC protein chemokine receptor (CCR5) HDGNR10. This is the amino acid  
 CC sequence of human immunoglobulin sequence associated with the antibodies  
 CC against HDGNR10  
 XX SQ Sequence 121 AA;  
 Query Match 84.0%; Score 547; DB 5; Length 121;  
 Best Local Similarity 86.0%; Pred. No. 1.6e-38;  
 Matches 104; Conservative 8; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISTYYNSWIRQPPKGLWIGYIYTGNTY 60  
 DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISFFYNSWIRQPPKGLWIGRIYTGNTY 60

Search completed: November 9, 2005, 12:55:32  
Job time : 75.6015 secs

(CANC) 2000-0000-0000-0000



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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:29:55 ; Search time 18.802 Seconds  
(without alignments)  
480.403 Million cell updates/sec

Title: US-10-660-357A-37

Perfect score: 651

Sequence: 1 QVQLQESGPGLVKPSSETLSL.....WLVPDAFDWQGTMTSVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	538.5	82.7	120	4	US-09-424-840B-20
2	536	82.3	119	3	US-09-025-769B-39
3	536	82.3	119	3	US-09-025-769B-65
4	536	82.3	119	4	US-09-490-070A-39
5	536	82.3	119	4	US-09-490-070A-65
6	536	82.3	119	4	US-09-490-153-39
7	536	82.3	119	4	US-09-490-153-65
8	536	82.3	119	4	US-09-490-324-39
9	536	82.3	119	4	US-09-490-324-65
10	525.5	80.7	118	3	US-09-025-769B-25
11	525.5	80.7	118	4	US-09-490-070A-25
12	525.5	80.7	118	4	US-09-490-153-25
13	525.5	80.7	118	4	US-09-490-324-25
14	525.5	80.7	244	3	US-09-138-091A-77
15	525.5	80.7	244	4	US-09-138-091A-77
16	520.5	80.0	473	3	US-09-049-672A-4
17	513	78.8	117	4	US-09-720-493-2
18	511	78.5	142	2	US-08-480-774A-2
19	510.5	78.4	122	1	US-08-360-125-11
20	510.5	78.4	122	2	US-08-450-578-11
21	510.5	78.4	122	2	US-09-017-628-11
22	510.5	78.4	122	2	US-09-014-880-11
23	510.5	78.4	122	4	US-08-450-363-11
24	510.5	78.4	122	4	US-09-467-903-11
25	498.5	76.6	487	4	US-09-800-729-145
26	497.5	76.4	172	4	US-09-472-087-7
27	497.5	76.4	172	4	US-09-472-087-86

28 496.5 76.3 139 4 US-09-471-276-837 Sequence 837, Appl  
29 496 76.2 119 1 US-08-360-125-5 Sequence 5, Appli  
30 496 76.2 119 2 US-08-450-578-5 Sequence 5, Appli  
31 496 76.2 119 2 US-09-017-628-5 Sequence 5, Appli  
32 496 76.2 119 2 US-09-014-880-5 Sequence 5, Appli  
33 496 76.2 119 4 US-08-450-363-5 Sequence 5, Appli  
34 496 76.2 119 4 US-09-467-903-5 Sequence 5, Appli  
35 491 75.4 123 3 US-08-793-450-4 Sequence 4, Appli  
36 488 75.0 116 3 US-08-545-809A-140 Sequence 140, App  
37 488 75.0 472 3 US-08-793-450-8 Sequence 8, Appli  
38 482.5 74.1 98 1 US-08-478-039-75 Sequence 75, Appl  
39 482.5 74.1 98 1 US-08-476-349A-75 Sequence 75, Appl  
40 482.5 74.1 278 3 US-09-260-527-3 Sequence 3, Appli  
41 480 73.7 119 2 US-08-652-816A-10 Sequence 10, Appl  
42 480 73.7 155 4 US-09-471-276-888 Sequence 888, App  
43 478 73.4 117 4 US-09-232-290-47 Sequence 47, Appl  
44 477 73.3 118 3 US-08-545-809A-142 Sequence 142, App  
45 475.5 73.0 139 4 US-09-203-768A-2 Sequence 2, Appli

#### ALIGNMENTS

##### RESULT 1

US-09-424-840B-20  
; Sequence 20, Application US/09424840B  
; Patent No. 6790938  
; GENERAL INFORMATION:  
; APPLICANT: Berchtold, Peter  
; APPLICANT: Escher, Robert F. A.  
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES  
; FILE REFERENCE: 100564-09049  
; CURRENT APPLICATION NUMBER: US/09/424,840B  
; CURRENT FILING DATE: 1999-12-03  
; PRIOR APPLICATION NUMBER: DE 19820663.1  
; PRIOR FILING DATE: 1998-05-08  
; PRIOR APPLICATION NUMBER: DE 19755227.7  
; PRIOR FILING DATE: 1997-12-12  
; PRIOR APPLICATION NUMBER: DE 19723904.8  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 20  
; LENGTH: 120  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-424-840B-20

Query Match 82.7%; Score 538.5; DB 4; Length 120;  
Best Local Similarity 85.4%; Pred. No. 1.9e-46;  
Matches 105; Conservative 6; Mismatches 7; Indels 5; Gaps 3;  
Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISTYVWSMIRQPPGKLEWIGYIYTGNTYYN 60  
Db 1 QVQLKESGPGLVKPSSETLSLTCTVSGSFSTYVWSMIRQPPGKLEWIGYIYSGNTYYN 60  
Qy 61 PSLSKRVTVSVDFSKNQSFKLSNVTAAADTAVVYCA--RDPGQWLVPDAFDWQGTMTVS 118  
Db 61 PSLSKRATISVDTSKNQFSLKLSVTAADTAVVYCARLNDG-W--NDGFDWQGTMTV 117  
Qy 119 VSS 121  
Db 118 VSS 120

##### RESULT 2

US-09-025-769B-39  
; Sequence 39, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic

```
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA: US/09/025,769B
; FILING DATE: 18-AUG-1995
; APPLICATION NUMBER: EP 95 11 3021.0
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-39

Query Match 82.3%; Score 536; DB 3; Length 119;
Best Local Similarity 85.1%; Pred. No. 3.4e-46;
Matches 103; Conservative 7; Mismatches 9; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISTYVWSWIRQPPGKLEWIGIYYTNTYYN 60
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Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISYYVWSWIRQPPGKLEWIGIYYTNTYYN 60
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QY 61 PSLKSRVTISVDTSKNQPSLKNSVTAADTAVYYCARDPGQWLVPDADFINGOGTMTVS 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 PSLKSRVTISVDTSKNQPSLKNSVTAADTAVYYCARDPGQWLVPDADFINGOGTMTVS 118
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QY 121 $ 121
|
Db 119 $ 119

RESULT 4
US-09-490-070A-39
; Sequence 39, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
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; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA: US/09/025,769B
; FILING DATE: 18-AUG-1995
; APPLICATION NUMBER: EP 95 11 3021.0
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-39

Query Match 82.3%; Score 536; DB 3; Length 119;
Best Local Similarity 85.1%; Pred. No. 3.4e-46;
Matches 103; Conservative 7; Mismatches 9; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISTYVWSWIRQPPGKLEWIGIYYTNTYYN 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISYYVWSWIRQPPGKLEWIGIYYTNTYYN 60
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QY 61 PSLKSRVTISVDTSKNQPSLKNSVTAADTAVYYCARDPGQWLVPDADFINGOGTMTVS 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 PSLKSRVTISVDTSKNQPSLKNSVTAADTAVYYCARDPGQWLVPDADFINGOGTMTVS 118
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QY 121 $ 121
|
Db 119 $ 119

RESULT 3
US-09-025-769B-65
; Sequence 65, Application US/09025769B
; Patent No. 630064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
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APPLICATION NUMBER: US/09/490,070A  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Colin G. Sandercock, Esq.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37629-0005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 912-2000  
TELEFAX: (202) 912-2020  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-490-070A-39

Query Match 82.3%; Score 536; DB 4; Length 119;  
Best Local Similarity 85.1%; Pred. No. 3.4e-46;  
Matches 103; Conservative 7; Mismatches 9; Indels 2; Gaps 1;  
Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIISYYSWIRQPPKGLGWIGYIYTGNTYIN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIISYYSWIRQPPKGLGWIGYIYSGNTYN 60  
Qy 61 PSLKSRVTISVDTSKNPSLKLNSVTAADTAIVYICARDPGQWLVPDAPDINGQGTMSVS 120  
Db 61 PSLKSRVTISVDTSKNPSLKLNSVTAADTAIVYICARDPGQWLVPDAPDINGQGTMTVS 118  
Qy 121 \$ 121  
Db 119 \$ 119

RESULT 5  
US-09-490-070A-65  
Sequence 65, Application US/09490070A  
Patent No. 6696248  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
White & McAuliffe  
STREET: 1666 K Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,070A  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37629-0005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 912-2000  
TELEFAX: (202) 912-2020  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 65:  
US-09-490-070A-65  
Query Match 82.3%; Score 536; DB 4; Length 119;  
Best Local Similarity 85.1%; Pred. No. 3.4e-46;  
Matches 103; Conservative 7; Mismatches 9; Indels 2; Gaps 1;  
Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIISYYSWIRQPPKGLGWIGYIYTGNTYIN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIISYYSWIRQPPKGLGWIGYIYSGNTYN 60  
Qy 61 PSLKSRVTISVDTSKNPSLKLNSVTAADTAIVYICARDPGQWLVPDAPDINGQGTMSVS 120  
Db 61 PSLKSRVTISVDTSKNPSLKLNSVTAADTAIVYICARDPGQWLVPDAPDINGQGTMTVS 118  
Qy 121 \$ 121  
Db 119 \$ 119  
RESULT 6  
US-09-490-153-39  
Sequence 39, Application US/09490153  
Patent No. 6706484  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,153  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID
US-09-490-153-39

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	Query Match	82.3%; Score 536; DB 4; Length 119;
	Best Local Similarity	85.1%; Pred. No. 3.4e-46;
	Matches 103; Conservative	7; Mismatches 9; Indels 2; Gaps 1;
Qy	1 QVQLQSGLGVPKPSSETLSLTCTVS	GSGISITYYWSWIRPPKGLEWIGIYYTGTNYYN 60
Dd	1 QVQLQSGLGVPKPSSETLSLTCTVS	GSGISITYYWSWIRPPKGLEWIGIYYSGSYN 60
Qy	61 PSLSKRVTYSVDTSKNQFSLKLNSVTAA	TAVYYCARDPGQWLVPDAFDIWGGQTMTSVS 120
Dd	61 PSLSKRVTISVDTSKNQFSLKLNSVTAA	TAVYYCARWGDDGFY--AMDYWGGQTIVTVS 118
Qy	121 S	121
Dd	119 S	119

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Dd		119 S	119			

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Query Match 82.3%; Score 536; DB 4; Length 119;  
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Db 61 PSLKSRVTISVDTSKNQFSLKLSVTAADTAATVYVCARDPQGWLPDAPFDIWDGQGTWVS 118

Qy 121 S 121  
Db 119 S 119

## RESULT 9

US-09-490-324-65

; Sequence 65, Application US/09490324

; Patent No. 6828422

; GENERAL INFORMATION:

; APPLICANT: Knappik, Achim

; Pack, Peter

; Ilag, Vic

; Ge, Liming

; Moroney, Simon

; Plueckthun, Andreas

; TITLE OF INVENTION: Protein/(Poly)peptide libraries

; NUMBER OF SEQUENCES: 373

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish &amp; Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10021

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/490,324

; FILING DATE: 24-Jan-2000

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/025,769

; FILING DATE: 18-FEB-1998

; APPLICATION NUMBER: EP 95 11 3021.0

; FILING DATE: 18-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: James F. Haley, Jr., Esq.

; REGISTRATION NUMBER: 27,794

; REFERENCE/DOCKET NUMBER: MORPHO/5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)596-9000

; TELEFAX: (212)596-9090

; INFORMATION FOR SEQ ID NO: 65:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 119 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 65:

US-09-490-324-65

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STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,324  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 25:  
US-09-490-324-25

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QY 121 S 121  
DB 118 S 118

RESULT 14  
US-08-918-148-79  
Sequence 79, Application US/08918148A  
Patent No. 6342220  
GENERAL INFORMATION:  
APPLICANT: Adams, Camellia  
APPLICANT: W.  
APPLICANT: Carter, Paul J.  
APPLICANT: Fendly, Brian M.  
APPLICANT: Gurney, Austin L.  
TITLE OF INVENTION: Agonist Antibodies  
FILE REFERENCE: P0979  
CURRENT APPLICATION NUMBER: US/08/918,148A  
CURRENT FILING DATE: 1997-08-25  
NUMBER OF SEQ ID NOS: 79  
SEQ ID NO 79  
LENGTH: 244  
TYPE: PRT  
ORGANISM: artificial  
US-08-918-148-79

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Best Local Similarity 82.6%; Pred. No. 9.2e-45;

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QY 121 S 121  
DB 116 S 116

RESULT 15  
US-09-138-091A-77  
Sequence 77, Application US/09138091A  
Patent No. 6737249  
GENERAL INFORMATION:  
APPLICANT: Adams, Camellia W.  
APPLICANT: Carter, Paul J.  
APPLICANT: Fendly, Brian M.  
APPLICANT: Gurney, Austin L.  
TITLE OF INVENTION: Agonist Antibodies  
FILE REFERENCE: 9491-013-27  
CURRENT APPLICATION NUMBER: US/09/138,091A  
CURRENT FILING DATE: 1998-08-21  
PRIOR APPLICATION NUMBER: US 60/056,736  
PRIOR FILING DATE: 1997-08-22  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 77  
LENGTH: 244  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: single chain antibody (scFv) fragments  
US-09-138-091A-77

Query Match 80.7%; Score 525.5; DB 4; Length 244;  
Best Local Similarity 82.6%; Pred. No. 9.2e-45;  
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QY 121 S 121  
DB 116 S 116

Search completed: November 9, 2005, 11:46:42  
Job time: 19.802 secs

(2010) 2010 2010 2010



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:40:37 ; Search time 67.2222 Seconds  
(without alignments)  
753.137 Million cell updates/sec

Title: US-10-660-357A-37

Perfect score: 651

Sequence: 1 QVQLQESGPGLVKPSSTLSL.....WLVPDAFDIWGQGTWVSVS 121

Scoring table: BLOSUM62

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Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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  - 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*
  - 18: /cgn2\_6/ptodata/1/pubpaa/US10F\_PUBCOMB.pep.\*
  - 19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*
  - 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
  - 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
  - 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	651	100.0	121	14	US-10-330-613-37
2	651	100.0	121	14	US-10-330-530-37
3	651	100.0	121	16	US-10-660-357-37
4	598	91.9	121	14	US-10-330-613-9
5	598	91.9	121	14	US-10-330-530-9
6	598	91.9	121	16	US-10-660-357-9
7	597	91.7	121	14	US-10-330-613-1
8	597	91.7	121	14	US-10-330-613-17
9	597	91.7	121	14	US-10-330-530-1
10	597	91.7	121	14	US-10-330-530-17
11	597	91.7	121	16	US-10-660-357-1

12	597	91.7	121	16	US-10-660-357-17	Sequence 17, Appl
13	554	85.1	125	15	US-10-309-762-11	Sequence 11, Appl
14	552	84.8	142	17	US-10-893-576-37	Sequence 37, Appl
15	547.5	84.1	118	15	US-10-292-088-142	Sequence 142, App
16	547	84.0	121	14	US-10-067-800-60	Sequence 60, Appl
17	547	84.0	121	18	US-10-994-679-60	Sequence 60, Appl
18	546	83.9	123	15	US-10-371-942-102	Sequence 102, App
19	544.5	83.6	121	14	US-10-010-729-11	Sequence 11, Appl
20	544	83.6	121	17	US-10-893-576-191	Sequence 191, App
21	543.5	83.5	118	15	US-10-292-088-109	Sequence 109, App
22	543	83.4	125	15	US-10-309-762-8	Sequence 8, Appl1
23	543	83.4	125	15	US-10-309-762-16	Sequence 16, Appl
24	541.5	83.2	122	15	US-10-309-762-25	Sequence 25, Appl
25	541.5	83.2	122	15	US-10-309-762-29	Sequence 29, Appl
26	541	83.1	119	17	US-10-937-596-23	Sequence 23, Appl
27	539	82.8	125	15	US-10-309-762-153	Sequence 153, App
28	539	82.8	446	17	US-10-644-277-62	Sequence 62, Appl
29	538.5	82.7	120	16	US-10-844-424-20	Sequence 20, Appl
30	537.5	82.6	118	17	US-10-727-155-178	Sequence 178, App
31	537.5	82.6	122	15	US-10-309-762-24	Sequence 24, Appl
32	537.5	82.6	122	15	US-10-309-762-27	Sequence 27, Appl
33	537.5	82.6	122	15	US-10-309-762-71	Sequence 71, Appl
34	537.5	82.6	141	15	US-10-309-762-90	Sequence 90, Appl
35	537	82.5	148	17	US-10-893-576-31	Sequence 31, Appl
36	536.5	82.4	139	17	US-10-893-576-39	Sequence 39, Appl
37	536.5	82.4	143	16	US-10-693-629-44	Sequence 44, Appl
38	536.5	82.4	193	15	US-10-264-049-4331	Sequence 4331, Ap
39	536	82.3	119	14	US-10-125-687-5	Sequence 5, Appl1
40	536	82.3	119	18	US-10-596-191-5	Sequence 5, Appl1
41	534.5	82.1	120	15	US-10-309-762-4	Sequence 4, Appl1
42	534.5	82.1	120	15	US-10-309-762-102	Sequence 102, App
43	534.5	82.1	128	15	US-10-173-551-24	Sequence 24, Appl
44	533.5	82.0	122	15	US-10-309-762-73	Sequence 73, Appl
45	533.5	82.0	141	15	US-10-309-762-94	Sequence 94, Appl

ALIGNMENTS

RESULT 1  
US-10-330-613-37  
; Sequence 37, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330, 613  
; PRIOR FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 37  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-37

Query Match 100.0%; Score 651; DB 14; Length 121;  
Best Local Similarity 100.0%; Pred. No. 2.4e-51;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 QVQLQESGPGLVKPSSTLSLCTCTVSGSGISSTYTWISWIRQPPGKLEWIGYIYTGNTYIN 60  
Db 1 QVQLQESGPGLVKPSSTLSLCTCTVSGSGISSTYTWISWIRQPPGKLEWIGYIYTGNTYIN 60  
  
Qy 61 PSLSKRVTVSDVTSKNQFSLKLNSTVTAADTAVYVCARDPGQWLVPDAFDIWGQGTWVSVS 120  
Db 61 PSLSKRVTVSDVTSKNQFSLKLNSTVTAADTAVYVCARDPGQWLVPDAFDIWGQGTWVSVS 120  
  
Qy 121 S 121  
|

```
Db      121 S 121

RESULT 2
US-10-330-530-37
; Sequence 37, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-37

Query Match      100.0%; Score 651; DB 14; Length 121;
Best Local Similarity 100.0%; Pred. No. 2.4e-51;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QVQLQESGPGLVKPSSETLSLTCTVSGGISITYYMSWIRQPPGKGLEWIGYIYTGNTYYN 60
Db      1 QVQLQESGPGLVKPSSETLSLTCTVSGGISITYYMSWIRQPPGKGLEWIGYIYTGNTYYN 60

Qy      61 PSLKSRVTVSVDTSKNQFSLKLSNVTAAADTAVYYCARDPGQWLVPDAFDIWGQGTWVS 120
Db      61 PSLKSRVTVSVDTSKNQFSLKLSNVTAAADTAVYYCARDPGQWLVPDAFDIWGQGTWVS 120

Qy      121 S 121
Db      121 S 121

RESULT 3
US-10-660-357-37
; Sequence 37, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-37

Query Match      100.0%; Score 651; DB 16; Length 121;
Best Local Similarity 100.0%; Pred. No. 2.4e-51;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QVQLQESGPGLVKPSSETLSLTCTVSGGISITYYMSWIRQPPGKGLEWIGYIYTGNTYYN 60
Db      1 QVQLQESGPGLVKPSSETLSLTCTVSGGISITYYMSWIRQPPGKGLEWIGYIYTGNTYYN 60

Qy      61 PSLKSRVTVSVDTSKNQFSLKLSNVTAAADTAVYYCARDPGQWLVPDAFDIWGQGTWVS 120
Db      61 PSLKSRVTVSVDTSKNQFSLKLSNVTAAADTAVYYCARDPGQWLVPDAFDIWGQGTWVS 120

Qy      121 S 121
Db      121 S 121

RESULT 4
US-10-330-613-9
; Sequence 9, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-9

Query Match      91.9%; Score 598; DB 14; Length 121;
Best Local Similarity 90.9%; Pred. No. 1.5e-46;
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy      1 QVQLQESGPGLVKPSSETLSLTCTVSGGISITYYMSWIRQPPGKGLEWIGYIYTGNTYYN 60
Db      1 QVQLQESGPGLVKPSSETLSLTCTVSGGISITYYMSWIRQPPGKGLEWIGYIYTGNTYYN 60

Qy      61 PSLKSRVTVSVDTSKNQFSLKLSNVTAAADTAVYYCARDPGQWLVPDAFDIWGQGTWVS 120
Db      61 PSLKSRVTVSVDTSKNQFSLKLSNVTAAADTAVYYCARDPGQWLVPDAFDIWGQGTWVS 120

Qy      121 S 121
Db      121 S 121

RESULT 5
US-10-330-530-9
; Sequence 9, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-9

Query Match      91.9%; Score 598; DB 14; Length 121;
Best Local Similarity 90.9%; Pred. No. 1.5e-46;
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy      1 QVQLQESGPGLVKPSSETLSLTCTVSGGISITYYMSWIRQPPGKGLEWIGYIYTGNTYYN 60
Db      1 QVQLQESGPGLVKPSSETLSLTCTVSGGISITYYMSWIRQPPGKGLEWIGYIYTGNTYYN 60

Qy      61 PSLKSRVTVSVDTSKNQFSLKLSNVTAAADTAVYYCARDPGQWLVPDAFDIWGQGTWVS 120
Db      61 PSLKSRVTVSVDTSKNQFSLKLSNVTAAADTAVYYCARDPGQWLVPDAFDIWGQGTWVS 120

Qy      121 S 121
Db      121 S 121
```

Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGGTMTVTS 120  
121 S 121  
|  
Db 121 S 121

## RESULT 6

US-10-660-357-9  
; Sequence 9, Application US/10660357  
; Publication No. US20040115205A1  
; GENERAL INFORMATION:  
; APPLICANT: Bar-El, Menashe  
; APPLICANT: Green, Larry L.  
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18  
; FILE REFERENCE: ABGENIX.030C1  
; CURRENT APPLICATION NUMBER: US/10/660,357  
; CURRENT FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 10/330,580  
; PRIOR FILING DATE: 2002-12-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-660-357-9

Query Match 91.9%; Score 598; DB 16; Length 121;  
Best Local Similarity 90.9%; Pred. No. 1.5e-46;  
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISSTYYWSMIROPPGKLEWIGYIYTGNTYNN 60  
|  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISSTYYWSMIROPPGKLEWIGYIYTGNTYNN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDPQGWLVDPDAFDIWGGTMTVSVS 120  
|  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGWLLPDAFDIWGGTMTVTS 120

QY 121 S 121  
|  
Db 121 S 121

## RESULT 7

US-10-330-613-1  
; Sequence 1, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-1

Query Match 91.7%; Score 597; DB 14; Length 121;  
Best Local Similarity 90.9%; Pred. No. 1.9e-46;  
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISSTYYWSMIROPPGKLEWIGYIYTGNTYNN 60  
|  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISSTYYWSMIROPPGKLEWIGYIYTGNTYNN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDPQGWLVDPDAFDIWGGTMTVSVS 120  
|  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120

QY 121 S 121  
|  
Db 121 S 121

## RESULT 8

US-10-330-613-17  
; Sequence 17, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-17

Query Match 91.7%; Score 597; DB 14; Length 121;  
Best Local Similarity 90.9%; Pred. No. 1.9e-46;  
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISSTYYWSMIROPPGKLEWIGYIYTGNTYNN 60  
|  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISSTYYWSMIROPPGKLEWIGYIYTGNTYNN 60

QY 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDPQGWLVDPDAFDIWGGTMTVSVS 120  
|  
Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGWLLPDAFDIWGGTMTVTS 120

QY 121 S 121  
|  
Db 121 S 121

## RESULT 9

US-10-330-530-1  
; Sequence 1, Application US/10330530  
; Publication No. US20030152514A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES  
; FILE REFERENCE: ABGENIX.031A  
; CURRENT APPLICATION NUMBER: US/10/330,530  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: US 60/346414  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-530-1

Query Match 91.7%; Score 597; DB 14; Length 121;  
Best Local Similarity 90.9%; Pred. No. 1.9e-46;  
Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISSTYYWSMIROPPGKLEWIGYIYTGNTYNN 60  
|  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISSTYYWSMIROPPGKLEWIGYIYTGNTYNN 60

Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRPPGKGLEWIGYIYYTWTSNYN 60

QY 61 PSLKSRVTISVDTSKNQFSLKLSNVTAAADVYYCARDPGQWLVPDAFDIWGGQTMVSVS 120

Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADVYYCARDQGWLLPDAFDIWGGQTMVTVS 120

QY 121 S 121

Db 121 S 121

## RESULT 10

US-10-330-530-17

; Sequence 17, Application US/10330530

; Publication No. US20030152514A1

; GENERAL INFORMATION:

; APPLICANT: Gudas, Jean

; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES

; FILE REFERENCE: ABGENIX.031A

; CURRENT APPLICATION NUMBER: US/10/330,530

; CURRENT FILING DATE: 2002-12-26

; PRIOR APPLICATION NUMBER: US 60/346414

; PRIOR FILING DATE: 2001-12-18

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 17

; LENGTH: 121

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-330-530-17

## Query Match

Best Local Similarity 91.7%; Score 597; DB 14; Length 121;

Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRPPGKGLEWIGYIYYTWTSNYN 60

Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRPPGKGLEWIGYIYYTWTSNYN 60

QY 61 PSLKSRVTISVDTSKNQFSLKLSNVTAAADVYYCARDPGQWLVPDAFDIWGGQTMVSVS 120

Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADVYYCARDQGWLLPDAFDIWGGQTMVTVS 120

QY 121 S 121

Db 121 S 121

## RESULT 11

US-10-660-357-1

; Sequence 1, Application US/10660357

; Publication No. US20040115205A1

; GENERAL INFORMATION:

; APPLICANT: Bar-Eli, Menashe

; APPLICANT: Green, Larry L.

; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18

; FILE REFERENCE: ABGENIX.030C1

; CURRENT APPLICATION NUMBER: US/10/660,357

; CURRENT FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 10/330,580

; PRIOR FILING DATE: 2002-12-26

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 121

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-660-357-1

## Query Match

Best Local Similarity 91.7%; Score 597; DB 16; Length 121;

Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRPPGKGLEWIGYIYYTWTSNYN 60

Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRPPGKGLEWIGYIYYTWTSNYN 60

QY 61 PSLKSRVTISVDTSKNQFSLKLSNVTAAADVYYCARDPGQWLVPDAFDIWGGQTMVSVS 120

Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADVYYCARDQGWLLPDAFDIWGGQTMVTVS 120

QY 121 S 121

Db 121 S 121

## RESULT 12

US-10-660-357-17

; Sequence 17, Application US/10660357

; Publication No. US20040115205A1

; GENERAL INFORMATION:

; APPLICANT: Bar-Eli, Menashe

; APPLICANT: Green, Larry L.

; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18

; FILE REFERENCE: ABGENIX.030C1

; CURRENT APPLICATION NUMBER: US/10/660,357

; CURRENT FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 10/330,580

; PRIOR FILING DATE: 2002-12-26

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 17

; LENGTH: 121

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-660-357-17

## Query Match

Best Local Similarity 91.7%; Score 597; DB 16; Length 121;

Matches 110; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRPPGKGLEWIGYIYYTWTSNYN 60

Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRPPGKGLEWIGYIYYTWTSNYN 60

QY 61 PSLKSRVTISVDTSKNQFSLKLSNVTAAADVYYCARDPGQWLVPDAFDIWGGQTMVSVS 120

Db 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADVYYCARDQGWLLPDAFDIWGGQTMVTVS 120

QY 121 S 121

Db 121 S 121

## RESULT 13

US-10-309-762-11

; Sequence 11, Application US/10309762

; Publication No. US20040018198A1

; GENERAL INFORMATION:

; APPLICANT: Gudas, Jean

; APPLICANT: Foltz, Ian

; APPLICANT: Handa, Masahisa

; APPLICANT: Gallo, Michael

; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX

; FILE REFERENCE: ABGENIX.027A

; CURRENT APPLICATION NUMBER: US/10/309,762

; CURRENT FILING DATE: 2002-12-02

; PRIOR APPLICATION NUMBER: 60/337275

; PRIOR FILING DATE: 2001-12-03

; NUMBER OF SEQ ID NOS: 246

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 11

; LENGTH: 125



(1234) 5678 9012 3456

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OM protein - protein search, using sw model

Run on: November 9, 2005, 12:25:58 ; Search time 13.0401 Seconds  
(without alignments)  
892.802 Million cell updates/sec

Title: US-10-660-357A-37

Perfect score: 651

Sequence: 1 QVQLQESGPGLVKPSSETLSL.....WLVPDAFDIWGQGTWVSVS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	537	82.5	140	2 I37782	Ig variable region
2	536	82.3	155	2 S31512	Ig heavy chain - h
3	531	81.6	155	2 S31511	Ig heavy chain - h
4	527	81.0	130	2 S31690	Ig heavy chain v r
5	524	80.5	147	2 S13519	Ig heavy chain v r
6	522.5	80.3	139	2 S31586	Ig heavy chain v r
7	517	79.4	135	2 S78051	Ig heavy chain pre
8	515.5	79.2	118	2 S20780	Ig heavy chain v r
9	512.5	78.7	130	2 S30534	Ig heavy chain v r
10	507.5	78.0	137	2 S31676	Ig heavy chain v r
11	498	76.5	121	2 S44113	Ig heavy chain v r
12	497	76.3	105	2 S44125	Ig lambda chain v
13	492.5	75.7	140	2 S78052	Ig heavy chain pre
14	489	75.1	97	2 S26906	Ig heavy chain v r
15	488	75.0	116	2 B26340	Ig heavy chain pre
16	488	75.0	123	2 S30530	Ig heavy chain v r
17	486	74.7	97	2 S12416	Ig heavy chain v r
18	485	74.5	146	2 S09711	Ig heavy chain v r
19	484	74.3	99	2 S26802	Ig heavy chain v r
20	484	74.3	99	2 S26803	Ig heavy chain v r
21	483.5	74.3	110	2 S44110	Ig heavy chain v r
22	483	74.2	139	2 S31696	Ig heavy chain v-D
23	483	74.2	140	2 A49045	Ig heavy chain v r
24	477.5	73.3	129	2 S44114	Ig heavy chain v r
25	477	73.0	118	2 A26340	Ig heavy chain pre
26	475	73.0	99	2 S26801	Ig heavy chain v r
27	475	73.0	146	2 S09710	Ig heavy chain v r
28	471	72.4	99	2 S12418	Ig heavy chain v r
29	470.5	72.3	126	2 S47010	Ig heavy chain V4.

30	469.5	72.1	118	2 S24443	Ig heavy chain v r
31	469	72.0	135	2 S31604	Ig heavy chain v r
32	469	72.0	140	2 A24770	hypothetical hybri
33	468.5	72.0	145	2 S78055	Ig heavy chain pre
34	468	71.9	97	2 PH0876	Ig heavy chain v r
35	468	71.9	143	2 B49028	Ig heavy chain v r
36	466	71.6	220	2 A49444	Ig gamma-1 heavy c
37	465	71.4	99	2 S12412	Ig heavy chain v r
38	462	71.0	99	2 S26800	Ig heavy chain v r
39	462	71.0	124	2 S31684	Ig heavy chain v r
40	462	71.0	129	1 D2HUMA	Ig heavy chain v r
41	461.5	70.9	137	2 S31585	Ig heavy chain v r
42	461	70.8	97	2 S26804	Ig heavy chain v r
43	461	70.8	116	2 S18557	Ig heavy chain v r
44	460.5	70.7	98	2 S12421	Ig heavy chain v r
45	460	70.7	116	2 S37456	Ig mu chain - huma

ALIGNMENTS

RESULT 1

I37782

Ig variable region (VDJ) (clone T23-9) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999

C;Accession: I37782; S25476

R;Demaïson, C.; Chastagner, P.; Theze, J.; Zouali, M.

Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994

A;Title: Somatic diversification in the heavy chain variable region genes expressed by

A;Reference number: A36876; MUID:94119917; PMID:8290556

A;Accession: I37782

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-140 <RES>

A;Cross-references: EMBL:X67906; NID:G33582; PIDN:CAA48104.1; PID:G33583

C;Superfamily: immunoglobulin v region; immunoglobulin homology

F;46-128/Domain: immunoglobulin homology <IMW>

Query Match 82.5%; Score 537; DB 2; Length 140;  
Best Local Similarity 84.3%; Pred. No. 1.le-40;  
Matches 102; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSSETLSLCTVSGSISTYVWSWIRQPPGKLEWIGYIYTGNTYNN 60

Db 20 QVQLQESGPGLVKPSSETLSLCTVSGSISTYVWSWIRQPPGKLEWIGYIYTGNTYNN 79

Qy 61 PSLKSRVTYSDTSKNQFSLKLSNVTAAADTAVYVCARDPGQWLVPDAFDIWGQGTWVSVS 120

Db 80 PSLKSRVTISVDTSKNQFSLKLSNVTAAADTAVYVCARDHNSSSWVGRYFDYWGQGTLTVTS 139

Qy 121 \$ 121

Db 140 \$ 140

RESULT 2

S31512

Ig heavy chain - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999

C;Accession: S31512

R;Chastagner, P.; Demaïson, C.; Theze, J.; Zouali, M.

Submitted to the EMBL Data Library, December 1992

A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA au

A;Reference number: S31509

A;Accession: S31512

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-155 <CHA>

A;Cross-references: EMBL:X69860; NID:G33082; PIDN:CAA49494.1; PID:G33083

C;Superfamily: immunoglobulin v region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;47-129/Domain: immunoglobulin homology <IMM>

Query Match 82.3%; Score 536; DB 2; Length 155;  
Best Local Similarity 82.1%; Pred. No. 1.5e-40;  
Matches 101; Conservative 8; Mismatches 12; Indels 2; Gaps 1;

QY 1 OVQLOESGPGLVKPESETLSLTCTVSGSISTYYWMIROPPGKLEWIGYIYTGNTY 60  
DB 33 OVQLOESGPGLVKPESETLSLTCTVSGSISTYYWMIROPPGKLEWIGYIYTGNTY 92

QY 61 PSLKSRVTVSVDTSKNQFSLKNSVTAADTAVYVCARDPG--QWLVPDAFDIWGQGTWVS 118  
DB 93 PPIKSRVTISVDTSKNQFSLKNSVTAADTAVYVCARGGSISSWYDYGNDVWGQGTVT 152

QY 119 VSS 121  
DB 153 VSS 155

#### RESULT 3

S31511  
Ig heavy chain - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S31511  
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto-  
A;Reference number: S31509  
A;Accession: S31511  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-155 <CHA>  
A;Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID:g33095  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;47-129/Domain: immunoglobulin homology <IMM>

Query Match 81.6%; Score 531; DB 2; Length 155;  
Best Local Similarity 82.1%; Pred. No. 4.2e-40;  
Matches 101; Conservative 7; Mismatches 13; Indels 2; Gaps 1;

QY 1 OVQLOESGPGLVKPESETLSLTCTVSGSISTYYWMIROPPGKLEWIGYIYTGNTY 60  
DB 33 OVQLOESGPGLVKPESETLSLTCTVSGSISTYYWMIROPPGKLEWIGYIYTGNTY 92

QY 61 PSLKSRVTVSVDTSKNQFSLKNSVTAADTAVYVCARDPG--QWLVPDAFDIWGQGTWVS 118  
DB 93 PPIKSRVTISVDTSKNQFSLKNSVTAADTAVYVCARGGSISSWYDYGNDVWGQGTVT 152

QY 119 VSS 121  
DB 153 VSS 155

#### RESULT 4

S31690  
Ig heavy chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S31690  
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.  
submitted to the EMBL Data Library, June 1992  
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A;Reference number: S31585  
A;Accession: S31690  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-130 <CUI>  
A;Cross-references: EMBL:Z14199; NID:g30984; PIDN:CAA78568.1; PID:g30985  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;20-102/Domain: immunoglobulin homology <IMM>

Query Match 81.0%; Score 527; DB 2; Length 130;  
Best Local Similarity 81.1%; Pred. No. 7.8e-40;  
Matches 103; Conservative 8; Mismatches 8; Indels 8; Gaps 2;

QY 1 OVQLOESGPGLVKPESETLSLTCTVSGSISTYYWMIROPPGKLEWIGYIYTGNTY 60  
DB 6 OVQLOESGPGLVKPESETLSLTCTVSGSISTYYWMIROPPGKLEWIGYIYTGNTY 65

QY 61 PSLKSRVTVSVDTSKNQFSLKNSVTAADTAVYVCARDP-----QWLVPDAFDIWGQGTWVS 114  
DB 66 PSLKSRVTISVDTSKNQFSLKNSVTAADTAVYVCARGSSVLLMFGLLY--YFDYWGQGTWVS 123

QY 115 TMVSVSS 121  
DB 124 TLVTVSS 130

#### RESULT 5

S31519  
Ig heavy chain V region precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S31519  
R;Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.  
Nucleic Acids Res. 19, 673, 1991  
A;Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked  
A;Reference number: S31519; MUID:91187691; PMID:2011536  
A;Accession: S31519  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-147 <MOR>  
A;Cross-references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;41-125/Domain: immunoglobulin homology <IMM>

Query Match 80.5%; Score 524; DB 2; Length 147;  
Best Local Similarity 82.9%; Pred. No. 1.6e-39;  
Matches 102; Conservative 9; Mismatches 8; Indels 4; Gaps 3;

QY 1 OVQLOESGPGLVKPESETLSLTCTVSGSI--STYYWMIROPPGKLEWIGYIYTGNTY 58  
DB 27 QLQLOESGPGLVKPESETLSLTCTVSGSISSSSYWMIROPPGKLEWIGISYISGTY 86

QY 59 YNPGLSRVTVSVDTSKNQFSLKNSVTAADTAVYVCARDPGQWLVPDAFDIWGQGTWVS 118  
DB 87 YNPGLSRVTISVDTSKNQFSLKNSVTAADTAVYVCAR-PLLWP-GELFDYWGQGTWVT 144

QY 119 VSS 121  
DB 145 VSS 147

#### RESULT 6

S31586  
Ig heavy chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S31586  
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.  
submitted to the EMBL Data Library, June 1992  
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A;Reference number: S31585  
A;Accession: S31586  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-139 <CUI>  
A;Cross-references: EMBL:Z14196; NID:g30978; PIDN:CAA78565.1; PID:g30979  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;34-116/Domain: immunoglobulin homology <IMM>



```
Query Match      80.3%; Score 522.5; DB 2; Length 139;
Best Local Similarity 85.1%; Pred. No. 2.1e-39;
Matches 103; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYIYWSWIRQPPGKLEWIGIYYTGTNTY 60
Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGSISYIYWSWIRQPPGKLEWIGIYYTGTNTY 79

QY 61 PSLKSRVTVSVDTSKNQFSLKNSVTAADTAVYYCARDPGQWLVPDAFDIWGGQTMVSVS 120
Db 80 PSLKSRVTMSVDTSKNQFSLKLSVTAADTAVYYCARG-GLGIRRGAFDIWGGQTMVTVS 138

QY 121 S 121
Db 139 S 139

RESULT 7
S78051
Ig heavy chain precursor V-D-J region (clone mAB 61VH) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78051; S23716
R;Harindranath, N.
submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78051
A;Molecule type: mRNA
A;Residues: 1-135 <HAR>
A;Cross-references: EMBL:X54437; NID:G37814; PIDN:CAA38306.1; PID:G930117
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.B.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.
A;Reference number: S23716; MUID:92031262; PMID:1718404
A;Accession: S23716
A;Molecule type: mRNA
A;Residues: 13-111 <HAW>
A;Cross-references: EMBL:X54437
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-13/Domain: signal sequence (fragment) #status predicted <SIG>
F;14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;27-111/Domain: immunoglobulin homology <IMM>

Query Match      79.4%; Score 517; DB 2; Length 135;
Best Local Similarity 80.6%; Pred. No. 6.2e-39;
Matches 100; Conservative 11; Mismatches 9; Indels 4; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSIS- -TYYSWIRQPPGKLEWIGIYYTGTNTY 58
Db 13 QVQLQESGPGLVKPSSETLSLTCTVSGSISRGSHYWGIRQPPGKLEWIGIYYTGTNTY 72

QY 59 YNPSSLKSRVTVSVDTSKNQFSLKNSVTAADTAVYYCAR-DPGQWLVPDAFDIWGGQTMV 117
Db 73 FNPSSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARLGPDDYTL-DGMDVWGQGTIV 131

QY 118 SVSS 121
Db 132 TVSS 135

RESULT 8
S20780
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S20780
R;Wortari, F.; Wang, J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A;Description: Analysis of human cord blood Ig heavy chain IgA and IgG repertoire.
A;Reference number: S20764
A;Accession: S20780
A;Molecule type: mRNA
```

```
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-118 <WOR>
A;Cross-references: EMBL:Z11958; NID:G33893; PIDN:CAA78015.1; PID:G33894
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match      79.2%; Score 515.5; DB 2; Length 118;
Best Local Similarity 82.6%; Pred. No. 7.3e-39;
Matches 100; Conservative 8; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYIYWSWIRQPPGKLEWIGIYYTGTNTY 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISGHYWSWIRQPPGKLEWIAFIRYTGSTHYN 60

QY 61 PSLKSRVTVSVDTSKNQFSLKNSVTAADTAVYYCARDPGQWLVPDAFDIWGGQTMVSVS 120
Db 61 PSLKSRVTMSVDTSKNQFSLKMTSVTAADTAVYSCARDGR- -DGGFDIWGGQTMVTVS 117

QY 121 S 121
Db 118 S 118

RESULT 9
S30534
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C;Accession: S30534
R;Mariette, X.
submitted to the EMBL Data Library, October 1992
A;Reference number: S30520
A;Accession: S30534
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <MAR>
A;Cross-references: EMBL:Z18320
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match      78.7%; Score 512.5; DB 2; Length 130;
Best Local Similarity 80.0%; Pred. No. 1.5e-38;
Matches 104; Conservative 7; Mismatches 10; Indels 9; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSIS- -TYYSWIRQPPGKLEWIGIYYTGTNTY 58
Db 1 QVQLQESGPGLVKPSQTLSLTCTVSGSISSGSYWSWIRQPPGKLEWIGIRIYTSSTN 60

QY 59 YNPSSLKSRVTVSVDTSKNQFSLKNSVTAADTAVYYCARDPGQ-WL- - - - -VPDAPDIW 111
Db 61 YNPSSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARDKGGFWSGYVTRNSRAAPDIW 120

QY 112 GQGTWVSVS 121
Db 121 GQGTWTVSVS 130

RESULT 10
S31676
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31676
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31676
A;Status: preliminary
A;Molecule type: mRNA
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A;Residues: 1-137 <GUI>  
A;Cross-references: EMBL:Z14182; NID:g31031; PIDN:CAA78551.1; PID:g31032  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-116/Domain: immunoglobulin homology <IMM>  
  
Query Match 78.0%; Score 507.5; DB 2; Length 137;  
Best Local Similarity 82.0%; Pred. No. 4.4e-38; Mismatches 9; Indels 5; Gaps 2;  
Matches 100; Conservative 8;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIYSTYYWIRQPPGKGLWIGIYYTGTNTY 60  
Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSIYSTYYWIRQPPGKGLWIGIYYTGTNTY 79  
QY 61 PSLKSRVTVSVDTSKNQFSLKNSVTAADTAVYYCARD-PGQWLVPDAPFDINGQGTMTVS 119  
Db 80 PSLKSRVTMTSVDTSKNQFSLKLSVTAADTAVYYCARDAPLMY----GMDVMVGQGTITTV 135  
QY 120 SS 121  
Db 136 SS 137  
  
RESULT 11  
S44113  
Ig heavy chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
C;Accession: S44113  
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
submitted to the EMBL Data Library, March 1994  
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable  
A;Reference number: S44105  
A;Accession: S44113  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-121 <HAW>  
A;Cross-references: EMBL:Z31389; NID:g472967; PIDN:CAA83264.1; PID:g940524  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-99/Domain: immunoglobulin homology <IMM>  
  
Query Match 76.5%; Score 498; DB 2; Length 121;  
Best Local Similarity 78.9%; Pred. No. 2.6e-37; Mismatches 9; Indels 4; Gaps 2;  
Matches 97; Conservative 9;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGG--SISTYYWIRQPPGKGLWIGIYYTGTNTY 58  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGYISSSSYWGWTRQPPGKGLWIGIYYSGSY 60  
QY 59 YNPSLKSRVTVSVDTSKNQFSLKNSVTAADTAVYYCARDPPGQWLVPDAPFDINGQGTMTVS 118  
Db 61 YNPSLKSRVTLSVDTSKNQFSLKLSVTAADTGVYCSRLSGGY--SDFDYMSQGTITVT 118  
QY 119 VSS 121  
Db 119 VSS 121  
  
RESULT 12  
S44125  
Ig lambda chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
C;Accession: S44125  
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
submitted to the EMBL Data Library, March 1994  
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable  
A;Reference number: S44105  
A;Accession: S44125  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-105 <HAW>

A;Cross-references: EMBL:Z31383; NID:g472978; PIDN:CAA83258.1; PID:g940535  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-97/Domain: immunoglobulin homology <IMM>  
  
Query Match 76.3%; Score 497; DB 2; Length 105;  
Best Local Similarity 92.9%; Pred. No. 2.8e-37; Mismatches 6; Indels 0; Gaps 0;  
Matches 92; Conservative 6;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIYSTYYWIRQPPGKGLWIGIYYTGTNTY 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIYSTYYWIRQPPGKGLWIGIYYTGTNTY 60  
QY 61 PSLKSRVTVSVDTSKNQFSLKNSVTAADTAVYYCARDP 99  
Db 61 PSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARNP 99  
  
RESULT 13  
S78052  
Ig heavy chain precursor V-D-J region (clone mAB 63VH) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 19-Nov-1997 #sequence\_revision 05-Dec-1997 #text\_change 23-Jul-1999  
C;Accession: S78052; S23717  
R;Harindranath, N.  
submitted to the EMBL Data Library, August 1990  
A;Reference number: S78051  
A;Accession: S78052  
A;Molecule type: mRNA  
A;Residues: 1-140 <HAR>  
A;Cross-references: EMBL:X54441; NID:g37815; PIDN:CAA38308.1; PID:g930118  
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin  
Int. Immunol. 3, 865-875, 1991  
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and  
patient.  
A;Reference number: S23716; MUID:92031262; PMID:1718404  
A;Accession: S23717  
A;Molecule type: mRNA  
A;Residues: 15-111 <HAW>  
A;Cross-references: EMBL:X54441  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;1-14/Domain: signal sequence (fragment) #status predicted <SIG>  
F;15-140/Product: Ig heavy chain (fragment) #status predicted <MAT>  
F;29-111/Domain: immunoglobulin homology <IMM>  
  
Query Match 75.7%; Score 492.5; DB 2; Length 140;  
Best Local Similarity 75.4%; Pred. No. 9.5e-37; Mismatches 11; Indels 5; Gaps 1;  
Matches 95; Conservative 11;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIYSTYYWIRQPPGKGLWIGIYYTGTNTY 60  
Db 15 QVQLQOQGAGLLKPSSETLSLTCAVYGSFSGYYWIRQPPGKGLWIGIYHSGSTNY 74  
QY 61 PSLKSRVTVSVDTSKNQFSLKNSVTAADTAVYYCARDPG----QWLVPDAPFDINGQGT 115  
Db 75 PSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGSVLRFLEWLLYPADYWGQGT 134  
QY 116 MVSVSS 121  
Db 135 LVTVSS 140  
  
RESULT 14  
S26906  
Ig heavy chain V region (DP-71 / VH 4.11 / 4.15) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S26906; S09421; S12415  
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of  
A;Reference number: S26885; MUID:93021117; PMID:1404388

Search completed: November 9, 2005, 13:08:05  
Job time : 13.0401 secs

A;Accession: S26906  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-97 <TOM>  
A;Cross-references: EMBL:Z12371; NID:g32962; PIDN:CAA78241.1; PID:g32963  
A;Note: designated DP-71  
R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.  
EMBO J. 8, 3741-3748, 1989  
A;Title: The smaller human V(H) gene families display remarkably little polymorphism.  
A;Reference number: S09421; MUID:90059975; PMID:2511001  
A;Accession: S09421  
A;Status: preliminary; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-97 <SAN>  
A;Cross-references: EMBL:X56355  
A;Note: designated 4.11  
A;Accession: S12415  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-97 <SA2>  
A;Cross-references: EMBL:X56359  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 75.1%; Score 489; DB 2; Length 97;  
Best Local Similarity 93.8%; Pred. No. 1.3e-36;  
Matches 91; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIISTYYWSWIRQPPGKGLEWIGYIYTGNTYYN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIISTYYWSWIRQPPGKGLEWIGYIYTGNTYYN 60

QY 61 PSLKSRVTYSVDTSKNQFSLKLSNVTAAADTAVYYCAR 97  
Db 61 PSLKSRVTISVDTSKNQFSLKLSNVTAAADTAVYYCAR 97

RESULT 15  
B26340  
Ig heavy chain precursor V-II region (71-4) - human  
C;Species: Homo sapiens (man)  
C;Date: 05-Jun-1988 #sequence\_revision 30-Jun-1991 #text\_change 23-Jul-1999  
C;Accession: B26340  
R;Kodaira, M.; Kinashi, T.; Umemura, I.; Matsuda, F.; Noma, T.; Ono, Y.; Honjo, T.  
J. Mol. Biol. 190, 529-541, 1986  
A;Title: Organization and evolution of variable region genes of the human immunoglobulin  
A;Reference number: A26340; MUID:87061007; PMID:3097326  
A;Accession: B26340  
A;Molecule type: DNA  
A;Residues: 1-116 <KOD>  
A;Cross-references: GB:X05711; NID:g33602; PIDN:CAA29183.1; PID:g296660  
A;Note: the authors translated the codon GAG for residue 25 as Gln  
C;Genetics:  
A;Introns: 16/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-116/Product: Ig heavy chain V region 71-4 #status predicted <MAT>  
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 488; DB 2; Length 116;  
Best Local Similarity 92.8%; Pred. No. 1.9e-36;  
Matches 90; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIISTYYWSWIRQPPGKGLEWIGYIYTGNTYYN 60  
Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSIISTYYWSWIRQPPGKGLEWIGYIYTGNTYYN 79

QY 61 PSLKSRVTYSVDTSKNQFSLKLSNVTAAADTAVYYCAR 97  
Db 80 PSLKSRVTISVDTSKNQFSLKLSNVTAAADTAVYYCAR 116

(11/10/10) 11/10/10

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 11:46:52 ; Search time 62.4712 Seconds  
(without alignments)  
991.843 Million cell updates/sec

Title: US-10-660-357A-37

Perfect score: 651

Sequence: 1 QVQLQESGPGLVKPSSETLSL.....WLVPDAFDWVGQTMVSVS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	538	82.6	476	2	Q6GMX1
2	513	78.8	119	2	Q9UL73
3	505.5	77.6	478	2	Q7Z379
4	504.5	77.5	465	2	Q6GMX6
5	503.5	77.3	620	2	Q96EY0
6	502.5	77.2	477	2	Q6GMX7
7	495	76.0	139	2	Q86SX2
8	487	74.8	492	2	Q7Z374
9	485.5	74.6	150	2	Q95973
10	474.5	72.9	496	2	Q96KX8
11	465.5	71.5	576	2	Q6P418
12	462	71.0	129	1	HV2F HUMAN
13	452	69.4	478	2	Q6NYH3
14	449.5	69.0	146	1	HV2I HUMAN
15	448	68.8	595	2	Q8WUX4
16	448	68.8	597	2	Q6GMX5
17	448	68.8	597	2	Q9BU10
18	448	68.8	625	2	Q96AA6
19	444	68.2	597	2	Q9BQB8
20	441.5	67.8	130	2	Q81ZD7
21	431	66.2	117	1	HV2G HUMAN
22	420.5	64.6	116	2	Q7Z3Y6
23	418.5	64.3	473	2	Q8TC63
24	406	62.4	479	2	Q99W22
25	402	61.8	476	2	Q6MZX7
26	401.5	61.7	122	2	Q9UL75
27	397.5	61.1	136	2	Q6LBQ5
28	396	60.8	137	1	HV46_MOUSE
29	392	60.2	262	2	Q65Z11
30	391	60.1	113	1	HV47_MOUSE
31	370.5	56.9	116	1	P18532

32 369.5 56.8 116 1 HV60\_MOUSE  
33 369.5 56.8 482 2 Q91X92  
34 365 56.2 117 1 HV62\_MOUSE  
35 360.5 55.4 121 2 Q99NG4  
36 353 54.2 144 1 HV43\_MOUSE  
37 350.5 53.8 135 1 HV02\_XENLA  
38 343.5 52.8 118 2 Q811U5  
39 343.5 52.8 613 2 Q8WUK1  
40 342 52.5 470 2 Q6PJA4  
41 339 52.1 118 2 Q9UL74  
42 339 52.1 466 2 Q6IN78  
43 333 51.2 240 2 Q65ZC9  
44 331.5 50.9 118 2 Q9UL91  
45 331 50.8 121 2 Q9UL96

P18531 mus musculus  
Q91X92 mus musculus  
P18533 mus musculus  
Q99NG4 mus musculus  
P01819 mus musculus  
P20957 xenopus lae  
Q811U5 mus musculus  
Q8WUK1 homo sapien  
Q6PJA4 homo sapien  
Q9UL74 homo sapien  
Q6IN78 homo sapien  
Q65ZC9 homo sapien  
Q9UL91 homo sapien  
Q9UL96 homo sapien

#### ALIGNMENTS

RESULT 1  
Q6GMX1 PRELIMINARY; PRT; 476 AA.  
ID Q6GMX1  
AC Q6GMX1;  
DT 05-JUL-2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
ON NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McQuellano N.A., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Strausberg R.;  
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073773; AAH73773.1; -;  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF07654; Cl-set; 3.  
DR Pfam; PF00047; IG; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.

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KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABAS62DD9D CRC64;

Query Match      82.6%; Score 538; DB 2; Length 476;
Best Local Similarity 81.2%; Pred. No. 7.5e-45;
Matches 104; Conservative 10; Mismatches 6; Indels 8; Gaps 3;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIST--YYWSWIRQPPGKLEWIGYIYYTGNTY 58
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLQESGPGLVKPSQTSLSLTCTVSGGSISGGYYWSWIRQPPGKLEWIGYIYSGSTY 79
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 59 YNPSSLSRVTVSVDTSKNQFSKLNSVTAADTAVYVCARDPGQW-----LVPADFQWGO 113
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 YNPSSLSRVTVSVDTSKNQFSKLNSVTAADTAVYFCAR-AGVWGFRSVAIDGFNIWGO 138
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 114 GTWVSVSS 121
    |||||:|||||
Db 139 GTWVTVSS 146
    |||||:|||||

RESULT 2
Q9UL73 PRELIMINARY; PRT; 119 AA.
AC Q9UL73;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RC MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
  Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035041; AAD56277.1; -.
DR PIR; PH0876; PH0876.
DR PIR; S12416; S12416.
DR HSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;

Query Match      78.8%; Score 513; DB 2; Length 119;
Best Local Similarity 81.8%; Pred. No. 5e-43;
Matches 99; Conservative 8; Mismatches 12; Indels 2; Gaps 2;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISTYYWSWIRQPPGKLEWIGYIYYTGNTY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISCSYWSWIRQPPGKLEWIGYIYSGSTNYT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 PSLKSRVTVSVDTSKNQFSKLNSVTAADTAVYVCARDPGQWLVDPADFQWGOQTVSVS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 PSLKSRVTVSVDTSKNQFSKLNSVTAADTAVYFCAR-LSNW-GPYFYFDWGOQTLTVS 118
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 121 S 121
    |||||:|||||
Db 119 S 119
    |||||:|||||

RESULT 3
Q72379 PRELIMINARY; PRT; 478 AA.
ID Q72379
```

```
AC Q72379;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686K04218 (Fragment).
GN Name=DKFZp686K04218;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloecker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
  Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538066; CAD97996.1; -.
DR HSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;

Query Match      77.6%; Score 505.5; DB 2; Length 478;
Best Local Similarity 76.4%; Pred. No. 1.2e-41;
Matches 94; Conservative 18; Mismatches 6; Indels 5; Gaps 2;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIST--YYWSWIRQPPGKLEWIGYIYYTGNTY 58
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 19 QVQLQESGPGLVKPSQTSLSLTCTVSGGSISGGDYFWSWIRQPPGKLEWIGYIYSGSTY 78
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 59 YNPSSLSRVTVSVDTSKNQFSKLNSVTAADTAVYVCARDPGQWLVDPADFQWGOQTVS 118
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 79 YNPSSLSRLSISIDTSKNQFSKLNSLTAADTAVYFCARGVG--LGTAFDIWGOQTVTVT 135
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 119 VSS 121
    |||||
Db 136 VSS 138
    |||||

RESULT 4
Q6GMX6 PRELIMINARY; PRT; 465 AA.
ID Q6GMX6;
AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
  Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
  Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
```

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,  
 RA Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073766; AAH73766.1; -;  
 DR InterPro; IPR003599; Ig-like.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR Pfam; PF00047; Ig; 4.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein  
 SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FD8B1386E CRC64;

Query Match 77.5%; Score 504.5; DB 2; Length 465;  
 Best Local Similarity 82.6%; Pred. No. 1.5e-41;  
 Matches 100; Conservative 8; Mismatches 8; Indels 5; Gaps 2;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIITYYWSWIRQPPGKLEWIGYIYTGNTYYN 60  
 Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSIITYYWSWIRQPPGKLEWIGYIYTGNTYYN 79  
 Qy 61 PSLSKRVTVSDTSKNQFSLKLSVTAADTAATVAVYCARDPGQWLVPDADFIMGOGTWSVS 120  
 Db 80 PSLSKRVTVSDTSKNQFSLKLSVTAADTAATVAVYCARDPGQWLVPDADFIMGOGTWSVS 134  
 Qy 121 S 121  
 Db 135 S 135

RESULT 5  
 Q96EYO ID Q96EYO PRELIMINARY; PRT; 620 AA.  
 AC Q96EYO;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE IGHM protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,  
 RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC011857; AAH11857.2; -;  
 DR PIR; S15590; S15590.  
 DR HSP; P01820; IG7J.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 4.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 4.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
 KW Hypothetical protein  
 SQ SEQUENCE 620 AA; 68125 MW; 990A1A4A6E8FF27B CRC64;

Query Match 77.3%; Score 503.5; DB 2; Length 620;  
 Best Local Similarity 81.1%; Pred. No. 2.6e-41;  
 Matches 99; Conservative 8; Mismatches 12; Indels 3; Gaps 2;

Qy 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIITYYWSWIRQPPGKLEWIGYIYTGNTYYN 60  
 Db 27 QVQLQESGPGLVKPSSETLSLTCTVSGGSIITYYWSWIRQPPGKLEWIGYIYTGNTYYN 86  
 Qy 61 PSLSKRVTVSDTSKNQFSLKLSVTAADTAATVAVYCARDPGQWLVPDADFIMGOGTWSVS 119  
 Db 87 PSLSKRVTVSDTSKNQFSLKLSVTAADTAATVAVYCARDPGQWLVPDADFIMGOGTWSVS 144  
 Qy 120 S 121  
 Db 145 S 146

RESULT 6  
 Q6GMX7 ID Q6GMX7 PRELIMINARY; PRT; 477 AA.  
 AC Q6GMX7;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,  
 RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

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RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smillus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RC Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC073765; AAH73765.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig.cl.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF07654; C1-set; 2.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00409; IG; 4.
DR SMART: SM00407; IGC1; 3.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS0835; IG LIKE; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CF85 CRC64;

Query Match 77.2%; Score 502.5; DB 2; Length 477;
Best Local Similarity 81.0%; Pred. No. 2.5e-41;
Matches 98; Conservative 9; Mismatches 11; Indels 3; Gaps 2;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISTYVSWIRQPPGKLEWIGIYYTGTNTY 60
DB 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISTYVSWIRQPPGKLEWIGIYSHGTTYN 79

QY 61 PSLKSRVTVSVDTSKNQFSLKNSVTAADTAVYYCARDPQQLVPDAFDIWGGTVMVSVS 120
DB 80 PSLKSRVTLSLDTSKNQFSLRLNSVTAADTAVYYCAHG-SSW--DFAFDIWGGTTLTVTS 136

QY 121 S 121
DB 137 S 137

RESULT 7
Q86SX2 PRELIMINARY; PRT; 139 AA.
AC Q86SX2; 2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Full-length cDNA clone CS0DL004YM19 of B cells (Ramos cell line) of
DE Homo sapiens (human) (Fragment).
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=B cells;
RC Li W.B., Gruber C., Jessee J., Polayes D.;
RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=B cells;
RC Genoscope;
RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.

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DR EMBL: BX248300; CAD62627.1; -.
DR HSSP: P01820; 1G7J.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;

Query Match 76.0%; Score 495; DB 2; Length 139;
Best Local Similarity 93.9%; Pred. No. 3.6e-41;
Matches 92; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISTYVSWIRQPPGKLEWIGIYYTGTNTY 60
DB 33 QVQLQESGPGLVKPSSETLSLTCTVSGGSISTYVSWIRQPPGKLEWIGIYVSGSTNY 92

QY 61 PSLKSRVTVSVDTSKNQFSLKNSVTAADTAVYYCARD 98
DB 93 PSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARD 130

RESULT 8
Q7Z374 PRELIMINARY; PRT; 492 AA.
AC Q7Z374;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686C02218 (Fragment).
GN Name=DKFZp686C02218;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Human rectum tumor;
RC Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wienann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BX538077; CAD98001.1; -.
DR HSSP: P01820; 1G7J.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig.cl.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF07654; C1-set; 2.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;

Query Match 74.8%; Score 487; DB 2; Length 492;
Best Local Similarity 75.4%; Pred. No. 8.8e-40;
Matches 95; Conservative 8; Mismatches 13; Indels 10; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIS--TYVSWIRQPPGKLEWIGIYYTGTNTY 58
DB 32 QVQLQESGPGLVKPSSETLSLTCTVSGGSISNRNYWGIRQPPGKLEWIGISYYNTY 91

QY 59 YNPFLSKSRVTVSVDTSKNQFSLKNSVTAADTAVYYCAR---DPGQWLVPDAFDIWGGT 115
DB 92 YSPFLSKSRVTIFVDTSKNHFSLRLTSVTAADTAVYYCVRHVEGPGYGW-----FDPWGGT 146

QY 116 MVSVS 121
DB 147 LVTVS 152

RESULT 9

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O95973
ID O95973 PRELIMINARY; PRT; 150 AA.
AC O95973;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE V44 heavy chain variable region precursor (fragment).
GN Name=IGM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Suh C.-H., Song C.-H., Lee S.-K.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RE EMBL: AF103795; AAC79084.1; -
DR PIR: S31673; S31673.
DR HSP: S78056; S78056.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig cl.
DR InterPro: IPR003596; Ig v.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
KW Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 >150 V44 heavy chain variable region.
FT NON_TER 150 150
SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;

Query Match 74.6%; Score 485.5; DB 2; Length 150;
Best Local Similarity 77.2%; Pred. No. 3.4e-40;
Matches 95; Conservative 11; Mismatches 10; Indels 7; Gaps 2;

QY 1 QVQLQESGGPGLVKPSETLSLTCTVSGGSI--YYWVSWIRPPKGLWIGIYYTQNTY 58
Db 20 QIQQLQESGGPGLVKPSETLSLTCTVSGGSISSSYWVWIRPPKGLWIGIYYTQNTY 79
QY 59 YNPGLKSRVTVSDTSKNQPSLKNVTAADTAVYVCARDPGQWLVPDADFINGQGTMS 118
Db 80 YNPGLKSRVTVSDTSKNQPSLKNVTAADTAVYVCARDPGQWLVPDADFINGQGTMS 134
QY 119 VSS 121
Db 135 VSS 137

RESULT 10
Q96KX8
ID Q96KX8 PRELIMINARY; PRT; 496 AA.
AC Q96KX8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC27165 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Klausner R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RE EMBL: BC016369; AAH16369.1; -
DR HSP: P01876; IOW0.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig cl.
DR InterPro: IPR003006; Ig MHC.
DR InterPro: IPR003596; Ig v.
DR Pfam: PF07654; Cl-set; 2.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;

Query Match 72.9%; Score 474.5; DB 2; Length 496;
Best Local Similarity 74.8%; Pred. No. 1.5e-38;
Matches 95; Conservative 9; Mismatches 14; Indels 9; Gaps 3;

QY 1 QVQLQESGGPGLVKPSETLSLTCTVSGGSI--STVYVSWIRPPKGLWIGIYYTQNTY 58
Db 20 QIQQLQESGGPGLVKPSETLSLTCTVSGGSISSSYWVWIRPPKGLWIGIYYTQNTY 79
QY 59 YNPGLKSRVTVSDTSKNQPSLKNVTAADTAVYVCARDPGQWLVPDADFINGQGTMS 114
Db 80 YNPGLKSRVTVSDTSKNQPSLKNVTAADTAVYVCARDPGQWLVPDADFINGQGTMS 136
QY 115 TVSVSS 121
Db 137 TVTVSS 143

RESULT 11
Q6P4I8
ID Q6P4I8 PRELIMINARY; PRT; 576 AA.
AC Q6P4I8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHD protein.
GN Names=IGHD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

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DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 2.  
 DR SMART; SM00409; IG; 4.  
 DR SMART; SM00407; IGC1; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS0835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 478 AA; 51856 MW; 5F8B98F60F077256 CRC64;

Query Match 69.4%; Score 452; DB 2; Length 478;  
 Best Local Similarity 71.1%; Pred. No. 2.5e-36;  
 Matches 86; Conservative 16; Mismatches 17; Indels 2; Gaps 1;

Qy 1 QVQLQESGPGLVKPESETLSLTCTVSGSGISITSYWYWSWIRQPPGKGLEWIGIYYTGTNYN 60  
 Db 20 QVDLQESGPGLVKPESETLSLTCTVSGSDSIASYWYWSWIRKSPQGMWIGIYFHSGLTYN 79  
 Qy 61 PSLKSRVTVSDTSKNQFSLKNSVTAADTAATVAVYCARDPGQWLVPDADFIMWQGTWVS 120  
 Db 80 PSLKSRVTVSDTSKNQFSLKNSVTAADTAATVAVYCARDPGQWLVPDADFIMWQGTWVS 137  
 Qy 121 S 121  
 Db 138 S 138

RESULT 14  
 HV21 HUMAN STANDARD; PRT; 146 AA.  
 AC P06331;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V-II region ARH-77 precursor.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85205332; PubMed=3922855; DOI=10.1016/0378-1119(85)90092-7;  
 RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;  
 RT "A cloned human immunoglobulin heavy chain gene with a novel direct-repeat sequence in 5' flanking region.";  
 RL Gene 33:181-189(1985).  
 DR PIR; A02101; G1HUH2.  
 DR HSP; P01825; 7FAB.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; P:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS0835; IG LIKE; 1.  
 KW Immunoglobulin v region; Signal.

FT SIGNAL 1 19  
 FT CHAIN 20 146 Ig heavy chain V-II region ARH-77.  
 FT DOMAIN 20 117 V segment.  
 FT DOMAIN 118 127 D segment.  
 FT DOMAIN 128 146 J segment.  
 FT DISULFID 42 115 By similarity.  
 FT NON TER 146 146  
 SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52B218171F CRC64;

Query Match 69.0%; Score 449.5; DB 1; Length 146;  
 Best Local Similarity 71.4%; Pred. No. 1.2e-36;  
 Matches 90; Conservative 11; Mismatches 20; Indels 5; Gaps 2;

Qy 1 QVQLQESGPGLVKPESETLSLTCTVSGSGISITSYWYWSWIRQPPGKGLEWIGIYYTGTNYN 60

Db 21 QVQLQWAGLVKPESETLSLTCAVFGSGFSGYWYWSWIRQPPGKLEWIGIYHSGSTNYK 80  
 Qy 61 PSLKSRVTVSDTSKNQFSLKNSVTAADTAATVAVYCARD--PGQWLVPDAP---DIWQGT 115  
 Db 81 TSLKSRVTISLDTSKNLSLGLSVTAADTAATVAVYCARDLRLGGWVDVYYGMVDWQGT 140  
 Qy 116 MVSVSS 121  
 Db 141 TVTVSS 146

RESULT 15  
 Q8WUX4

ID Q8WUX4 PRELIMINARY; PRT; 595 AA.  
 AC Q8WUX4;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
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 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RA Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC019235; AAH19235.2; -.  
 DR PIR; G34964; G34964.  
 DR HSP; P01861; IADQ.  
 DR Pfam; PF07654; C1-set; 4.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGC1; 4.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS0835; IG LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 595 AA; 65290 MW; 0D4B50776545714E CRC64;

Query Match 68.8%; Score 448; DB 2; Length 595;  
 Best Local Similarity 70.5%; Pred. No. 7.9e-36;  
 Matches 91; Conservative 9; Mismatches 17; Indels 12; Gaps 3;

Qy 1 QVQLQESGPGLVKPESETLSLTCTVSGSGISITSYWYWSWIRQPPGKLEWIGIYYTGTNYN 60  
 Db 27 QVQLQWAGLVKPESETLSLTCTVSGSGISITSYWYWSWIRQPPGKLEWIGIYHSGSTNYN 86

Qy 61 PSLKSRVTVSVDTSKNQFSIKLNSVTAADTAVVYCAR-----DPGQWLVPD---AFDIWG 112  
Db 87 PSLKSRVTIISVDTSKKQLSLKSSVNAADTAVVYCARVITRASP-----TDGRYGMVWG 142  
Qy 113 QGTWVSYS 121  
Db 143 QGTTTVSS 151

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